

```

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP 1-6
RA Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by DKFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 6 BP: 0 A; 2 C; 2 G; 0 T; 2 other;
Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 5 G 5
RESULT 30
LOCUS BE726686 6 bp mRNA linear EST 14-SEP-2000
DEFINITION 894095D11.Y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
ACCESSION BE726686
VERSION BE726686.1 GI:10128110
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 6)
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
Mcdermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Vascular Plants: Project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
source
1..6
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap

```

```

II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
Mcdermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in YAP (acetate-containing) medium in the
light, YAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT
ORIGIN
0 a 1 c 5 g 0 t

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```

RESULT 31
LOCUS BE726686 6 bp mRNA linear EST 14-SEP-2000
DEFINITION 894095D11.Y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
ACCESSION BE726686
VERSION BE726686.1 GI:10128110
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 6)
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
Mcdermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Vascular Plants: Project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
source
1..6
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap

```

```

/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
Mcdermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in YAP (acetate-containing) medium in the
light, YAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

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BASE COUNT 0 a 1 c 5 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 6:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 G 2

RESULT 32

BC897546 standard; RNA; EST; 7 BP.

AC BC897546;
SV BC897546.1
XX

DT 09-JUN-2001 (Rel. 68, Created)
DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA
DE sequence.

DE EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX

XX MEDLINE: 21482651.

RX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
RT Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
RT Identification and initial characterization of 5000 expressed sequenced
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
RT libraries*;
RL Osteoarthritic Cartilage 9(7):641-653(2001).

XX

CC Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
CC Tel: 610-270-7245
CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com
CC Seq primer: T7.

XX

XX Key Location/Qualifiers

XX source

FT 1..7 /db_xref="taxon:9606"

FT /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
FT Directional"

FT /organism="Homo sapiens"

FT /clone_lib="HOA (Human Osteoarthritic Cartilage)"

FT /tissue_type="Cartilage"

FT /lab_host="E.coli DH10 B"

XX

SO Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

OY 1 g 1
1

Query Match 100.0%; Score 1; DB 2; Length 7:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 G 6

RESULT 33

BC897546/C
ID BC897546 standard; RNA; EST; 7 BP.

XX BC897546;
XX

SV BC897546.1
XX

DT 09-JUN-2001 (Rel. 68, Created)
DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA
DE sequence.

DE EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX

XX MEDLINE: 21482651.

RX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
RT Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
RT Identification and initial characterization of 5000 expressed sequenced
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
RT libraries*;
RL Osteoarthritic Cartilage 9(7):641-653(2001).

XX

XX Contact: Sanjay Kumar

XX UW2109

CC GlaxoSmithKline
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
CC Tel: 610-270-7245
CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com
CC Seq primer: T7.

XX

XX Key Location/Qualifiers

XX source

FT 1..7 /db_xref="taxon:9606"

FT /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
FT Directional"

FT /organism="Homo sapiens"

FT /clone_lib="HOA (Human Osteoarthritic Cartilage)"

FT /tissue_type="Cartilage"

FT /lab_host="E.coli DH10 B"

XX

SO Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

OY 1 g 1
1

Query Match 100.0%; Score 1; DB 2; Length 7:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 G 7

RESULT 34

HSMD007412
ID HSM007412 standard; RNA; EST; 7 BP.

XX AL042562;
XX

SV AL042562.1

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XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA: EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
DE EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
DB 2 G 2

RESULT 35
HSM007412/c
ID HSM007412 standard; RNA; EST: 7 BP.
XX
AC AL042562;
XX
SV AL042562.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA: EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
XX EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL

```

```

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
DB 1 G 1

RESULT 36
HSM007502
ID HSM007502 standard; RNA; EST: 7 BP.
XX
AC AL042652;
XX
SV AL042652.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA: EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
XX EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434N1921"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"

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FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
DB      2 G 2

RESULT 37
HSM007502/c standard; RNA; EST; 7 BP.
XX
AC      AL042652;
XX
SV      AL042652.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN      [1]
RP      1-7
RA      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
CC      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key
FH      Location/Qualifiers
FT      source
FT      1..7
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434N1921"
FT      DH10B; sites NotI + SalI
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
DB      1 G 1

RESULT 38
CS8888

LOCUS      CS8888
DEFINITION      C58888 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
ACCESSION      C58888
VERSION      C58888
KEYWORDS      EST.
SOURCE      EST.
ORGANISM      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
1 (bases 1 to 7)
REFERENCE      Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano
AUTHORS      'M., Miyata, A. and Nishiyaki, A.
TITLE      Expression map of the C. elegans genome
JOURNAL      Unpublished (1996)
COMMENT      Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1..7
Location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="C1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="YK383a7"
/clone_id="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT      2 a 0 c 1 g 3 t 1 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 1; DB 10; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
DB      7 G 7

RESULT 39
HSM001420/c standard; RNA; EST; 8 BP.
XX
AC      AL037095;
XX
SV      AL037095.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp564L2064_r1 (from clone DKFZp564L2064)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN      [1]
RP      1-8
RA      Duysterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
CC      Clone from S. Wiemann, sequenced by Qiagen within the CDNA
CC      sequencing consortium of the German Genome Project

```



```

CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT
FT 1.8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp564L071"
FT /clone_11b="564 (synonym: hfbz2). Vector pAMP1; host
FT x1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX
SQ Sequence 8 BP: 2 A; 3 C; 0 G; 3 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 7 G 7

RESULT 40
HSM001743/c standard; RNA; EST; 8 BP.
XX
AC AL037413:
XX
SV AL037413.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp564L071_s1 (from clone DKFZp564L071)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX
RN [1]
RP 1-8
RA Blocker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by GBF within the CDNA
CC sequencing consortium of the German Genome Project
CC No r1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT
FT source
FT 1.8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp564L071"
FT /clone_11b="564 (synonym: hfbz2). Vector pAMP1; host
FT x1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX
SQ Sequence 8 BP: 1 A; 7 C; 0 G; 0 T; 0 other;

```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 7 G 7

RESULT 41
HSM004451 standard; RNA; EST; 8 BP.
XX
AC AL039975:
XX
SV AL039975.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX
RN [1]
RP 1-8
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT
FT source
FT 1.8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434K0712"
FT /clone_11b="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 8 BP: 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 G 1

RESULT 42
HSM004451/c standard; RNA; EST; 8 BP.
XX
AC AL039975:
XX

```

```

SV      AL039975.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
DE
XX      EST: expressed sequence tag.
XX
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      (1)
RN      1-8
RA      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by Olagen within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key
FH      Location/Qualifiers
FH      source
FH      1..8
FH      /db_xref="taxon:9606"
FH      /organism="Homo sapiens"
FH      /clone="DKFZp434K0712"
FH      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FH      DH10B; sites NotI + SalI"
FH      /dev_stage="adult"
FH      /tissue_type="testis"
XX
XX      Sequence 8 BP; 2 A; 2 G; 2 T; 0 other:
SO
Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 g 1
Db      8 C 8

```

```

RESULT 43
HSM007277
ID      HSM007277 standard; RNA; EST; 8 BP.
AC
XX      AL042427;
SV
XX      AL042427.1
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
DE
XX      EST: expressed sequence tag.
XX
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      (1)
RN      1-8
RA      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key
FH      Location/Qualifiers
FH      source
FH      1..8
FH      /db_xref="taxon:9606"
FH      /organism="Homo sapiens"
FH      /clone="DKFZp434C2421"
FH      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FH      DH10B; sites NotI + SalI"
FH      /dev_stage="adult"
FH      /tissue_type="testis"
XX
XX      Sequence 8 BP; 2 A; 2 G; 2 T; 0 other:
SO
Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 g 1
Db      1 G 1

```

```

RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key
FH      Location/Qualifiers
FH      source
FH      1..8
FH      /db_xref="taxon:9606"
FH      /organism="Homo sapiens"
FH      /clone="DKFZp434C2421"
FH      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FH      DH10B; sites NotI + SalI"
FH      /dev_stage="adult"
FH      /tissue_type="testis"
XX
XX      Sequence 8 BP; 2 A; 2 G; 2 T; 0 other:
SO
Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 g 1
Db      1 G 1

```

FT DH10B: sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX

SQ Sequence 8 BP: 2 A: 2 C: 2 G: 2 T: 0 other:

Query Match Best Local Similarity 100.0%; Score 1: DB 2: Length 8:

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1
 DB 8 C 8

RESULT 45

HSM007323

ID HSM007323 standard; RNA; EST; 8 BP.

AC AL042473:

SV AL042473.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFP434F0121_r1 (from clone DKFP434F0121)

XX EST; expressed sequence tag.

KW Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.

XX

RN

RP

1-8

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC No s1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

FT

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FT

Search completed: July 15, 2002, 20:07:36
 Job time: 14494 sec

SQ Sequence 8 BP: 2 A: 2 C: 2 G: 2 T: 0 other:

Query Match

Best Local Similarity 100.0%; Score 1: DB 2: Length 8:

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1
 DB 1 C 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:57:00 ; Search time 808.35 Seconds

(without alignments)
2.105 Million cell updates/sec

Title: US-09-375-248-1_COPY_3141_3141

Sequence: 1 g 1

Scoring table:

Gapco 60.0, Gapext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Pending Patents, NA, New: *
1: /cgn2_6/prodata/2/pna/PC7_NEW_COMB.seq: *
2: /cgn2_6/prodata/2/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/prodata/2/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/prodata/2/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/prodata/2/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq: *
7: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	1	100.0	2	6	US-10-027-632-51869
C 2	1	100.0	2	6	US-10-027-632-52280
C 3	1	100.0	2	6	US-10-027-632-52357
C 4	1	100.0	2	6	US-10-027-632-53003
C 5	1	100.0	2	6	US-10-027-632-58305
6	1	100.0	2	6	US-10-027-632-175312
7	1	100.0	2	6	US-10-027-632-175312
8	1	100.0	2	6	US-10-027-632-175312
9	1	100.0	2	6	US-10-027-632-175312
10	1	100.0	2	6	US-10-027-632-175312
11	1	100.0	2	6	US-10-027-632-175403
12	1	100.0	2	6	US-10-027-632-175415
13	1	100.0	2	6	US-10-027-632-175419
14	1	100.0	2	6	US-10-027-632-175426
15	1	100.0	2	6	US-10-027-632-175433
16	1	100.0	2	6	US-10-027-632-175849
17	1	100.0	2	6	US-10-027-632-175849
18	1	100.0	2	6	US-10-027-632-175849
19	1	100.0	2	6	US-10-027-632-175880
20	1	100.0	2	6	US-10-027-632-178420
21	1	100.0	2	6	US-10-027-632-178440
22	1	100.0	2	6	US-10-027-632-178440
23	1	100.0	2	6	US-10-027-632-178617
24	1	100.0	2	6	US-10-027-632-178617
25	1	100.0	3	1	PC7-US02-00351-20
26	1	100.0	3	6	US-10-027-632-52136
			3	6	US-10-027-632-52402

C 27	1	100.0	3	6	US-10-027-632-52403	Sequence 52403, A
C 28	1	100.0	3	6	US-10-027-632-52404	Sequence 52404, A
C 29	1	100.0	3	6	US-10-027-632-52410	Sequence 52410, A
C 30	1	100.0	3	6	US-10-027-632-52417	Sequence 52417, A
C 31	1	100.0	3	6	US-10-027-632-52418	Sequence 52418, A
C 32	1	100.0	3	6	US-10-027-632-52419	Sequence 52419, A
C 33	1	100.0	3	6	US-10-027-632-52425	Sequence 52425, A
C 34	1	100.0	3	6	US-10-027-632-52495	Sequence 52495, A
C 35	1	100.0	3	6	US-10-027-632-52495	Sequence 52495, A
C 36	1	100.0	3	6	US-10-027-632-52496	Sequence 52496, A
C 37	1	100.0	3	6	US-10-027-632-52508	Sequence 52508, A
C 38	1	100.0	3	6	US-10-027-632-52512	Sequence 52512, A
C 39	1	100.0	3	6	US-10-027-632-52513	Sequence 52513, A
C 40	1	100.0	3	6	US-10-027-632-52615	Sequence 52615, A
C 41	1	100.0	3	6	US-10-027-632-52633	Sequence 52633, A
C 42	1	100.0	3	6	US-10-027-632-52651	Sequence 52651, A
C 43	1	100.0	3	6	US-10-027-632-52753	Sequence 52753, A
C 44	1	100.0	3	6	US-10-027-632-52758	Sequence 52758, A
C 45	1	100.0	3	6	US-10-027-632-52761	Sequence 52761, A

ALIGNMENTS

```

RESULT 1
US-10-027-632-51869/c
; Sequence 51869, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 51869
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51869

Query Match
Best Local Similarity 100.0%: Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 G 2

RESULT 2
US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome

```

```
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218.006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198.676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193.483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185.218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167.363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156.358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146.002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52280
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52280
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 2 g 2
```

```
RESULT 3
US-10-027-632-52357/c
Sequence 52357, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218.006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198.676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193.483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185.218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167.363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156.358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146.002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52357
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52357
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
```

```
Db 2 g 2
RESULT 4
US-10-027-632-53003/c
Sequence 53003, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218.006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198.676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193.483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185.218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167.363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156.358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146.002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53003
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-53003
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 2 g 2
```

```
RESULT 5
US-10-027-632-58305/c
Sequence 58305, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218.006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198.676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193.483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185.218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167.363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156.358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146.002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58305
```

LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-58305

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 6
US-10-027-632-175312
Sequence 175312, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 175312
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-175312

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 7
US-10-027-632-175337
Sequence 175337, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 175337
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-175337

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 8
US-10-027-632-175354
Sequence 175354, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 175354
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-175354

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 9
US-10-027-632-175401
Sequence 175401, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.

```

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
Db      1 g 1
```

```
RESULT 10
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
Db      1 g 1
```

```
RESULT 11
US-10-027-632-175415
; Sequence 175415, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175415
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
Db      1 g 1
```

```
RESULT 12
US-10-027-632-175419
; Sequence 175419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
```



```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175419
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1

RESULT 13
US-10-027-632-175426
; Sequence 175426, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1

RESULT 14
US-10-027-632-175433
; Sequence 175433, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
```

```
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175433
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1

RESULT 15
US-10-027-632-175849
; Sequence 175849, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175849
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1

RESULT 16
US-10-027-632-176848
; Sequence 176848, Application US/10027632
```

```

: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176848
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176848
```

```

Query Match      100.0%: Score 1: DB 6: Length 2:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 g 1
   |
Db 1 g 1

RESULT 17
US-10-027-632-176849
: Sequence 176849, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176849
```

Query Match 100.0%: Score 1: DB 6: Length 2:

```

Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 g 1
   |
Db 1 g 1
```

```

RESULT 18
US-10-027-632-176880
: Sequence 176880, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176880
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176880
```

```

Query Match      100.0%: Score 1: DB 6: Length 2:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 g 1
   |
Db 1 g 1

RESULT 19
US-10-027-632-178420
: Sequence 178420, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
```

```

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178420
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178420
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
   |
Db 1 g 1
```

```

RESULT 20
US-10-027-632-178440
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
   |
Db 1 g 1
```

```

RESULT 21
US-10-027-632-178440/c
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```

; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
   |
Db 2 g 2
```

```

RESULT 22
US-10-027-632-178617
; Sequence 178617, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178617
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
   |
Db 2 g 2
```

RESULT 23

```
US-10-027-632-178640
; Sequence 178640, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178640
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 2 g 2
```

```
RESULT 24
PCT-US02-00351-20/c
; Sequence 20, Application PC/TUS0200351
; GENERAL INFORMATION:
; APPLICANT: Chet, Ian
; APPLICANT: Viterbo, Ada
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING
; FILE REFERENCE: 02/23682
; CURRENT APPLICATION NUMBER: PCT/US02/00351
; CURRENT FILING DATE: 2002-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: motif found in the URSS of both ech42 and prb1 genes
PCT-US02-00351-20
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 3 g 3
```

RESULT 25

```
US-10-027-632-52136
; Sequence 52136, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52136
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52136
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 3 g 3
```

```
RESULT 26
US-10-027-632-52402/c
; Sequence 52402, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52402
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52402
```

```
Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
    |
Db 2 G 2
```

```
RESULT 27
US-10-027-632-52403/c
; Sequence 52403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52403
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52403
```

```
Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
    |
Db 2 G 2
```

```
RESULT 28
US-10-027-632-52404/c
; Sequence 52404, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52404
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52404
```

```
Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
    |
Db 2 G 2
```

```
RESULT 29
US-10-027-632-52410/c
; Sequence 52410, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52410
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52410
```

```
Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
    |
Db 3 G 3
```

```
RESULT 30
US-10-027-632-52417/c
; Sequence 52417, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
```

```
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 52417
;; LENGTH: 3
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-52417
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 2 G 2
```

```
RESULT 31
US-10-027-632-52418/c
; Sequence 52418, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52418
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52418
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 2 G 2
```

```
RESULT 32
US-10-027-632-52419/c
; Sequence 52419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52419
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52419
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 2 G 2
```

```
RESULT 33
US-10-027-632-52425/c
; Sequence 52425, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52425
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
```

US-10-027-632-52425

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
DB 3 g 3

RESULT 34

US-10-027-632-52491
; Sequence 52491, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 52491
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52491

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
DB 2 g 2

RESULT 35

US-10-027-632-52495/C
; Sequence 52495, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 52495

; LENGTH: 3

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-52495

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
DB 3 g 3

RESULT 36

US-10-027-632-52496
; Sequence 52496, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 52496
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52496

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
DB 2 g 2

RESULT 37

US-10-027-632-52508
; Sequence 52508, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

```

; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52508
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52508
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 2 g 2
```

```

RESULT 38
US-10-027-632-52512/c
; Sequence 52512, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52512
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52512
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 2 g 2
```

```

Db 3 G 3
```

```

RESULT 39
US-10-027-632-52513
; Sequence 52513, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52513
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52513
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 2 g 2
```

```

RESULT 40
US-10-027-632-52615
; Sequence 52615, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52615
; LENGTH: 3
```


TYPE: DNA
ORGANISM: Human
US-10-027-632-52615

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 g 2

RESULT 41
US-10-027-632-52633

Sequence 52633, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52633
LENGTH: 3
TYPE: DNA
ORGANISM: Human
US-10-027-632-52633

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 g 2

RESULT 42
US-10-027-632-52651

Sequence 52651, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52651
LENGTH: 3
TYPE: DNA
ORGANISM: Human
US-10-027-632-52651

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 g 2

RESULT 43
US-10-027-632-52753

Sequence 52753, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52753
LENGTH: 3
TYPE: DNA
ORGANISM: Human
US-10-027-632-52753

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 g 2

RESULT 44

US-10-027-632-52758/c
Sequence 52758, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52758
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52758

```

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
        |
Db       1 G 1

```

```

RESULT 45
US-10-027-632-52761
; Sequence 52761, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52761
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52761

```

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
        |
Db       1 G 1

```

Search completed: July 16, 2002, 02:57:00
Job time: 24558 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:26 ; Search time 12941.8 Seconds

(without alignments)
1.672 Million cell updates/sec

Title: US-09-375-248-1_COPY_3141_3141

Perfect score: 1 g 1

Sequence: 1 g 1

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 21979536 seqs, 10817449327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

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SUMMARIES			
Result No.	Score	% Query Match	Description
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2	100.0	2	US-08-107-721-46
3	100.0	2	US-08-107-721B-46
4	100.0	2	US-09-172-828-15
5	100.0	2	US-09-387-777-7
6	100.0	2	US-09-387-777-8
7	100.0	2	US-09-387-777-9
8	100.0	2	US-09-387-777-10
9	100.0	2	US-09-387-777-11
10	100.0	2	US-09-387-777-12
11	100.0	2	US-09-387-777-13
12	100.0	2	US-09-387-777-14
13	100.0	2	US-09-387-777-15
14	100.0	2	US-09-387-777-16
15	100.0	2	US-09-387-777-17
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19	100.0	2	US-09-387-777-21
20	100.0	2	US-09-387-777-22
21	100.0	2	US-09-387-777-23
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37	100.0	2	US-09-387-777-39
38	100.0	2	US-09-387-777-40
39	100.0	2	US-09-387-777-41
40	100.0	2	US-09-387-777-42
41	100.0	2	US-09-387-777-43
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46	100.0	2	US-09-387-777-48
47	100.0	2	US-09-387-777-49
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50	100.0	2	US-09-387-777-52
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52	100.0	2	US-09-387-777-54
53	100.0	2	US-09-387-777-55
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64	100.0	2	US-09-387-777-66
65	100.0	2	US-09-387-777-67
66	100.0	2	US-09-387-777-68
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68	100.0	2	US-09-387-777-70
69	100.0	2	US-09-387-777-71
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73	100.0	2	US-09-387-777-75
74	100.0	2	US-09-387-777-76
75	100.0	2	US-09-387-777-77

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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33 1 100.0 2 24 US-09-634-306B-175403 Sequence 175403,
34 1 100.0 2 24 US-09-634-306B-175415 Sequence 175415,
35 1 100.0 2 24 US-09-634-306B-175419 Sequence 175419,
36 1 100.0 2 24 US-09-634-306B-175426 Sequence 175426,
37 1 100.0 2 24 US-09-634-306B-175433 Sequence 175433,
38 1 100.0 2 24 US-09-634-306B-175449 Sequence 175449,
39 1 100.0 2 24 US-09-634-306B-176848 Sequence 176848,
40 1 100.0 2 24 US-09-634-306B-176849 Sequence 176849,
41 1 100.0 2 24 US-09-634-306B-176880 Sequence 176880,
42 1 100.0 2 24 US-09-634-306B-178420 Sequence 178420,
43 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440,
44 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440,
45 1 100.0 2 24 US-09-634-306B-178617 Sequence 178617,

ALIGNMENTS

RESULT 1
US-07-934-385-14
; Sequence 14, Application US/07934385
; GENERAL INFORMATION:
; APPLICANT: LATHAM, JOHN
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES
; TITLE OF INVENTION: CONTAINING MODIFIED NUCLEOTIDE RESIDUES
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,385
; FILING DATE: 19920821
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 24610-20022.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1, "")
; OTHER INFORMATION: /note="This position is a
; OTHER INFORMATION: biotin-17 nucleotide stretch of random sequences."
US-07-934-385-14

Query Match
Best Local Similarity 100.0%; Score 1; DB 3; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 g 2

RESULT 2
US-08-107-721-46
; Sequence 46, Application US/08107721
; GENERAL INFORMATION:
; APPLICANT: TOOLE, JOHN J.
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: BOCK, LOUIS C.
; APPLICANT: LATHAM, JOHN A.
; APPLICANT: MUENCHAU, DARYL D.
; APPLICANT: KRAMCZYK, STEVEN
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: GILEAD SCIENCES, INC.
; STREET: 344 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,721
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28216
; REFERENCE/DOCKET NUMBER: 24610-20022.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)574-3000
; TELEFAX: (415)578-9264
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note="This is a biotin-17
; OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-107-721-46

Query Match
Best Local Similarity 100.0%; Score 1; DB 5; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 g 2

RESULT 3
US-08-107-721B-46
; Sequence 46, Application US/08107721B
; GENERAL INFORMATION:
; APPLICANT: TOOLE, JOHN J.
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: BOCK, LOUIS C.
; APPLICANT: LATHAM, JOHN A.
; APPLICANT: MUENCHAU, DARYL D.
; APPLICANT: KRAMCZYK, STEVEN
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING

NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: GILEAD SCIENCES, INC.
STREET: 344 LAKE SIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,721B
FILING DATE: 20-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28216
REFERENCE/DOCKET NUMBER: 24610-20022.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)574-3000
TELEFAX: (415)578-9264
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "this is a biotin-17
US-08-107-721B-46
nucleotide stretch of abasic residues."

Query Match 100.0%; Score 1; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 2 G 2

RESULT 4
US-09-172-828-15
Sequence 15, Application US/09172828
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
APPLICANT: Klagsbrun, Michael
APPLICANT: Elenius, Klaus
APPLICANT: Corfas, Gabriel
TITLE OF INVENTION: Novel Human EGF Receptors and Use
FILE REFERENCE: 47758-PCT
CURRENT APPLICATION NUMBER: US/09/172,828
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 2
TYPE: DNA
ORGANISM: mouse
US-09-172-828-15

Query Match 100.0%; Score 1; DB 15; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 5
US-09-284-725-201/c
Sequence 201, Application US/09284725
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
APPLICANT: Van Doorn, Leendert
TITLE OF INVENTION: Probes, methods and kits for detection and
TITLE OF INVENTION: typing of Helicobacter pylori nucleic acids in biological
NUMBER OF SEQUENCES: 280
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/284,725
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP96/870131.8
FILING DATE: 16-OCT-1996
APPLICATION NUMBER: PCT/EP97/05614
FILING DATE: 10-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: INNOG2.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 760-0404
TELEFAX: (949) 760-9395
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-284-725-201

Query Match 100.0%; Score 1; DB 16; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 2 G 2

RESULT 6
US-09-306-333A-32
Sequence 32, Application US/09306333A
GENERAL INFORMATION:
APPLICANT: Academy of Applied Science
TITLE OF INVENTION: BRCAl and hMLH1 Gene Primer Sequences and Method for
TITLE OF INVENTION: Testing
FILE REFERENCE: BRCAl
CURRENT APPLICATION NUMBER: US/09/306,333A
CURRENT FILING DATE: 1999-05-06

PRIOR APPLICATION NUMBER: PCT/IB00/01607
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 2
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-333A-32

Query Match
Best Local Similarity 100.0%; Score 1; DB 17; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 7
US-09-306-333A-32/c
Sequence 32, Application US/09306333A
GENERAL INFORMATION:
APPLICANT: Academy of Applied Science
TITLE OF INVENTION: BRCA1 and hMLH1 Gene Primer Sequences and Method for
FILE REFERENCE: BRCA1
CURRENT APPLICATION NUMBER: US/09/306,333A
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: PCT/IB00/01607
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 2
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-333A-32

Query Match
Best Local Similarity 100.0%; Score 1; DB 17; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 8
US-09-387-777-2/c
Sequence 2, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-8907X
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
to an ASCII file

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-2

Query Match
Best Local Similarity 100.0%; Score 1; DB 17; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 9
US-09-387-777-3
Sequence 3, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-8907X
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-3

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 10
US-09-387-777-5/c
Sequence 5, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-5

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 G 1

RESULT 11

US-09-387-777-6/c
Sequence 6, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-6

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 12
US-09-387-777-7
Sequence 7, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk


```

: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-387-777-7

Query Match          100.0%; Score 1: DB 17; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 g 2

RESULT 13
US-09-387-777-7/C
: Sequence 7, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedmam c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
```

```

: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-387-777-7
```

```

Query Match          100.0%; Score 1: DB 17; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 14
US-09-387-777-8/C
: Sequence 8, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedmam c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-387-777-8
```

```

Query Match          100.0%; Score 1: DB 17; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
```

Db 1 G 1

RESULT 15

US-09-387-777-9

Sequence 9, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: to an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-387-777-9

Query Match

Best Local Similarity 100.0%; Score 1; DB 17; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 1 G 1

RESULT 16

US-09-387-777-10

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington

STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: to an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-387-777-10

Query Match

Best Local Similarity 100.0%; Score 1; DB 17; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 1 G 1

RESULT 17

US-09-387-777-10/c

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: to an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-10

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 18
US-09-387-777-11
Sequence 11, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: to an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-11

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 G 1

RESULT 19
US-09-387-777-12
Sequence 12, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: to an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-12

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 G 1

RESULT 20
US-09-387-777-14/C
Sequence 14, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-14
Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 2 g 2
RESULT 21
US-09-387-777-15
Sequence 15, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-15
Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 2 g 2
RESULT 22
US-09-472-035A-19
Sequence 19, Application US/09472035A
GENERAL INFORMATION:
APPLICANT: Yechezkel Kashi et al.
TITLE OF INVENTION: ABUNDANT, WELL-DISTRIBUTED AND
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472,035A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 74/77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-472-035A-19

Query Match
Best Local Similarity 100.0%; Score 1; DB 18; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
db 1 g 1

RESULT 23
US-09-472-035A-20/C
Sequence 20: Application US/09472035A
GENERAL INFORMATION:
APPLICANT: Yechezkel Kasht et al.
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
NUMBER OF SEQUENCES: PROKARYOTE CLASSIFICATION AND TYPING
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-8907X
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472.035A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 74/77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-472-035A-20

Query Match
Best Local Similarity 100.0%; Score 1; DB 18; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
db 2 g 2
RESULT 24

US-09-634-306B-51869/C
Sequence 51869, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51869
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-51869

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
db 2 g 2

RESULT 25
US-09-634-306B-52280/C
Sequence 52280, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52280
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-52280

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      2 g 2
```

```
RESULT 26
US-09-634-306B-52357/c
; Sequence 52357, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52357
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52357
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      2 g 2
```

```
RESULT 27
US-09-634-306B-53003/c
; Sequence 53003, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53003
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-53003
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      2 g 2
```

```
RESULT 28
US-09-634-306B-58305/c
; Sequence 58305, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58305
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58305
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      1 g 1
```

```
RESULT 29
US-09-634-306B-175312
; Sequence 175312, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
```

```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175312
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Oy 1 g 1
Db 1 g 1
```

```

RESULT 30
US-09-634-306B-175337
; Sequence 175337, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175337
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Oy 1 g 1
Db 1 g 1
```

```

RESULT 31
US-09-634-306B-175354
; Sequence 175354, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175354
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Oy 1 g 1
Db 1 g 1
```

```

RESULT 32
US-09-634-306B-175401
; Sequence 175401, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
```

US-09-634-306B-175401

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 33
US-09-634-306B-175403

Sequence 175403, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 175403
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-175403

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 34
US-09-634-306B-175415

Sequence 175415, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 175415

LENGTH: 2

TYPE: DNA

ORGANISM: Human

US-09-634-306B-175415

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 35
US-09-634-306B-175419

Sequence 175419, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 175419
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-175419

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 36
US-09-634-306B-175426

Sequence 175426, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129


```

; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175426
```

```

Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 g 1
      |
Db      1 g 1
```

```

RESULT 37
US-09-634-306B-175433
; Sequence 175433, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175433
```

```

Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 g 1
      |
```

```

Db      1 g 1
```

```

RESULT 38
US-09-634-306B-175849
; Sequence 175849, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175849
```

```

Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 g 1
      |
Db      1 g 1
```

```

RESULT 39
US-09-634-306B-176848
; Sequence 176848, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176848
; LENGTH: 2
```

TYPE: DNA
ORGANISM: Human
US-09-634-306B-176848

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 40
US-09-634-306B-176849
Sequence 176849, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176849
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-176849

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 41
US-09-634-306B-176880
Sequence 176880, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176880
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-176880

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 42
US-09-634-306B-178420
Sequence 178420, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 178420
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-178420

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 43
US-09-634-306B-178440
Sequence 178440, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178440
```

```

Query Match          100.0%: Score 1; DB 24; Length 2:
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 44
US-09-634-306B-178440/C
; Sequence 178440, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178440
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Query Match          100.0%: Score 1; DB 24; Length 2:
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 g 1
Db 2 g 2
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RESULT 45
US-09-634-306B-178617
; Sequence 178617, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178617
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Query Match          100.0%: Score 1; DB 24; Length 2:
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 g 1
Db 2 g 2
```

Search completed: July 16, 2002, 02:50:26
Job time: 31279 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:38 ; Search time 223.79 Seconds
(without alignments)
1.098 Million cell updates/sec

Title: US-09-375-248-1-COPY_3141_3141

Sequence score: 1 9 1

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: Issued_Patents_NA:*
2: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*
3: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	100.0	1	2	US-08-268-679B-8	Sequence 8, Appl1
2	100.0	1	2	US-08-484-192-16	Sequence 16, Appl1
3	100.0	2	4	US-08-361-024-3	Sequence 3, Appl1
4	100.0	2	4	US-08-361-024-3	Sequence 3, Appl1
5	100.0	3	1	US-07-791-213D-46	Sequence 46, Appl1
6	100.0	3	1	US-07-791-213D-46	Sequence 46, Appl1
7	100.0	3	1	US-07-791-213D-46	Sequence 62, Appl1
8	100.0	3	1	US-07-791-213D-62	Sequence 62, Appl1
9	100.0	3	1	US-08-268-679B-7	Sequence 7, Appl1
10	100.0	3	1	US-08-602-036A-2	Sequence 2, Appl1
11	100.0	3	1	US-08-602-036A-2	Sequence 2, Appl1
12	100.0	3	1	US-08-293-150A-46	Sequence 46, Appl1
13	100.0	3	1	US-08-293-150A-46	Sequence 46, Appl1
14	100.0	3	1	US-08-293-150A-62	Sequence 62, Appl1
15	100.0	3	1	US-08-293-150A-62	Sequence 62, Appl1
16	100.0	3	2	US-08-502-374A-2	Sequence 2, Appl1
17	100.0	3	2	US-08-502-374A-2	Sequence 2, Appl1
18	100.0	3	2	US-08-642-407A-2	Sequence 2, Appl1
19	100.0	3	2	US-08-642-407A-2	Sequence 2, Appl1
20	100.0	3	3	US-08-873-709-9	Sequence 9, Appl1
21	100.0	3	3	US-09-032-365A-36	Sequence 36, Appl1
22	100.0	3	4	US-08-793-634B-12	Sequence 12, Appl1
23	100.0	3	4	US-08-793-634B-12	Sequence 12, Appl1
24	100.0	4	1	US-07-755-462-2	Sequence 2, Appl1
25	100.0	4	1	US-07-755-462-2	Sequence 2, Appl1
26	100.0	4	1	US-08-169-950-6	Sequence 6, Appl1
27	100.0	4	1	US-08-169-950-6	Sequence 6, Appl1

28	100.0	4	1	US-07-630-288A-7	Sequence 7, Appl1
29	100.0	4	1	US-07-630-288A-11	Sequence 11, Appl1
30	100.0	4	1	US-07-630-288A-11	Sequence 11, Appl1
31	100.0	4	1	US-07-630-288A-13	Sequence 13, Appl1
32	100.0	4	1	US-07-630-288A-14	Sequence 14, Appl1
33	100.0	4	1	US-07-630-288A-14	Sequence 14, Appl1
34	100.0	4	1	US-07-630-288A-34	Sequence 34, Appl1
35	100.0	4	1	US-07-630-288A-34	Sequence 34, Appl1
36	100.0	4	1	US-08-126-594-25	Sequence 25, Appl1
37	100.0	4	1	US-08-126-594-25	Sequence 25, Appl1
38	100.0	4	1	US-08-188-943-1	Sequence 1, Appl1
39	100.0	4	1	US-08-188-943-1	Sequence 1, Appl1
40	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
41	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
42	100.0	4	1	US-08-465-811A-25	Sequence 25, Appl1
43	100.0	4	1	US-08-465-811A-25	Sequence 25, Appl1
44	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1
45	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-268-679B-8
Sequence 8, Application US/08268679B
Patent No. 5674729
GENERAL INFORMATION:
APPLICANT: WINNER, ECKARD, MOLLA,
AKHTERUZZAMAN, PAUL, ANIKO V.
TITLE OF INVENTION: DE NOVO CELL-FREE
SYNTHESIS PICORNAVIRUS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,679B
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/846,914
FILING DATE: 06-MAR-1992
CLASSIFICATION: 435
APPLICATION NUMBER: 07/719,761
FILING DATE: 24-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C. H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 0887-4095 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE: N.A.

POSITION IN GENOME: N.A.
US-08-268-6798-8

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 2
US-08-484-192-16
Sequence 16, Application US/08484192
Patent No. 5756291
GENERAL INFORMATION:
APPLICANT: GRIFFIN, LINDA C.
APPLICANT: ALBRECHT, GLENN
APPLICANT: LATHAM, JOHN
APPLICANT: LEUNG, LAWRENCE
APPLICANT: VERMAAS, ERIC
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
TITLE OF INVENTION: METHODS OF MAKING
NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,192
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,387
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 246102002221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc.difference
LOCATION: replace(1,"")
OTHER INFORMATION: /note= "this is a blotin-17
OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-484-192-16

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 1 g 1

Db 2 G 2

RESULT 3
US-08-361-024-3
Sequence 3, Application US/08361024
Patent No. 6207368
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
TITLE OF INVENTION: Method, Reagent and Kit
TITLE OF INVENTION: for Detection and
TITLE OF INVENTION: Amplification of
TITLE OF INVENTION: Nucleic Acid Sequence
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
COUNTRY: USA
ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,024
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/925,059
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Burgeon, Richard P.
REGISTRATION NUMBER: 34,787
REFERENCE/DOCKET NUMBER: 128D-126
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: yes
ANTI-SENSE: no
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 4
US-08-361-024-3/C
Sequence 3, Application US/08361024
Patent No. 6207368
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
TITLE OF INVENTION: Method, Reagent and Kit
TITLE OF INVENTION: for Detection and
TITLE OF INVENTION: Amplification of
TITLE OF INVENTION: Nucleic Acid Sequence

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
COUNTRY: USA
ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,024
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/925,059
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Burgoon, Richard P.
REGISTRATION NUMBER: 34,787
REFERENCE/DOCKET NUMBER: 128D-126
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: yes
ANTI-SENSE: no
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 5
US-07-791-213D-46
Sequence 46, Application US/07/91213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF INVENTIONS: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 6
US-07-791-213D-46/C
Sequence 46, Application US/07/91213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF INVENTIONS: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

;; INFORMATION FOR SEQ ID NO: 46:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 3 g 3

RESULT 7
US-07-791-213D-62
; Sequence 62, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshihiro
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22133-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1

Db 2 g 2

RESULT 8
US-07-791-213D-62/c
; Sequence 62, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshihiro
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22133-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 3 g 3

RESULT 9
US-08-268-679B-7
; Sequence 7, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD, MOLLA,
; APPLICANT: AKTERUZZAMAN, PAUL, ANIRO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,679B
FILING DATE: 30-JUN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/846,914
FILING DATE: 06-MAR-1992
CLASSIFICATION: 435
APPLICATION NUMBER: 07/719,761
FILING DATE: 24-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C.H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 0887-4095 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE: N.A.
POSITION IN GENOME: N.A.
US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 g 2

RESULT 10
US-08-602-036A-2
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
NUMBER OF SEQUENCES: 23
METHODS OF INHIBITING METASTATIC CANCER
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 1 g 1

RESULT 11
US-08-602-036A-2/c
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
NUMBER OF SEQUENCES: 23
METHODS OF INHIBITING METASTATIC CANCER
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
|
Db 3 G 3

RESULT 12
US-08-293-150A-46
; Sequence 46, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-293-150A-46

Query Match 100.0%; Score 1; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
|
Db 2 G 2

RESULT 13
US-08-293-150A-46/C
; Sequence 46, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-293-150A-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
|
Db 3 G 3

RESULT 14
US-08-293-150A-62
; Sequence 62, Application US/08293150A
; Patent No. 5792629

GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 g 2

RESULT 15
US-08-293-150A-62/c
Sequence 62, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 3 g 3

RESULT 16
US-08-502-374A-2
Sequence 2, Application US/08502374A
Patent No. 5872007
GENERAL INFORMATION:
APPLICANT: Fodstad, Oeystein
APPLICANT: Engedaaten, Olav
APPLICANT: Hovig, Elvind
APPLICANT: Maelandmo, Gunhild H.
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,374A
FILING DATE: 14-Jul-1995

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 9 1
1 1
DB 1 G 1

RESULT 17
US-08-502-374A-2/C
Sequence 2, Application US/08502374A
Patent No. 5872007
GENERAL INFORMATION:
APPLICANT: Fodstad, Oeystein
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,374A
FILING DATE: 14-Jul-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO

ANTI-SENSE: YES
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 9 1
1 1
DB 3 G 3

RESULT 18
US-08-642-407A-2
Sequence 2, Application US/08642407A
Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 9 1
1 1
DB 1 G 1

RESULT 19
US-08-642-407A-2/C
Sequence 2, Application US/08642407A

Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oystein, Fodstad
APPLICANT: Hovig, Eivind
APPLICANT: Enebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-6000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-2

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1
DB 3 G 3

RESULT 20
US-08-873-709-9
Sequence 9, Application US/08873709
Patent No. 6037126
GENERAL INFORMATION:
APPLICANT: Grossman, Abraham
TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND
APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF
PROTEIN COMPONENT OF TELOMERASE ENZYME
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abraham Grossman
STREET: 666 Washington Avenue
CITY: Pleasantville
STATE: NY
COUNTRY: USA
ZIP: 10570
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,709
FILING DATE: 12-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: 0001/002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-747-9108
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-873-709-9

Query Match
Best Local Similarity 100.0%; Score 1; DB 3; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1
DB 1 G 1

RESULT 21
US-09-032-365A-36
Sequence 36, Application US/09032365A
Patent No. 6114502
GENERAL INFORMATION:
APPLICANT: No. 6114502th, Michael
APPLICANT: Nishina, Patsy
APPLICANT: Naggart, Juergen
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
NEUROSENSORY DEFECTS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM compatible
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-2CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:

LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-032-365A-36

Query Match 100.0%; Score 1; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
OY 1 g 1
DB 1 g 1

RESULT 22
US-08-793-634B-12
Sequence 12, Application US/08793634B
Patent No. 6211431
GENERAL INFORMATION:
APPLICANT: Boevink, Petra C.
APPLICANT: Surin, Brian P.
APPLICANT: Keese, Paul K.
APPLICANT: Chu, Paul W.G.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Khan, Rafiqul I.
APPLICANT: Larkin, Philip J.
APPLICANT: Marchall, Jerry S.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,634B
FILING DATE: June 9, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10530
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-793-634B-12

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
OY 1 g 1
DB 2 g 2

RESULT 23
US-08-973-568-55
Sequence 55, Application US/08973568B
Patent No. 6277634
GENERAL INFORMATION:
APPLICANT: McCall, Maxine J.
APPLICANT: Hendry, Philip
APPLICANT: Lockett, Trevor
TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF
FILE REFERENCE: 47203bpcus
CURRENT APPLICATION NUMBER: US/08/973,568B
CURRENT FILING DATE: 1998-05-18
NUMBER OF SEQ. ID NOS: 55
SOFTWARE: Patentin Ver. 2.1
SEQ. ID NO 55
LENGTH: 3
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
FEATURE: Synthetic Ribozyme or portion thereof
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
US-08-973-568-55

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
OY 1 g 1
DB 1 g 1

RESULT 24
US-07-755-462-2
Sequence 2, Application US/07755462
Patent No. 5273881
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Zarling, David A.
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Denlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,462
FILING DATE: 19910904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4255-0001.30
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 1 g 1

RESULT 25
US-07-755-462-2/c
Sequence 2, Application US/07755462
Patent No. 5273881
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calhoun, Cornelia J.
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,462
FILING DATE: 19910904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4255-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 4 g 4

RESULT 26

US-08-169-950-6
Sequence 6, Application US/08169950
Patent No. 5366882

GENERAL INFORMATION:

APPLICANT: LUNNEN, KEITH D.

APPLICANT: WILSON, GEOFFREY G.

TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI

TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &

STREET: 130 WATER STREET

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/169,950

FILING DATE: 17-DEC-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RESNICK, DAVID S.

REGISTRATION NUMBER: 34235

REFERENCE/DOCKET NUMBER: 43959

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 523-3400

TELEFAX: (617) 523-6440

TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 27

US-08-169-950-6/c

Sequence 6, Application US/08169950
Patent No. 5366882

GENERAL INFORMATION:

APPLICANT: LUNNEN, KEITH D.

APPLICANT: WILSON, GEOFFREY G.

TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI

TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,950
FILING DATE: 17-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1
|
DB 4 G 4

RESULT 28
US-07-630-288A-7
Sequence 7, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Giesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Giesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-7

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1
|
DB 1 G 1

RESULT 29
US-07-630-288A-11
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Giesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Giesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
Db 1 g 1

RESULT 30
US-07-630-288A-11/C
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630.288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370.218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252.243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
Db 1 g 1

Db 4 G 4

RESULT 31
US-07-630-288A-13
Sequence 13, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630.288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370.218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252.243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-13

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
Db 1 g 1

RESULT 32
US-07-630-288A-14
Sequence 14, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gieser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2443
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1 1
Db 1 g 1

RESULT 33
US-07-630-288A-14/C
Sequence 14, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Gieser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gieser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2443
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1 1
Db 4 g 4

RESULT 34
US-07-630-288A-34
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Gieser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gieser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2443
INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
Db 2 G 2

RESULT 35
US-07-630-288A-34/c
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glessner
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 435
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glessner, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
Db 4 G 4

RESULT 36
US-08-126-594-25
Sequence 25, Application US/08126594
Patent No. 5482845
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/ANC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
Db 3 G 3

RESULT 37
US-08-126-594-25/c
Sequence 25, Application US/08126594
Patent No. 5482845
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPM/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-25

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
DB 4 G 4

RESULT 38
US-08-188-943-1
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESS: C/O Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
DB 3 G 3

RESULT 39
US-08-188-943-1/c
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESS: C/O Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
|
Db 4 G 4

RESULT 40

US-08-188-943-2
; Sequence 2, Application US/08188943
; Patent No. 5635347
; GENERAL INFORMATION:
; APPLICANT: Link, John R.
; APPLICANT: Gudibande, Satyanarayana R.
; TITLE OF INVENTION: Rapid Assays for Amplification
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,943
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,602
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370068-3630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
|
Db 1 G 1

RESULT 41

US-08-188-943-2/c
; Sequence 2, Application US/08188943
; Patent No. 5635347
; GENERAL INFORMATION:
; APPLICANT: Link, John R.
; APPLICANT: Gudibande, Satyanarayana R.
; TITLE OF INVENTION: Rapid Assays for Amplification
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,943
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,602
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370068-3630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
|
Db 2 G 2

RESULT 42

US-08-465-811A-25
; Sequence 25, Application US/08465811A
; Patent No. 5637685
; GENERAL INFORMATION:
; APPLICANT: Soares, M. Bento
; APPLICANT: Efstratiadis, Argiris
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
; TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, c/o Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,811A
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JPM/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 3 G 3

RESULT 43
US-08-465-811A-25/c
Sequence 25, Application US/08465811A
Patent No. 5637665
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstratiadis, Argiris
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,811A
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPM/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 4 G 4

RESULT 44
US-08-199-317-2
Sequence 2, Application US/08199317
Patent No. 5670316
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calhoun, Cornelia J.
APPLICANT: Zarling, David A.
TITLE OF INVENTION: Diagnostic Applications of Double D-loop
TITLE OF INVENTION: Formation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,317
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,791
FILING DATE: 09-JUL-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/755,462
FILING DATE: 04-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 9150-0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for Dpn I
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 1 G 1

RESULT 45
US-08-199-317-2/C
: Sequence 2, Application US/08199317
: Patent No. 5670316
: GENERAL INFORMATION:
: APPLICANT: Sena, Elissa P.
: APPLICANT: Calhoun, Cornelia J.
: APPLICANT: Zarling, David A.
: TITLE OF INVENTION: Diagnostic Applications of Double D-loop
: TITLE OF INVENTION: Formation
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Ave., Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/199,317
: FILING DATE: 25-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/910,791
: FILING DATE: 09-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/755,462
: FILING DATE: 04-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/520,321
: FILING DATE: 07-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Stratford, Carol A.
: REGISTRATION NUMBER: 34,444
: REFERENCE/DOCKET NUMBER: 9150-0004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-324-0880
: TELEFAX: 415-324-0960
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Cleavage site for Dpn I
: US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 1 g 1
DB 4 G 4

Search completed: July 15, 2002, 23:07:38
Job time: 22991 sec

Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -

PT useful to inhibit metastatic cancer, partic. osteosarcoma
XX
XX Claim 2: Page 56; 70pp; English.
XX

CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
CC expression may include the trinucleotide GUC (AAT33326, given in 5'
CC to 3' direction) found in codon 14 of CAPL mRNA. These and
CC other antisense oligonucleotides (AAT33327-36) complementary to
CC specific regions of the CAPL gene (see also AAT33345), as well as
CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
CC patient as a means of inhibiting metastatic cancer.
XX
XX

Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
3 g 3
Db

RESULT 2
AAT33326/C
ID AAT33326 standard; RNA; 3 BP.
XX
XX AAT33326;

DT 12-NOV-1996 (first entry)

DE CAPL trinucleotide.

KW CAPL: antisense oligonucleotide; ribozyme; cancer; metastasis;
osteosarcoma; therapy; ss.

OS Synthetic.

PN MO9625499-A1.

PD 22-AUG-1996.

PF 16-FEB-1996; 96MO-US02108.

PR 17-FEB-1995; 95US-0391375.

PA (HYBR-) HYBRIDON INC.

PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.

PI Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandsmo GJ;
PI Von Hofe E;

DR WP1: 1996-393400/39.

PT Synthetic oligonucleotide(s) inhibiting CAPL gene expression -
PT useful to inhibit metastatic cancer, partic. osteosarcoma
XX
XX Claim 2: Page 56; 70pp; English.

CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
CC expression may include the trinucleotide GUC (AAT33326, given in 5'
CC to 3' direction) found in codon 14 of CAPL mRNA. These and
CC other antisense oligonucleotides (AAT33327-36) complementary to
CC specific regions of the CAPL gene (see also AAT33345), as well as
CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
CC patient as a means of inhibiting metastatic cancer.
XX
XX

Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
1
3 g 1
Db

RESULT 3
AAA94655
ID AAA94655 standard; DNA; 3 BP.
XX
XX AAA94655;

DT 15-JAN-2001 (first entry)

DE Human TUB gene probe #2.

KW Human: TULP; neurosensory defect; retina; retinal dystrophy; probe;
TUB; ss.

OS Homo sapiens.

PN US6114502-A.

PD 05-SEP-2000.

PF 27-FEB-1998; 98US-0032365.

PR 22-AUG-1996; 96US-0701380.

PR 04-SEP-1996; 96US-0706292.

PR 10-APR-1996; 96US-0630592.

PR 17-SEP-1996; 96US-0714991.

PR 30-APR-1997; 97US-0850218.

PR 01-AUG-1997; 97US-0904699.

PR 17-SEP-1997; 97US-0932306.

PA (AXYS-) AXYS PHARM INC.

PI North M, Nishina P, Noben-Trauth K, Naggett J;

DR WP1: 2000-586483/55.

PT Mammalian proteins expressed in retina and brain, useful for producing
PT antibodies and for diagnosing neurosensory defects including cochlear
PT degeneration, peripheral retinal degeneration and cone-rod retinal
PT dystrophy -
XX
XX

PS Disclosure; Columns 81-82; 61pp; English.

CC The present invention relates to human and murine cDNAs from a
CC neurosensory defect associated gene family. The novel cDNAs are mouse
CC tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB
CC form 6 (see AAA94632), human TUB form I (see AAA94633), human TULP1 (see
CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
CC immunogens to raise antibodies that specifically identify TUB/TULP
CC expressing cells and in drug screening assays directed at neurosensory
CC defects. The novel proteins encoded by the present sequence can be used
CC for the treatment of neurosensory degenerative conditions e.g. retinal
CC dystrophies. The present sequence is a probe used to isolate the novel
CC genes of the present invention.
XX
XX

Sequence 3 BP: 0 A; 0 C; 3 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
3 g 1
Db

```

RESULT 4
AAL20244/C
ID AAL20244 standard; cDNA: 3 BP.
XX
AC AAL20244:
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 12701.
XX
KW Human breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN MO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001MO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI; 2001-451856/48.
XX
JT New peptide useful as a marker for the diagnosis of breast cancer -
XX
XX Claim 1; Page 2245; 3695pp; English.
XX
PS The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

Query Match      100.0%; Score 1; DB 22; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
   |
DB 2 G 2

RESULT 5
AAO81664
ID AAO81664 standard; RNA: 4 BP.
XX
AC AAO81664:
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KM bubble structure; pseudoknot; receptor; heparin; competition;
XX bubble structure; pseudoknot; receptor; heparin; competition;
XX

```

```

KM Inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO9500528-A.
XX
PD 05-JAN-1995.
XX
PF 17-JUN-1994; 94WO-US06884.
XX
PR 18-JUN-1993; 93US-0079677.
PR 07-JAN-1994; 94US-0179491.
XX
XX (PHAR-) PHARMAGENICS INC.
XX
PI Beutel BA, Joesten ME;
XX
DR WPI; 1995-051992/07.
XX
PT New oligo-nucleotide(s) that bind to basic fibroblast growth
XX factor - modulating, esp. inhibiting, its activity; useful in
XX treating cancer, preventing metastasis, and diagnosis.
XX
PS Claim 3; Page 25; 44pp; English.
XX
CC The sequences given in AAO81642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AAO81664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.
XX
SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match      100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
   |
DB 1 g 1

RESULT 6
AAO81664/C
ID AAO81664 standard; RNA: 4 BP.
XX
AC AAO81664:
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KM bubble structure; pseudoknot; receptor; heparin; competition;
XX inhibition; enhance; neovascularisation; solid tumour; cancer;
XX metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO9500528-A.
XX

```

```

PD 05-JAN-1995.
XX
XX 17-JUN-1994; 94WO-US06884.
XX
XX 18-JUN-1993; 93US-0079677.
PR 07-JAN-1994; 94US-0179491.
XX
PA (PHAR-) PHARMAGENICS INC.
XX
XX Beutel BA, Joesten ME;
XX
XX WPI: 1995-051992/07.
XX
PT New oligo-nucleotide(s) that bind to basic fibroblast growth
PT factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.
XX
XX
XX Claim 3; Page 25; 44pp; English.
XX
CC The sequences given in AA081642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AA081664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.
XX
SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other:

```

```

Query Match      100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
   1
Db 4 G 4

```

```

RESULT 7
AA081665
ID AA081665 standard; RNA; 4 BP.
XX
AC AA081665;
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #2.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PN W09500528-A.
XX
PD 05-JAN-1995.
XX
XX 17-JUN-1994; 94WO-US06884.
XX
XX 18-JUN-1993; 93US-0079677.
PR 07-JAN-1994; 94US-0179491.
XX

```

```

PA (PHAR-) PHARMAGENICS INC.
XX
XX Beutel BA, Joesten ME;
XX
XX WPI: 1995-051992/07.
XX
XX
XX New oligo-nucleotide(s) that bind to basic fibroblast growth
XX factor - modulating, esp. inhibiting, its activity, useful in
XX treating cancer, preventing metastasis, and diagnosis.
XX
XX
XX Claim 3; Page 25; 44pp; English.
XX
CC The sequences given in AA081642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AA081664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.
XX
SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other:

```

```

Query Match      100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
   1
Db 3 g 3

```

```

RESULT 8
AA081665/C
ID AA081665 standard; RNA; 4 BP.
XX
AC AA081665;
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #2.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PN W09500528-A.
XX
PD 05-JAN-1995.
XX
XX 17-JUN-1994; 94WO-US06884.
XX
XX 18-JUN-1993; 93US-0079677.
PR 07-JAN-1994; 94US-0179491.
XX
XX (PHAR-) PHARMAGENICS INC.
XX
XX Beutel BA, Joesten ME;
XX
XX WPI: 1995-051992/07.
XX
PT New oligo-nucleotide(s) that bind to basic fibroblast growth

```

PT factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.
PS Claim 3: Page 25; 44pp; English.
XX

CC The sequences given in AA081642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AA081644-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.
XX

Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
DB 4 G 4

RESULT 9

AA086385
ID AA086385 standard; DNA; 4 BP.

AC AA086385;

DT 23-APR-1998 (first entry)

DE Probe for target nucleic acid sequence P0.

KW Point mutation detection; nucleic acid sequence analysis; probe;

KW viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

Key Location/Qualifiers

FT modified_base 1 /*tag= a
FT /note= "C-5'phosphate"

PN W09738131-A1.

PD 16-OCT-1997.

PE 11-APR-1996; 96WO-RU00087.

PR 11-APR-1996; 96WO-RU00087.

PA (DYMS/) DYMSHITS G M.

PA (IVAN/) IVANOVA E M.

PA (KRIV/) KRIVENKO A A.

PA (KULI/) KULIKOVA V F.

PA (LOKH/) LOKHOV S G.

PA (PYSH/) PYSHNY D V.

PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
PI Lokhov SG, Pyshny DV;

WP1: 1997-512737/47.

PT Detection of target nucleic acid sequence - based on ligation of
PT hybridised short probe to flanking target-complementary sequences
XX
PS Example; Page 4; 15pp; Russian.
XX

CC This sequence represents a probe for the target sequence P0 (shown in
CC AA086376). This sequence was used to test the method of the invention.
CC The method of the invention is for detecting a nucleic acid sequence to
CC be analysed, and comprises hybridisation of an oligonucleotide probe
CC complementary to the sequence to be analysed and bearing a reporter
CC group, the novelty is that detection of a sequence is based on the
CC ligation of a short oligonucleotide (with a length of 4-6 units) with
CC flanking oligonucleotide sequences (or their derivatives bearing
CC polycyclic aromatic groups). The method is especially useful for
CC detecting point mutations. Diagnosis of viral, genetic and other
CC diseases is also mentioned.
XX

Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
DB 3 g 3

RESULT 10

AA086385/c
ID AA086385 standard; DNA; 4 BP.

AC AA086385;

DT 23-APR-1998 (first entry)

DE Probe for target nucleic acid sequence P0.

KW Point mutation detection; nucleic acid sequence analysis; probe;

KW viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

Key Location/Qualifiers

FT modified_base 1 /*tag= a
FT /note= "C-5'phosphate"

PN W09738131-A1.

PD 16-OCT-1997.

PE 11-APR-1996; 96WO-RU00087.

PR 11-APR-1996; 96WO-RU00087.

PA (DYMS/) DYMSHITS G M.

PA (IVAN/) IVANOVA E M.

PA (KRIV/) KRIVENKO A A.

PA (KULI/) KULIKOVA V F.

PA (LOKH/) LOKHOV S G.

PA (PYSH/) PYSHNY D V.

PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
PI Lokhov SG, Pyshny DV;

WP1: 1997-512737/47.

PT Detection of target nucleic acid sequence - based on ligation of
PT hybridised short probe to flanking target-complementary sequences
XX
PS Example; Page 4; 15pp; Russian.

XX This sequence represents a probe for the target sequence p0 (shown in
 CC AAT86376). This sequence was used to test the method of the invention.
 CC The method of the invention is for detecting a nucleic acid sequence to
 CC be analysed, and comprises hybridisation of an oligonucleotide probe
 CC complementary to the sequence to be analysed and bearing a reporter
 CC group, the novelty is that detection of a sequence is based on the
 CC ligation of a short oligonucleotide (with a length of 4-6 units) with
 CC flanking oligonucleotide sequences (or their derivatives bearing
 CC polycyclic aromatic groups). The method is especially useful for
 CC detecting point mutations. Diagnosis of viral, genetic and other
 CC diseases is also mentioned.

SO Sequence 4 BP: 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 Db 4 G 4

RESULT 11

AAT77252
 ID AAT77252 standard; DNA: 4 BP.

XX AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome; vaccine;
 KW immune response; antigen; naked gene expression vector; IGE;
 KM antibody; immunotherapy; ss.
 XX

OS Synthetic.

XX WO9728259-A1.

XX 07-AUG-1997.

PF 28-JAN-1997; 97WO-US01277.

PR 30-JAN-1996; 96US-0593554.

PA (REGC) UNIV CALIFORNIA.

PI Carson DA, Raz E;

DR WPI; 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic
 PT polynucleotide - useful for selectively enhancing the TH1 immune
 PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16: Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide
 CC (ISP) comprised of at least one strand of a palindrome, which includes
 CC at least one dinucleotide consisting of adjacent, unethylated cytosine
 CC and guanine residues. ISP's could be used used in vaccination methods
 CC for enhancing the immune response of a host to an antigen. Administration
 CC of naked gene expression vectors which encode antigens or their
 CC immunostimulatory fragments suppresses IGE antibody production
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.

SO Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 Db 3 g 3

RESULT 12

AAT77252/C
 ID AAT77252 standard; DNA: 4 BP.

XX AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome; vaccine;
 KW immune response; antigen; naked gene expression vector; IGE;
 KM antibody; immunotherapy; ss.
 XX

OS Synthetic.

XX WO9728259-A1.

XX 07-AUG-1997.

PF 28-JAN-1997; 97WO-US01277.

PR 30-JAN-1996; 96US-0593554.

PA (REGC) UNIV CALIFORNIA.

PI Carson DA, Raz E;

DR WPI; 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic
 PT polynucleotide - useful for selectively enhancing the TH1 immune
 PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16: Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide
 CC (ISP) comprised of at least one strand of a palindrome, which includes
 CC at least one dinucleotide consisting of adjacent, unethylated cytosine
 CC and guanine residues. ISP's could be used used in vaccination methods
 CC for enhancing the immune response of a host to an antigen. Administration
 CC of naked gene expression vectors which encode antigens or their
 CC immunostimulatory fragments suppresses IGE antibody production
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.

SO Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 Db 2 g 2

RESULT 13

AAL17191
 ID AAL17191 standard; cDNA: 4 BP.

XX AAL17191;

DT 07-DEC-2001 (first entry)

```

XX DE Human breast cancer expressed polynucleotide 9648.
XX KW Human; breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-MAR-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 29-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX DR WPI: 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer
XX PS Claim 1; Page 1720; 3695pp; English.
XX SO The invention relates to human breast cancer expressed polynucleotides
    (AAL07544-AAL26789) and methods of assessing whether a patient is
    afflicted with breast cancer by examining the correlation between the
    expression of certain markers and the cancerous state of breast cells.
    The polynucleotides and encoded polypeptides are potential markers for
    detecting, diagnosing, monitoring, characterising treating and
    potentially preventing breast cancer. The polynucleotides and encoded
    polypeptides are also useful for isolating compounds with cytostatic
    activity.
    Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;
    Query Match          100.0%; Score 1; DB 22; Length 4;
    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Oy 1 g 1
    Db 1 g 1
    RESULT 14
    AAL17191/C
    ID AAL17191 standard; cDNA; 4 BP.
    AC AAL17191;
    XX
    XX 07-DEC-2001 (first entry)
    DE Human breast cancer expressed polynucleotide 9648.
    KW Human; breast cancer; cell marker; cytostatic; ss.
    OS Homo sapiens.
    XX
    XX PN WO200151628-A2.
    XX PD 19-JUL-2001.
    XX PF 10-JAN-2001; 2001WO-US00798.
    XX PR
    XX DR

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PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX DR WPI: 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer
XX PS Claim 1; Page 1720; 3695pp; English.
XX SO The invention relates to human breast cancer expressed polynucleotides
    (AAL07544-AAL26789) and methods of assessing whether a patient is
    afflicted with breast cancer by examining the correlation between the
    expression of certain markers and the cancerous state of breast cells.
    The polynucleotides and encoded polypeptides are potential markers for
    detecting, diagnosing, monitoring, characterising treating and
    potentially preventing breast cancer. The polynucleotides and encoded
    polypeptides are also useful for isolating compounds with cytostatic
    activity.
    Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;
    Query Match          100.0%; Score 1; DB 22; Length 4;
    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Oy 1 g 1
    Db 3 g 3
    RESULT 15
    AAL24357/C
    ID AAL24357 standard; cDNA; 4 BP.
    AC AAL24357;
    XX
    XX 07-DEC-2001 (first entry)
    DE Human breast cancer expressed polynucleotide 16814.
    KW Human; breast cancer; cell marker; cytostatic; ss.
    OS Homo sapiens.
    XX
    XX PN WO200151628-A2.
    XX PD 19-JUL-2001.
    XX PF 10-JAN-2001; 2001WO-US00798.
    XX PR 14-JAN-2000; 2000US-0176077.
    XX PR 14-MAR-2000; 2000US-0189167.
    XX PR 24-MAR-2000; 2000US-0192099.
    XX PR 29-MAR-2000; 2000US-0193480.
    XX PR 15-MAY-2000; 2000US-0205230.
    XX PR 09-JUN-2000; 2000US-0211315.
    XX PR 25-JUL-2000; 2000US-0220534.
    XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
    XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
    XX DR WPI: 2001-451856/48.

```

XX New peptide useful as a marker for the diagnosis of breast cancer -
PT
XX
PS Claim 1: Page 3087; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AA07544-AA126789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
SO
Sequence 4 BP; 0 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 3 G 3

RESULT 16
AA061450
ID AA061450 standard; RNA; 4 BP.
XX
AC AA061450;
XX
DT 18-JUN-2001 (first entry)
XX
DE Cyclin binding hammerhead ribozyme 3' catalytic fragment SEQ ID 19.
XX
KM Hammerhead ribozyme; cyclin E; restenosis; catalytic; angioplasty;
KM cyclin E2F1; vasotrophic; gene therapy; cell cycle arrest; ss.
XX
OS Synthetic.
XX
PN WO200121789-A1.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-1999; 99WO-EP07049.
XX
PR 22-SEP-1999; 99WO-EP07049.
XX
PA (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.
XX
PI Grassi G, Kuhn AC, Kandolf R;
XX
DR WPI: 2001-257985/26.
XX
PT New catalytically acting RNA molecule comprising hammerhead ribozyme
PT directed against mRNA molecules encoding cyclin E or E2F1, useful for
PT inhibiting vascular smooth muscle cell proliferation and restenosis -
PS
PS Claim 12: Page 28; 40pp; German.
XX
CC This invention describes a novel catalytic RNA molecule which is directed
CC against mRNA molecules (II) which encode the cell-relevant protein cyclin
CC E or E2F1. The products of the invention have vasotrophic activity and can
CC be used for gene therapy. The use of (I), or a DNA molecule or a plasmid
CC for inhibiting restenosis is claimed for obtaining a vector for gene therapy and
CC compositons containing these components are also claimed. (I)
CC efficiently induces cell cycle arrest by combined inactivation of cyclin
CC E and E2F1.
XX
SO Sequence 4 BP; 2 A; 0 C; 1 G; 0 U; 1 other;

Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 g 2

RESULT 17
AAN93676/C
ID AAN93676 standard; DNA; 5 BP.
XX
AC AAN93676;
XX
DT 24-JUN-1990 (first entry)
XX
DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber
DE variant (HSV-C) and HSV grape variant (HSV-g).
XX
KM Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.
XX
OS Hop growth retarding viroid.
XX
PN JP01040000-A.
XX
PD 10-FEB-1989.
XX
PF 05-AUG-1987; 87JP-0194377.
XX
PR 05-AUG-1987; 87JP-0195377.
XX
PA (YUKI) YUKI GOSHI YAKUHIN.
XX
DR WPI: 1989-089715/12.
XX
PT Fractionating and detecting hop growth retarding viroids -
PT using synthetic DNA probe contg. specific base sequence
XX
PS Disclosure; page 3; 5pp; Japanese.
XX
CC The synthetic probes is complementary to the RNA of HSV-g bases 53-59.
CC HSV, HSV-C and HSV-g are fractionated and detected using the synthetic
CC probe. The probe is 13-25mer. The probe can be used to diagnose HSV
CC infections in plants.
XX
SO Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 5 G 5

RESULT 18
AA068752
ID AA068752 standard; DNA; 5 BP.
XX
AC AA068752;
XX
DT 22-FEB-1995 (first entry)
XX
DE CHA255 heavy chain CDRI clone 3.3.3. coding sequence.
XX
KM Polymerase chain reaction; primer: PCR; amplify; heavy; light;
KM chain; complementarity determining region; CDR; variable; constant;
KW region; monoclonal antibody; Mab; binding affinity; EDTA; DOTA;

KM tumour: cancer: colorectal; breast; metal chelate; hapten; ss.
 XX Synthetic.
 OS
 XX AU9350602-A.
 PN
 XX 26-MAY-1994.
 PD
 X
 PF 10-NOV-1993; 93AU-0050602.
 XX
 PR 12-NOV-1992; 92US-0975230.
 XX
 PA (HYBR-) HYBRITTECH INC.
 XX
 PI Abtweller PM, Moore MD;
 XX
 DR WPI: 1994-209063/26.
 DR P-PSDB: AAR34150.
 XX
 PT Polypeptide used in imaging and treatment of carcinomas and
 PT tumours - comprising substd antibody CDR having binding affinity
 PT for metal chelate of EDTA or DETA or analogues
 XX
 PS Claim 25; Fig 3A; 61pp: English.
 CC
 CC The sequences given in AAQ68747-57 encode the wild type and mutagenised
 CC versions of the complementarity determining region 1 (CDR1) of the
 CC antibody designated CHA255. CHA255 is a murine monoclonal antibody
 CC (MAb) which is capable of binding complexes. Mutagenesis of these
 CC CDRs, causes the production of polypeptides with a particularly
 CC high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3
 CC of the heavy chain, and CDR2 and -3 of the light chain were targeted
 CC for mutagenesis. Five residues of both CDR1 and -3 of the CHA255
 CC nine light chain CDR3 residues were specifically targeted for
 CC codon-based mutagenesis. The mutagenised MAbs can be used in
 CC compositions for in vivo imaging of malignant tissues or tumours. They
 CC are also useful for the treatment of malignant tissues or tumours eg.
 CC colorectal or breast cancer. Both methods involve the use of
 CC radionuclides which bind to metal chelates or haptens which are
 CC specifically delivered to the target site by a targeting molecule. CDR
 CC derived peptides may be used to construct bi-functional antibodies
 CC having dual specificities, or as donor or recipients of CDR sequences.
 XX
 SO Sequence 5 BP; 0 A; 0 C; 1 G; 1 T; 3 other:

Query Match
 Best Local Similarity 100.0%; Score 1; DB 15; Length 5;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 1 g 1

RESULT 19
 AAQ81667/c
 ID AAQ81667 standard; RNA: 5 BP.
 XX
 AC AAQ81667;
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #4.
 XX
 KW Basic: fibroblast growth factor; bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KM inhibition; enhance; neovascularisation; solid tumour; cancer;
 KM metastasis; diagnosis; gene therapy; ss.
 XX
 OS Synthetic.
 XX

PN W09500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 XX
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI: 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 PT factor - modulating, esp. inhibiting, its activity, useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp: English.
 CC
 CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC affinity receptor or a closed, circular structure. bFGF binds to high
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SO Sequence 5 BP; 2 A; 2 C; 0 G; 1 U; 0 other:

Query Match
 Best Local Similarity 100.0%; Score 1; DB 16; Length 5;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 5 G 5

RESULT 20
 AAT12043/c
 ID AAT12043 standard; RNA: 5 BP.
 XX
 AC AAT12043;
 XX
 DT 17-JUL-1996 (first entry)
 XX
 DE Cleavable replicable-inhibiting sequence.
 XX
 KW Ribozyme; hairpin; hammerhead; probe; MDV-1; midvariant-1;
 KM replication; cleavage; ss.
 XX
 OS Synthetic.
 XX
 PN US5472840-A.
 XX
 PD 05-DEC-1995.
 XX
 PF 30-SEP-1988; 88US-0252243.
 XX
 PR 17-DEC-1990; 90US-0630288.
 XX
 PR 30-SEP-1988; 88US-0252243.
 PR 22-JUN-1989; 89US-0370218.

XX (STAD) AMOCO CORP.
PA
XX
PI Stefano JE;
XX
DR WPI: 1996-029807/03.
XX
PT Ribozyme-forming nucleic acid probes - contg. MDV-1 sequence and
XX cleavable replicable-inhibiting sequence.
XX
PS Claim 4: Column 62; 43pp: English.
XX
CC A composition comprises RNA of formula P4-P1-P2-P3 (Ia), a nucleic
CC acid of formula R1-R2 (Iii), where (Ia) and (Iii) bind to a target
CC nucleic acid of formula X2-X1-X3 (Ii) to form a hammerhead ribozyme,
CC where P1 is a MDV-1 sequence capable of autocatalytic replication in
CC the absence of P3; P2 is a sequence (AA112042 or AA112044) that binds
CC to (Ii) and forms a cleavage site between P1 and P3; P3 (AA112043)
CC is an inhibitory element that binds to X2 and interacts with a
CC region of P1 corresp. to nucleotides 81-126 of MDV-1; P4 contributes
CC nucleotides to form the ribozyme with X1 and P2, or is the terminal
CC nucleotide of P1; X1 is a target region of (Ii); X2 and X3 are
CC terminal nucleotides or second or third target regions of (Ii); R1
CC is a ribozyme-forming area of (Iii); and R2 is a terminal nucleotide
CC of R1 or an area of (Iii) that binds to (Ii). X1 and R1 are
CC mutually exclusive and are represented by the sequences of AA112040 and
CC AA112041. For hairpin ribozymes, P2 is AA112045 and R1 is AA112046.
CC Probes bearing ribozymes are produced in a single step by transcription
CC of DNA of appropriate sequence, thereby reducing costs. The ribozymes
CC produce specific cleavage events, leading to a product RNA with
CC defined replication properties.
XX
SQ Sequence 5 BP; 0 A; 1 C; 0 G; 2 U; 2 other;

Query Match 100.0%; Score 1; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 5 G 5

RESULT 21
AAV61663
ID AAV61663 standard; DNA: 5 BP.
XX
AC AAV61663;
XX
DT 03-DEC-1998 (first entry)
XX
DE Fusarium sp. 18S rRNA DNA fragment #7.
XX
KW 18S rRNA: detection: identification: fungus; ss.
XX
OS Fusarium sp.
XX
PN JP10234380-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-0062104.
XX
PR 28-FEB-1997; 97JP-0062104.
XX
PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
XX
DR WPI: 1998-535034/46.
XX
PT Use of oligo:nucleotide for detecting and identification of fungus
PT of Fusarium genus - as primer or probe to detect of identify
PT microbes rapidly and exactly

XX
PS Claim 1; Page 7; 20pp: Japanese.
XX
CC AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are
CC used in a method for the detection and identification of a fungus of
CC Fusarium genus. The process can be used to detect or identify microbes
CC rapidly and exactly.
XX
SQ Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 4 g 4

RESULT 22
AAV61663/C
ID AAV61663 standard; DNA: 5 BP.
XX
AC AAV61663;
XX
DT 03-DEC-1998 (first entry)
XX
DE Fusarium sp. 18S rRNA DNA fragment #7.
XX
KW 18S rRNA: detection: identification: fungus; ss.
XX
OS Fusarium sp.
XX
PN JP10234380-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-0062104.
XX
PR 28-FEB-1997; 97JP-0062104.
XX
PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
XX
DR WPI: 1998-535034/46.
XX
DT Use of oligo:nucleotide for detecting and identification of fungus
PT of Fusarium genus - as primer or probe to detect of identify
PT microbes rapidly and exactly
XX
PS Claim 1; Page 7; 20pp: Japanese.
XX
CC AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are
CC used in a method for the detection and identification of a fungus of
CC Fusarium genus. The process can be used to detect or identify microbes
CC rapidly and exactly.
XX
SQ Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 5 G 5

RESULT 23
AA196299
ID AA196299 standard; DNA: 5 BP.
XX

AC AAT96299;
 XX
 DT 08-APR-1998 (first entry)
 XX
 DE Fungal telomeric nucleic acid sequence.
 XX
 KM Detection; eukaryotic pathogen; telomeric nucleic acid sequence;
 KM telomerase activity; diagnosis; fungal infection; fungus; fungi;
 KM malarial infection; malaria; ss.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN US5695932-A.
 XX
 PD 09-DEC-1997.
 XX
 PF 13-MAY-1993; 93US-0060952.
 XX
 PR 13-MAY-1993; 93US-0060952.
 PR 13-MAY-1992; 92US-0882438.
 PR 24-MAR-1993; 93US-0038766.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;
 DR WPI: 1998-041292/04.
 XX
 PT Detection of eukaryotic pathogens, especially fungal or Plasmodium
 PT spp. - by detecting telomerase activity
 XX
 PS Claim 5: Columns 81-82; 82pp; English.
 XX
 CC The present sequence can be used in a novel method for detecting a
 CC eukaryotic pathogen in a patient. The method comprises obtaining a
 CC sample of somatic tissue or cells from the patient, determining if
 CC telomerase activity is present and correlating this with the
 CC presence of the pathogen. The method is useful for diagnosis of
 CC fungal infections, especially a fungus of the genus Candida,
 CC Kluveromyces, Saccharomyces, Sporothrix, Coccidioides,
 CC Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,
 CC Aspergillus, Mucor or Rhizopus, or malarial infections, especially
 CC Plasmodium vivax, P. ovale, P. malariae or P. falciparum.
 CC
 SO Sequence 5 BP; 0 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 2 g 2

RESULT 24
 AA210695
 ID AA210695 standard; DNA; 5 BP.
 XX
 AC AA210695;
 XX
 DT 23-NOV-1999 (first entry)
 XX
 DE Oligonucleotide sequence that increases p53 activity in a cell.
 XX
 KM p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
 KM UV-induced hyperproliferative disease; psoriasis; vitiligo;
 KM atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
 KM skin cancer; ss.
 XX
 OS Synthetic.

XX
 PN GB2336157-A.
 XX
 PD 13-OCT-1999.
 XX
 PF 24-MAR-1999; 99GB-0006758.
 XX
 PR 26-MAR-1998; 98US-0048927.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Gilchrest BA, Yaar M, Eller M;
 DR WPI: 1999-543520/46.
 XX
 PT DNA fragments useful for increasing p53 activity in a cell and reducing
 PT susceptibility to UV-induced hyperproliferative diseases -
 XX
 PS Claim 11; Page 30; 44pp; English.
 XX
 CC AA210692-97 represent DNA fragments that are used for increasing p53
 CC activity in a cell. The oligonucleotides are UV mimetics and
 CC protect cells against subsequent exposure to UV-irradiation or
 CC chemicals. The oligonucleotides are useful for increasing p53 activity
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
 CC and reducing susceptibility to skin cancer.
 CC
 SO Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 1 g 1

RESULT 25
 AA210696/c
 ID AA210696 standard; DNA; 5 BP.
 XX
 AC AA210696;
 XX
 DT 23-NOV-1999 (first entry)
 XX
 DE Oligonucleotide sequence that increases p53 activity in a cell.
 XX
 KM p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
 KM UV-induced hyperproliferative disease; psoriasis; vitiligo;
 KM atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
 KM skin cancer; ss.
 XX
 OS Synthetic.
 XX
 PN GB2336157-A.
 XX
 PD 13-OCT-1999.
 XX
 PF 24-MAR-1999; 99GB-0006758.
 XX
 PR 26-MAR-1998; 98US-0048927.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Gilchrest BA, Yaar M, Eller M;
 DR WPI: 1999-543520/46.
 XX
 PT DNA fragments useful for increasing p53 activity in a cell and reducing

PT susceptibility to UV-induced hyperproliferative diseases -
XX Claim 11; Page 30; 44pp: English.

CC AA210692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.

SO Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 5 G 5

RESULT 26
AA211611
ID AA211611 standard; DNA; 5 BP.
XX
AC AA211611;

DT 16-NOV-1999 (first entry)
XX

DE DNA enhancer sequence present in an upstream element.

KW Plant promoter; TATA motif; transcription start site; upstream element;
KM gene expression; oxalate oxidase; plant resistance; pathogen; maize;
KM ubi-1 promoter; Syn II core promoter; ss.

OS Synthetic.

XX WO9943838-A1.

XX 02-SEP-1999.

XX 23-FEB-1999; 99WO-US03863.

XX 24-FEB-1998; 98US-0028819.

XX (PION-) PIONEER HI-BRED INT INC.

XX Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;

XX WPI: 1999-540601/45.

PT New synthetic promoter functional in plants to provide non-tissue
PT specific, constitutive expression, particularly of oxalate oxidase for
PT increased resistance to pathogens
PS Claim 39; Page 47; 61pp: English.

XX The invention provides a new synthetic plant promoter that comprises a
CC TATA motif; a transcription start site (TSS) and a region between TATA
CC and TSS containing at least 64 percent GC content. The synthetic core
CC promoter, optionally containing additional upstream elements are used to
CC increase expression, provides non-tissue specific, constitutive
CC transcription of heterologous genes in any sort of plant, especially the
CC gene for oxalate oxidase for increasing plant resistance to pathogens.
CC The upstream activating elements can be used to increase transcription
CC from any promoter. A combination of the synthetic core promoter with
CC synthetic upstream elements can induce expression 10 times greater than
CC that provided by the maize ubi-1 promoter. The present sequence
CC represents a DNA enhancer OSC-like motif present in an upstream element

CC sequence.

XX Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 g 2

RESULT 27
AA211611/C
ID AA211611 standard; DNA; 5 BP.
XX
AC AA211611;

DT 16-NOV-1999 (first entry)
XX

DE DNA enhancer sequence present in an upstream element.

KW Plant promoter; TATA motif; transcription start site; upstream element;
KM gene expression; oxalate oxidase; plant resistance; pathogen; maize;
KM ubi-1 promoter; Syn II core promoter; ss.

OS Synthetic.

XX WO9943838-A1.

XX 02-SEP-1999.

XX 23-FEB-1999; 99WO-US03863.

XX 24-FEB-1998; 98US-0028819.

XX (PION-) PIONEER HI-BRED INT INC.

XX Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;

XX WPI: 1999-540601/45.

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PT specific, constitutive expression, particularly of oxalate oxidase for
PT increased resistance to pathogens
PS Claim 39; Page 47; 61pp: English.

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CC TATA motif; a transcription start site (TSS) and a region between TATA
CC and TSS containing at least 64 percent GC content. The synthetic core
CC promoter, optionally containing additional upstream elements are used to
CC increase expression, provides non-tissue specific, constitutive
CC transcription of heterologous genes in any sort of plant, especially the
CC gene for oxalate oxidase for increasing plant resistance to pathogens.
CC The upstream activating elements can be used to increase transcription
CC from any promoter. A combination of the synthetic core promoter with
CC synthetic upstream elements can induce expression 10 times greater than
CC that provided by the maize ubi-1 promoter. The present sequence
CC represents a DNA enhancer OSC-like motif present in an upstream element
XX sequence.

SO Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1

Db 5 G 5

RESULT 28
AAV72347/c
ID AAV72347 standard; DNA: 5 BP.
XX

AC AAV72347;
XX

DT 28-JUL-1999 (first entry)
XX

DE US908745 primer #4.
XX

KM DNA sequencing; disease-associated allele; polyacrylamide matrix;
KM continuous/contiguous stacking hybridization technique; detection;
KW mutation; diagnosis; primer; ss.
XX

OS Synthetic.
XX

PN US908745-A.
XX

PD 01-JUN-1999.
XX

PF 16-JAN-1996; 96US-0587332.
XX

PR 16-JAN-1996; 96US-0587332.
XX

PA (UYCH-) UNIV CHICAGO.
XX

PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
PI Parinov SV, Yershov GM;
XX

DR MPI: 1999-347002/29.
XX

PT Detecting disease-associated alleles using continuous/contiguous
stacking hybridization as a diagnostic tool
XX

PS Example 1; Column 9; 16pp; English.
XX

CC This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.
XX

SO Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
I
Db 5 G 5

RESULT 29

AAV72348
ID AAV72348 standard; DNA: 5 BP.
XX

AC AAV72348;
XX

DT 28-JUL-1999 (first entry)
XX

DE US908745 primer #5.
XX

KM DNA sequencing; disease-associated allele; polyacrylamide matrix;
KM continuous/contiguous stacking hybridization technique; detection;
KW mutation; diagnosis; primer; ss.
XX

OS Synthetic.
XX

PN US908745-A.
XX

PD 01-JUN-1999.
XX

PF 16-JAN-1996; 96US-0587332.
XX

PR 16-JAN-1996; 96US-0587332.
XX

PA (UYCH-) UNIV CHICAGO.
XX

PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
PI Parinov SV, Yershov GM;
XX

DR MPI: 1999-347002/29.
XX

PT Detecting disease-associated alleles using continuous/contiguous
stacking hybridization as a diagnostic tool
XX

PS Example 1; Column 9; 16pp; English.
XX

CC This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.
XX

SO Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
I
Db 2 g 2

RESULT 30

AAV72348/c
ID AAV72348 standard; DNA: 5 BP.
XX

AC AAV72348;
XX

DT 28-JUL-1999 (first entry)
XX

DE US908745 primer #5.
XX

KM DNA sequencing; disease-associated allele; polyacrylamide matrix;
KM continuous/contiguous stacking hybridization technique; detection;
KW mutation; diagnosis; primer; ss.
XX

OS Synthetic.
XX

PN US908745-A.
XX

PD 01-JUN-1999.
XX

XX 16-JAN-1996; 960S-0587332.
 PF 16-JAN-1996; 960S-0587332.
 XX (UYCH-) UNIV CHICAGO.
 PA Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
 PI Parinov SV, Yershov GM;
 XX WPI: 1999-347002/29.
 DR
 XX
 PT Detecting disease-associated alleles using continuous/contiguous
 XX stacking hybridization as a diagnostic tool
 PS
 XX Example 1: Column 9; 16pp; English.
 CC This invention describes novel methods for sequencing and analysing DNA
 CC samples to detect disease-associated alleles, by continuous/contiguous
 CC stacking hybridization techniques (utilizing universal bases) with
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
 CC be used to detect multiple DNA base mutations which are specific for
 CC certain diseases. The methods of the invention provide accurate and
 CC efficient and sensitive methods for diagnosing disease by detecting
 CC multiple mutation sequences in patient DNA. The method require the
 CC minimum number of oligonucleotides and few stacking hybridization steps
 CC than prior art methods. The methods are also efficient enough to
 CC discriminate between perfect and imperfect duplexes. The methods also
 CC obviate the need for the fabrication and array placement of large numbers
 CC of immobilized oligomers.
 CC
 SQ Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 9 1
 Db 5 G 5

RESULT 31
 AAV72349/C
 ID AAV72349 standard; DNA: 5 BP.
 XX
 AC AAV72349;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE US5908745 primer #6.
 XX
 DE US5908745 primer #6.
 XX
 KW DNA sequencing; disease-associated allele; polyacrylamide matrix;
 KW continuous/contiguous stacking hybridization technique; detection;
 XX mutation; diagnosis; primer; ss.
 OS Synthetic.
 XX
 PA US5908745-A.
 PN
 XX
 PD 01-JUN-1999.
 XX
 PF 16-JAN-1996; 960S-0587332.
 XX
 PR 16-JAN-1996; 960S-0587332.
 XX
 PA (UYCH-) UNIV CHICAGO.
 XX
 PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
 PI Parinov SV, Yershov GM;
 XX WPI: 1999-347002/29.
 DR

XX
 PT Detecting disease-associated alleles using continuous/contiguous
 PT stacking hybridization as a diagnostic tool
 XX
 PS
 XX Example 1: Column 9; 16pp; English.
 CC This invention describes novel methods for sequencing and analysing DNA
 CC samples to detect disease-associated alleles, by continuous/contiguous
 CC stacking hybridization techniques (utilizing universal bases) with
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
 CC be used to detect multiple DNA base mutations which are specific for
 CC certain diseases. The methods of the invention provide accurate and
 CC efficient and sensitive methods for diagnosing disease by detecting
 CC multiple mutation sequences in patient DNA. The method require the
 CC minimum number of oligonucleotides and few stacking hybridization steps
 CC than prior art methods. The methods are also efficient enough to
 CC discriminate between perfect and imperfect duplexes. The methods also
 CC obviate the need for the fabrication and array placement of large numbers
 CC of immobilized oligomers.
 CC
 SQ Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 9 1
 Db 5 G 5

RESULT 32
 AAV72350/C
 ID AAV72350 standard; DNA: 5 BP.
 XX
 AC AAV72350;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE US5908745 primer #7.
 XX
 DE US5908745 primer #7.
 XX
 PN US5908745-A.
 XX
 PD 01-JUN-1999.
 XX
 PF 16-JAN-1996; 960S-0587332.
 XX
 PR 16-JAN-1996; 960S-0587332.
 XX
 PA (UYCH-) UNIV CHICAGO.
 XX
 PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
 PI Parinov SV, Yershov GM;
 XX WPI: 1999-347002/29.
 DR
 XX
 PT Detecting disease-associated alleles using continuous/contiguous
 PT stacking hybridization as a diagnostic tool
 XX
 PS
 XX Example 1: Column 9; 16pp; English.
 CC This invention describes novel methods for sequencing and analysing DNA
 CC samples to detect disease-associated alleles, by continuous/contiguous
 CC stacking hybridization techniques (utilizing universal bases) with
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
 CC be used to detect multiple DNA base mutations which are specific for

CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.

XX
SQ Sequence 5 BP; 3 A; 2 C; 0 G; 0 U; 0 other;

Query Match

Best Local Similarity 100.0%; Score 1; DB 20; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
DB 5 G 5

RESULT 33

AA56964
ID AAX56964 standard; DNA; 5 BP.

AC AAX56964;

DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
cell growth inhibitor; treatment; cancer; ras protein; ss.

OS Synthetic.

PN WO9922772-A1.

XX 14-MAY-1999.

PF 28-OCT-1998; 98WO-US22821.

PK 31-OCT-1997; 97US-0961469.

PA (ISIS-) ISIS PHARM INC.

PI Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;

PT Templin MV;

DR WP1; 1999-313181/26.

PT Liposome-encapsulated oligonucleotides useful for treating or
preventing cancers associated with ras gene activation

XX Example 1; Page 107; 120pp; English.

CC This invention describes novel compositions comprising oligonucleotides
CC (AAX56957-X57017), entrapped within liposomes, that hybridize
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
CC ras protein. The products of the invention have anticancer activity and
CC specifically bring about the antisense inhibition of ras genes or mRNA.
CC The products of the invention are used to modulate expression of a ras
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
CC growth and especially to treat or prevent cancers associated with
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
CC rate at which it is cleared from the blood when compared with
CC non-encapsulated material, and the oligonucleotides become distributed to
CC practically all parts of the body.

XX Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match

100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
DB 2 g 2

RESULT 34

AA56964/C
ID AAX56964 standard; DNA; 5 BP.

AC AAX56964;

DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
cell growth inhibitor; treatment; cancer; ras protein; ss.

OS Synthetic.

PN WO9922772-A1.

PD 14-MAY-1999.

PF 28-OCT-1998; 98WO-US22821.

PK 31-OCT-1997; 97US-0961469.

PA (ISIS-) ISIS PHARM INC.

PI Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;

PT Templin MV;

DR WP1; 1999-313181/26.

PT Liposome-encapsulated oligonucleotides useful for treating or
preventing cancers associated with ras gene activation

XX Example 1; Page 107; 120pp; English.

CC This invention describes novel compositions comprising oligonucleotides
CC (AAX56957-X57017), entrapped within liposomes, that hybridize
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
CC ras protein. The products of the invention have anticancer activity and
CC specifically bring about the antisense inhibition of ras genes or mRNA.
CC The products of the invention are used to modulate expression of a ras
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
CC growth and especially to treat or prevent cancers associated with
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
CC rate at which it is cleared from the blood when compared with
CC non-encapsulated material, and the oligonucleotides become distributed to
CC practically all parts of the body.

XX Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match

Best Local Similarity 100.0%; Score 1; DB 20; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
DB 4 G 4

RESULT 35

AA56964/C
ID AAX21608 standard; DNA; 5 BP.

AC AAX21608;

The invention relates to oligonucleotides, which target a nucleic acid encoding human N-ras, and are capable of inhibiting human N-ras expression. The antisense oligonucleotides form a pharmaceutical composition, which is useful for modulating the expression of human N-ras, inhibiting the proliferation of cancer cells, and preventing or treating conditions arising from the activation of a human N-ras oncogene. The oligonucleotides are also useful in diagnostics, therapeutics, and as research reagents and kits. The oligonucleotides enable the specific modulation of activated human N-ras expression, which is associated with tumour formation. Sequences AAX21601-619 represent antisense oligonucleotides targeted to mutant H-ras.

```

RESULT 37
AAA56981
ID AAA56981 standard; cDNA; 5 BP.
XX
AC AAA56981;
XX
DT 14-NOV-2000 (first entry)
XX
DE Human colon cancer cell cDNA sequence #109.
XX
KW Human; arbitrary primer; cDNA synthesis; contig sequence construction;
XX open reading frame; ORF; low stringency; cDNA sequencing; ss.
XX OS Homo sapiens.
XX
XX WO20031299-A2.
XX
XX 02-JUN-2000.
XX
XX PD
XX
XX PF 19-NOV-1999; 99WO-US27430.
XX
XX PR 20-NOV-1998; 98US-0196716.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Simpson AJG, Dias Neto E, Brentani RR;
XX DR
XX WPI: 2000-400100/34.
XX
XX Method for determining open reading frames of the genome of an organism
XX using primers at low stringency conditions, useful in the construction

```

PT of contigs or constructs of sequenced nucleic acid molecules -
 XX
 PS Example 6: Page 47; 113pp; English.
 XX

CC The present sequence is a cDNA sequence obtained using a method for
 CC determining open reading frames (ORFs) of the genome of an
 CC organism. An aliquot of mRNA from human colon cancer cells was mixed
 CC with a single, arbitrary primer, Moloney murine leukemia virus reverse
 CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
 CC incubated under low stringency conditions to yield single stranded
 CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
 CC than providing nucleotide sequence information from the non-coding
 CC terminl of nucleic acid molecules, the method provides information on
 CC the more interesting and relevant internal portions, such as ORFs. The
 CC method also permits the construction of contigs of sequenced nucleic
 CC acid molecules.
 XX

SQ Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 g 1
 1
 Db 3 g 3

RESULT 38

AA56981/c

ID AA56981 standard; cDNA; 5 BP.

XX

AC AA56981;

XX

DT 14-NOV-2000 (first entry)

XX

DE Human colon cancer cell cDNA sequence #109.

XX

KW Human: arbitrary primer; cDNA synthesis; contig sequence construction;

XX

OS open reading frame; ORF; low stringency; cDNA sequencing; ss.

XX

PN Homo sapiens.

XX

PD WO200031299-A2.

XX

PF 02-JUN-2000.

XX

PR 19-NOV-1999; 99MO-US27430.

XX

PR 20-NOV-1998; 98US-0196716.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Simpson AUG, Dias Neto E, Brentani RR;

XX

DR WPI: 2000-400100/34.

XX

PT Method for determining open reading frames of the genome of an organism

XX

PS of contigs or constructs of sequenced nucleic acid molecules -

XX

Example 6: Page 47; 113pp; English.

XX

CC The present sequence is a cDNA sequence obtained using a method for

CC

CC determining open reading frames (ORFs) of the genome of an

CC

CC organism. An aliquot of mRNA from human colon cancer cells was mixed

CC

CC with a single, arbitrary primer, Moloney murine leukemia virus reverse

CC

CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was

CC

CC incubated under low stringency conditions to yield single stranded

CC

CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather

CC

CC than providing nucleotide sequence information from the non-coding

CC terminl of nucleic acid molecules, the method provides information on

CC the more interesting and relevant internal portions, such as ORFs. The
 CC method also permits the construction of contigs of sequenced nucleic
 CC acid molecules.
 XX

SQ Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 g 1
 1
 Db 5 G 5

RESULT 39

AA293601

ID AA293601 standard; DNA; 5 BP.

XX

AC AA293601;

XX

DT 24-JUL-2000 (first entry)

XX

DE Transcription factor binding site of tobacco gene promoter sequence.

XX

KW Regulatory sequence; meristem; genetic engineering;

XX

KW gene expression; crop protection; transgenic plant; resistance;

XX

KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

XX

OS Synthetic.

XX

OS Nicotiana acuminata.

XX

PN WO200012713-A1.

XX

PD 09-MAR-2000.

XX

PF 26-AUG-1999; 99MO-AU00692.

XX

PR 26-AUG-1998; 98AU-0005498.

XX

PA (UYOU) UNIV QUEENSLAND.

XX

PI Mudge SR, Birch RG;

XX

DR WPI: 2000-237875/20.

XX

PT Meristem-expressible nucleic acid sequences, useful for producing

XX

PT transgenic plants with improved characteristics such as resistance to

XX

PS pathogens

XX

Example 9; Page 51; 102pp; English.

XX

CC Isolated regulatory sequences of plants that are operable in

XX

CC dividing cells, in particular the meristem cells of plants are useful

XX

CC in the genetic engineering of plants. The regulatory sequences can

XX

CC be used to control the expression of foreign genes placed under their

XX

CC control. Such methods are useful for producing transgenic plants with

XX

CC altered shape and/or size. The sequences are also useful for

XX

CC producing transgenic plants capable of rapid regeneration following

XX

CC harvest or plants having improved resistance to pathogens. This

XX

CC sequence has been shown to bind a factor involved in the activation

XX

CC times in the meristem regulatory sequence of Tobacco described in

CC

CC GENES50 record AA293567.

XX

SQ Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 5 g 5

RESULT 40

AA293601/c
ID AA293601 standard; DNA: 5 BP.

XX
AC AA293601;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.
XX
KW Regulatory sequence; meristem; genetic engineering;
KW gene expression; crop protection; transgenic plant; resistance;
KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

OS Synthetic.
OS Nicotiana acuminata.
XX
PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing
transgenic plants with improved characteristics such as resistance to
pathogens

PS Example 9; Page 51; 102pp; English.

XX Isolated regulatory sequences of plants that are operable in
dividing cells. In particular the meristem cells of plants are useful
in the genetic engineering of plants. The regulatory sequences can
be used to control the expression of foreign genes placed under their
control. Such methods are useful for producing transgenic plants with
altered shape and/or size. The sequences are also useful for
producing transgenic plants capable of rapid regeneration following
harvest or plants having improved resistance to pathogens. This
sequence has been shown to bind a factor involved in the activation
of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three
times in the meristem regulatory sequence of Tobacco described in
GENESQ record AA293567.

SO Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 4 G 4

RESULT 41

AA293602/c
ID AA293602 standard; DNA: 5 BP.

XX
AC AA293602;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

XX
KW Regulatory sequence; meristem; genetic engineering;
KW gene expression; crop protection; transgenic plant; resistance;
KW tobacco; transcription factor; NIT2; nitrate; ss.

OS Synthetic.
OS Nicotiana acuminata.

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing
transgenic plants with improved characteristics such as resistance to
pathogens

PS Example 9; Page 51; 102pp; English.

XX Isolated regulatory sequences of plants that are operable in
dividing cells. In particular the meristem cells of plants are useful
in the genetic engineering of plants. The regulatory sequences can
be used to control the expression of foreign genes placed under their
control. Such methods are useful for producing transgenic plants with
altered shape and/or size. The sequences are also useful for
producing transgenic plants capable of rapid regeneration following
harvest or plants having improved resistance to pathogens. This
sequence has been shown to regulate nitrate metabolism in the
fungus Neurospora crassa. It occurs multiple times in the meristem
regulatory sequence of Tobacco described in GENESQ record AA293567.

SO Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 4 G 4

RESULT 42

AA289330/c
ID AA289330 standard; DNA: 5 BP.

XX
AC AA289330;

DT 13-JUN-2000 (first entry)

DE Human UCP3 promoter fragment #10.

XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
fat metabolism; ss.

OS Homo sapiens.

PN DE19838837-A1.

PD 02-MAR-2000.

```

Query Match      100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 9 1
db 2 G 2

```

```

Query Match          100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches      1; Conservative      0; Indels      0; Gaps      0
Qy           1 g 1
              |
db           4 g 4

```

RESULT 44
 AA289332
 ID AA289332 standard; DNA; 5 BP.
 AC AA289332;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human UCP3 promoter fragment #12.
 XX
 KM UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
 KM fat metabolism; ss.
 OS Homo sapiens.
 OS
 PN DE19838837-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 27-AUG-1998; 98DE-1038837.
 XX
 PR 27-AUG-1998; 98DE-1038837.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Esterbauer H, Oberkofler H, Patsch W;
 DR WPI; 2000-272214/24.
 XX
 PT Recombinant fat and muscle tissue specific uncoupling protein 3
 PT promoters useful for identifying UCP3 modulators -
 XX
 PS Claim 31; Page 12; 38pp; German.
 XX
 CC This invention describes novel recombinant DNA molecules containing
 CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
 CC cells but not functional in muscle cells or vice versa. The recombinant
 CC DNA molecules are useful for transcription of genes and, with host cells,
 CC to test for substances that can influence transcription. They can also be
 CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
 CC metabolism and control of the promoter is useful in combating diseases
 CC with inappropriate fat tissue metabolism. This sequence represents a
 CC fragment of the human UCP-3 promoter which is used to illustrate the
 CC method of the invention.
 XX
 SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 Db 4 g 4

Search completed: July 15, 2002, 23:10:11
 Job time: 18429 sec

RESULT 45
 AA248433
 ID AA248433 standard; DNA: 5 BP.
 XX
 AC AA248433:
 XX
 DT 27-MAR-2000 (first entry)
 XX
 DE First DNA arm segment.
 XX
 KM Microorganism: virus; polymerase chain reaction; food; cosmetic;
 KM Clinical diagnostic; molecular beacon; PCR primer; ss.
 XX
 OS Synthetic.
 OS
 PN WO963112-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 18-MAY-1999; 99WO-US10940.
 XX
 PR 18-MAY-1998; 98US-0086025.
 PR 17-MAY-1999; 99US-0086025.
 XX
 PA (HUNT-) HUNT WESSON INC.
 XX
 PI Romick TL, Fraser MS;
 PI
 DR WPI: 2000-086985/07.
 XX
 PT Detection of microorganisms and viruses, for use in the food and
 PT cosmetic industries and for clinical diagnostics .
 XX
 PS Claim 51; Page 40; 63pp: English.
 XX
 CC The invention provides a novel in vitro method for the detection of
 CC microorganisms and viruses. The method comprises: (1) forming a
 CC polymerase chain reaction (PCR) mixture by combining a predetermined
 CC volume of a sample to be tested for the presence of a nucleic acid
 CC sequence comprising 5'-TGAAGC-3', known amounts of a first primer
 CC comprising 5'-GCTAAGCTCCCAAGT-3', and a second primer comprising
 CC 5'-AGAAGCTCTCTCAAC-3', and PCR reagents; (2) forming a PCR product by
 CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,
 CC to replicate and attain 0.25-1000nmug nucleotide product/mul mixture; (3)
 CC adding a probe containing DNA comprising 5'-GGTGGCTCTCTCAAGCACC-3' to
 CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
 CC the nucleic acid sequence, if present, and change the conformation of the
 CC probe; and (4) determining whether or not bacteria are present in the
 CC sample by detecting the conformational change of the probe, a
 CC conformational change indicating the presence of bacteria in the sample.
 CC The methods can be used for the detection of viruses and microorganisms,
 CC including bacteria, yeast, molds and protoista. They can be used in the
 CC food and cosmetic industry and in clinical diagnostics. Using the method
 CC it is not necessary to remove non-hybridized probe from the system.
 XX
 SQ Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:28:08 ; Search time 9532.94 seconds
(without alignments) 2.195 Million cell updates/sec

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Sequence: 1 g 1

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Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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1: gb-da: *
2: gb-hcg: *
3: gb-in: *
4: gb-om: *
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7: gb-ph: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
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C	7	100.0	2	6	AX092447	Sequence
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar

AX092441
Sequence 2 from Patent WO0116366.
AX092441
GI:13444536
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Kless, H.
Oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 2 08-MAR-2001
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar

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OY 1 g 1
1
db 2 G 2

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LOCUS AX092442
DEFINITION Sequence 3 from Patent WO0116366.
ACCESSION AX092442
VERSION AX092442.1 GI:13444537
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
(IL)

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source Location/Qualifiers

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db 2 G 2

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AX092444/c AX092444 2 bp DNA linear PAT 23-MAR-2001
LOCUS AX092444
DEFINITION Sequence 5 from Patent WO0116366.
ACCESSION AX092444
VERSION AX092444.1 GI:13444539
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
(IL)

unidentified.
unclassified.
1 (bases 1 to 2)
Kless,H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 5 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
FEATURES
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BASE COUNT 1 a 1 c 0 g 0 t
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
db 1 G 1

RESULT 4

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LOCUS AX092445
DEFINITION Sequence 6 from Patent WO0116366.
ACCESSION AX092445
VERSION AX092445.1 GI:13444540
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
(IL)

FEATURES

source Location/Qualifiers

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/note="synthetic oligonucleotide;"
BASE COUNT 0 a 2 c 0 g 0 t
ORIGIN

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OY 1 g 1
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db 2 G 2

RESULT 5

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LOCUS AX092446
DEFINITION Sequence 7 from Patent WO0116366.
ACCESSION AX092446
VERSION AX092446.1 GI:13444541
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
(IL)

unidentified.
unclassified.
1 (bases 1 to 2)
Kless,H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 7 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
FEATURES
source Location/Qualifiers

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RESULT 6
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LOCUS AX092446
DEFINITION Sequence 7 from Patent WO0116366.
ACCESSION AX092446
VERSION AX092446.1 GI:13444541
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
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BASE COUNT 0 a 1 c 1 g 0 t
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Db 1 c 1

RESULT 7
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LOCUS AX092447
DEFINITION Sequence 8 from Patent WO0116366.
ACCESSION AX092447
VERSION AX092447.1 GI:13444542
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
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OY 1 g 1
Db 1 c 1

Db 1 c 1

RESULT 8
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LOCUS AX092448
DEFINITION Sequence 9 from Patent WO0116366.
ACCESSION AX092448
VERSION AX092448.1 GI:13444543
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
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BASE COUNT 1 a 0 c 1 g 0 t
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 c 1

RESULT 9
AX092449 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092449
DEFINITION Sequence 10 from Patent WO0116366.
ACCESSION AX092449
VERSION AX092449.1 GI:13444544
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
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/note="synthetic oligonucleotide;"

BASE COUNT 0 a 1 c 1 g 0 t
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 c 1

RESULT 10
AX092449/c

LOCUS

DEFINITION Sequence 10 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AX092449.1 GI:13444544
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 10 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES

source

1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 1 c 1 g 0 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 2 G 2

RESULT 11
AX092450

LOCUS

DEFINITION Sequence 11 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AX092450.1 GI:13444545
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 11 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES

source

1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 0 c 2 g 0 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 1 G 1

RESULT 12
AX092451

LOCUS

DEFINITION Sequence 15 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

VERSION

AX092451.1 GI:13444549
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 12 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES

source

1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 0 c 2 g 0 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 1 G 1

DEFINITION Sequence 12 from Patent WO0116366.
ACCESSION AX092451
VERSION AX092451.1 GI:13444546
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 12 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES

source

1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 0 c 1 g 1 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 1 G 1

RESULT 13
AX092453/c

LOCUS

DEFINITION Sequence 14 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AX092453.1 GI:13444548
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 14 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES

source

1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 1 c 0 g 1 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 2 G 2

RESULT 14
AX092454

LOCUS

DEFINITION Sequence 15 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

VERSION

AX092454.1 GI:13444549
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 12 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES

source

1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 1 c 0 g 1 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 2 G 2

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

unclassified.
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 15 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
(IL)
Location/Qualifiers
1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 0 c 1 g 1 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 2 c 2

RESULT 15
AX092528/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

AX092528
Sequence 89 from Patent W00116366.
AX092528
AX092528.1 GI:13444623
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 89 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
(IL)
Location/Qualifiers
1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
1 a 1 c 0 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 1 c 1

RESULT 16
AX092529/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

AX092529
Sequence 90 from Patent W00116366.
AX092529
AX092529.1 GI:13444624
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 90 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
(IL)
Location/Qualifiers
1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
1 a 1 c 0 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 1 c 1

unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 90 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
(IL)
Location/Qualifiers
1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 2 c 0 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 2 c 2

RESULT 17
AX092530
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

AX092530
Sequence 91 from Patent W00116366.
AX092530
AX092530.1 GI:13444625
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 91 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
(IL)
Location/Qualifiers
1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
1 a 0 c 1 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 2 c 2

RESULT 18
AX092538
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

AX092538
Sequence 99 from Patent W00116366.
AX092538
AX092538.1 GI:13444633
unclassified.
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 99 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
(IL)
Location/Qualifiers
1..2
/organism="unclassified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
1 a 0 c 1 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 2 c 2

TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 99-08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 19
AX175286
LOCUS AX175286 2 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 50 from Patent WO0144465.
ACCESSION AX175286
VERSION AX175286.1 GI:14598654
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.

REFERENCE
AUTHORS Phillips,N.C. and Pillon,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 50-21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source Location/Qualifiers
1..2
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 20
AX175287
LOCUS AX175287 2 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 51 from Patent WO0144465.
ACCESSION AX175287
VERSION AX175287.1 GI:14598655
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
1 (bases 1 to 2)
Phillips,N.C. and Pillon,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 51-21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source Location/Qualifiers
1..2
/organism="synthetic construct"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 g 2

RESULT 21
BD009609/c
LOCUS BD009609 2 bp DNA linear PAT 31-JAN-2002
DEFINITION Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples.
ACCESSION BD009609
VERSION BD009609.1 GI:18637982
KEYWORDS JP 2001502536-A/201.
SOURCE
ORGANISM
unidentified.
unclassified.
1 (bases 1 to 2)
Quint,W. and Doorn,L.J.V.
REFERENCE Probes, methods and kits for detection and typing of Helicobacter
AUTHORS pylori nucleic acids in biological samples
TITLE Patent: JP 2001502536-A 201-27-FEB-2001;
JOURNAL INNOGENETICS NV,DDL BV
COMMENT
OS Unidentified
PN JP 2001502536-A/201
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN
PC C1201/68,C07K14/205,C12N15/11
CC
FH
FT Key source Location/Qualifiers
1..2
/organism="unidentified".
Location/Qualifiers

FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 1 c 0 g 0 t 1 others
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 g 2

RESULT 22
CNS01C99
LOCUS CNS01C99 2 bp mRNA linear PLN 02-SEP-1999
DEFINITION Botrytis cinerea strain T4 CDNA library under conditions of nitrogen deprivation.
ACCESSION AL115237
VERSION AL115237.1 GI:5829686
KEYWORDS cdna library; nitrogen deprivation.
SOURCE Botryotinia fuckeliana.
ORGANISM Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE Biton,F., Lewis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
AUTHORS 1 (bases 1 to 2)

TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
REFERENCE 2 (bases 1 to 2)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 Evry cedex - FRANCE (E-mail : sequefr@genoscope.cns.fr)
COMMENT The cDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSIT
vector.

FEATURES
source
1..2
/organism="Botryotinia fuckeliana"
/strain="74"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W04F091"

BASE COUNT
0 a 0 c 1 g 1 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 8; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 23
AC079635
LOCUS Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC079635
AC079635.3 GI:14647267
VERSION HTG: HTGS-PHASE0.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3)
McCombie,W.R., Baker,J.P., Bahret,A., Yang,C., Ballia,V.,
Dedhia,N.N., de la Bastide,M., Kuit,K., King,L., Kirchoff,K.A.,
Miller,B., Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.R.,
Rodriguez,S., Santos,L., Shah,R.S., Spiegel,L.A., Palmer,L.,
Vil,M.D. and Zutavern,F.
Mouse Genomic Sequence
Unpublished
2 (bases 1 to 3)
McCombie,W.R.
Direct Submission
Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA
On Jul 10, 2001 this sequence version replaced gi:14595773.
* NOTE: This record contains 1 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
3: contig of 3 bp in length.
This entry has been temporarily removed. An update for RP23-152L20

FEATURES Will be submitted as soon as it becomes available.
source
1..3
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-152L20"

BASE COUNT
1 a 0 c 1 g 1 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 g 3

RESULT 24
CHKNCAMC5
LOCUS Chicken cardiac neural cell adhesion (NCAM) gene, exon 12D.
DEFINITION M23994 J04140
ACCESSION M23994 J04140
VERSION M23994.1 GI:212442
KEYWORDS 5 of 6
SEGMENT
SOURCE chicken.
ORGANISM Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 3)
Prediger,E.A., Hoffman,S., Edelman,G.M. and Cunningham,B.A.
Four exons encode a 93-base-pair insert in three neural cell
adhesion molecule mRNAs specific for chicken heart and skeletal
muscle.
Proc. Natl. Acad. Sci. U.S.A. 85 (24), 9616-9620 (1988)
JOURNAL MEDLINE
PUBMED 3200847
COMMENT Exon 12D represents a very small exon.
FEATURES
source
1..3
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pPC101B"
/tissue-type="Cardiac muscle"
/dev_stage="day 10 embryo"
1..3
/gene="NACW"
/number=12

BASE COUNT
2 a 0 c 1 g 0 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 1; DB 5; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 g 3

RESULT 25
A97991
LOCUS A97991
DEFINITION Sequence 21 from Patent W09914366.
ACCESSION A97991
VERSION A97991.1 GI:6781229
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

unclassified.

REFERENCE 1 (bases 1 to 3)

AUTHORS Pongers-Willems, M.J. and Van, D.J.
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL Patent: WO 914366-A 21 25-MAR-1999;
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)FEATURES
source Location/Qualifiers

1..3

/organism="unidentified"

BASE COUNT 0 a 1 c 2 g 0 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 2 g 2

RESULT 26

A97991/c

LOCUS A97991

DEFINITION Sequence 21 from Patent WO914366.

ACCESSION A97991

VERSION A97991.1 GI:6781229

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 3)

AUTHORS Pongers-Willems, M.J. and Van, D.J.

TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL Patent: WO 914366-A 21 25-MAR-1999;
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)

FEATURES

source

1..3

/organism="unidentified"

BASE COUNT 0 a 1 c 2 g 0 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 1 g 1

RESULT 27

AX092457/c

LOCUS AX092457

DEFINITION Sequence 18 from Patent WO0116366.

ACCESSION AX092457

VERSION AX092457.1 GI:13444552

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 3)

AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 18 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar

FEATURES

source

Location/Qualifiers

source

1..3

/organism="unidentified"

/db_xref="taxon:32644"

/note="synthetic oligonucleotide;"

BASE COUNT 2 a 1 c 0 g 0 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 3 g 3

RESULT 28

AX092458

LOCUS AX092458

DEFINITION Sequence 19 from Patent WO0116366.

ACCESSION AX092458

VERSION AX092458.1 GI:13444553

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 3)

AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 19 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar

FEATURES

source

1..3

/organism="unidentified"

/db_xref="taxon:32644"

/note="synthetic oligonucleotide;"

BASE COUNT 2 a 0 c 1 g 0 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 3 g 3

RESULT 29

AX092460/c

LOCUS AX092460

DEFINITION Sequence 21 from Patent WO0116366.

ACCESSION AX092460

VERSION AX092460.1 GI:13444555

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 3)

AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 21 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar

FEATURES

source

Location/Qualifiers

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/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
1
Db 2 G 2

RESULT 30
AX092461/c AX092461 3 bp DNA linear PAT 21-MAR-2001
LOCUS
DEFINITION Sequence 22 from Patent WO0116366.
ACCESSION AX092461
VERSION AX092461.1 GI:13444556
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 3)
TITLE Kless,H.
JOURNAL Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 22 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
1
Db 3 G 3

RESULT 31
AX092462 AX092462 3 bp DNA linear PAT 21-MAR-2001
LOCUS
DEFINITION Sequence 23 from Patent WO0116366.
ACCESSION AX092462
VERSION AX092462.1 GI:13444557
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 3)
TITLE Kless,H.
JOURNAL Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 23 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
1
Db 3 G 3

RESULT 32
AX092462/c AX092462 3 bp DNA linear PAT 21-MAR-2001
LOCUS
DEFINITION Sequence 23 from Patent WO0116366.
ACCESSION AX092462
VERSION AX092462.1 GI:13444557
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 3)
TITLE Kless,H.
JOURNAL Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 23 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
1
Db 2 G 2

RESULT 33
AX092463/c AX092463 3 bp DNA linear PAT 21-MAR-2001
LOCUS
DEFINITION Sequence 24 from Patent WO0116366.
ACCESSION AX092463
VERSION AX092463.1 GI:13444558
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 3)
TITLE Kless,H.
JOURNAL Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 24 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 2 G 2

RESULT 34
LOCUS AX092464 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 25 from Patent WO0116366.
ACCESSION AX092464
VERSION AX092464.1 GI:13444559
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE Kless,H.
AUTHORS 1 (bases 1 to 3)
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 25 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar
(IL)

FEATURES
source 1..3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 2 a 0 c 1 g 0 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 2 G 2

RESULT 35
LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE Kless,H.
AUTHORS 1 (bases 1 to 3)
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 26 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar
(IL)

FEATURES
source 1..3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 36
LOCUS AX092465/c 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE Kless,H.
AUTHORS 1 (bases 1 to 3)
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 26 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar
(IL)

FEATURES
source 1..3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 3 G 3

RESULT 37
LOCUS AX092466 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 27 from Patent WO0116366.
ACCESSION AX092466
VERSION AX092466.1 GI:13444561
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE Kless,H.
AUTHORS 1 (bases 1 to 3)
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 27 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar
(IL)

FEATURES
source 1..3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 2 g 0 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 2 G 2

RESULT 38
AX092467
LOCUS AX092467 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 28 from Patent WO0116366.
ACCESSION AX092467
VERSION AX092467.1 GI:13444562
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
1
Db 2 c 2

RESULT 39
AX092469/C
LOCUS AX092469 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 30 from Patent WO0116366.
ACCESSION AX092469
VERSION AX092469.1 GI:13444564
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
1
Db 2 c 2

RESULT 40
AX092470
LOCUS AX092470 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 31 from Patent WO0116366.
ACCESSION AX092470
VERSION AX092470.1 GI:13444565
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
1
Db 1 c 1

RESULT 41
AX092472/C
LOCUS AX092472 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 33 from Patent WO0116366.
ACCESSION AX092472
VERSION AX092472.1 GI:13444567
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
1
Db 1 c 1

RESULT 42
AX092473/C
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 34 from Patent WO0116366.
QY 1 g 1
1
Db 1 c 1

```

SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   unclassified.
AUTHORS     1 (bases 1 to 3)
TITLE       Kless,H.
JOURNAL      Template-dependent nucleic acid polymerization using
              oligonucleotide triphosphates building blocks
              Patent: WO 0116366-A 35 08-MAR-2001;
              YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
              (IL)
FEATURES
  source     Location/Qualifiers
              1..3
              /organism="unidentified"
              /db_xref="taxon:32644"
              /note="synthetic oligonucleotide;"
BASE COUNT  1 a          1 g          0 t
ORIGIN

```

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 1 G 1

```

RESULT	45				
AX092475/c					
LOCUS					
AX092475					
DEFINITION	Sequence	36 bp	DNA	linear	PAT 21-MAR-2001
ACCESSION	AX092475				
VERSION	AX092475.1				
KEYWORDS	GI:13444570				
SOURCE					
ORGANISM	unidentified.				
REFERENCE	unclassified.				
AUTHORS	1 (bases 1 to 3)				
TITLE	Kless,H.				
JOURNAL	Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks				
	PATENT: WO 0116366-A 36 08-MAR-2001;				
	VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)				
FEATURES					
source	1..3				
	Location/Qualifiers				
	/organism="unidentified"				
	/db_xref="taxon:32644"				
	/note="synthetic oligonucleotide;"				
BASE COUNT	1 a 1 c 0 g 1 t				
ORIGIN					

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Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
   | |
Db 1 g 1

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Search completed: July 15, 2002, 23:28:08
Job time: 24541 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 20:07:28 ; Search time 7067.1 Seconds
(without alignments)
899.530 Million cell updates/sec

Title: US-09-375-248-1_COPY_3044_3514
Perfect score: 471
Sequence: 1 ctgaccatggaagatctgt.....gacctgcattctcgagctg 471

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST: *
1: em_estha: *
2: em_esthum: *
3: em_estlin: *
4: em_estlun: *
5: em_estlov: *
6: em_estlpl: *
7: em_estro: *
8: em_hlc: *
9: *
10: gb_estl: *
11: gb_estl2: *
12: gb_hlc: *
13: em_gss_hum: *
14: em_gss_luv: *
15: em_gss_pln: *
16: em_gss_vrt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143	30.4	344	9	AA223868 zrl10h12.r
2	67	14.2	687	10	BE281514 601155083
3	54	11.5	920	10	BE778623 601466167
4	27	5.7	189	10	BC815223 dac02f10.
5	27	5.7	514	10	BC656884 df25411.y
6	26	5.5	525	9	AA637964 vrl30a02.r
7	26	5.5	542	9	AA911950 wr98e03.y
8	26	5.5	589	12	AZ645762 1M0511E24
9	26	5.5	748	10	BG518797 602578390
10	26	5.5	763	10	BG518797 602578390
11	26	5.5	789	10	B1118214 602920679
12	26	5.5	827	9	A1746873 ul108e07.y
13	26	5.5	846	10	BE279830 601157156
14	26	5.5	869	10	BG870441 602791353
15	26	5.5	876	10	BG932284 602825245
16	26	5.5	916	10	BF780935 602105450
17	26	5.5	1002	10	BF140383 601787895

18	25	5.3	722	10	BF320636
19	24	5.1	546	9	BE030526
20	23	4.9	357	9	A1556371
21	23	4.9	409	12	A0136157
22	23	4.9	455	9	AA709653 vva1f05.r
23	23	4.9	461	9	A1092636 q35d08.x
24	23	4.9	498	9	AL039890
25	23	4.9	604	10	BF523018
26	23	4.9	1003	12	CNS04372
27	23	4.9	1099	12	CNS03518
28	22	4.7	658	9	AL642415
29	22	4.7	743	10	BF1556970
30	22	4.7	793	10	BF136721
31	22	4.7	834	10	B1686934
32	22	4.7	888	12	CNS04EJU
33	22	4.7	903	12	CNS02ZER
34	22	4.7	967	12	CNS02YAK
35	22	4.7	978	12	CNS025AS
36	22	4.7	1023	12	CNS01UBA
37	22	4.7	3397	11	BC013342
38	21	4.5	359	9	AA895295
39	21	4.5	458	10	BF147285
40	21	4.5	711	12	AG094291
41	21	4.5	845	10	B111962
42	21	4.5	945	10	BF119392
43	21	4.5	1019	10	B1153717
44	21	4.5	2564	11	BC018230
45	20	4.2	253	9	AU129676

ALIGNMENTS

RESULT 1
LOCUS AA223868
DEFINITION zrl10h12.r1 Stragatene NT2 neuronal precursor 937230 Homo sapiens
CDNA clone IMAGE:651143 5' similar to gb:X68203 TYROSINE-PROTEIN
KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AA223868
VERSION AA223868.1 GI:1844453
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theisling, B.,
White, Y., Wyllie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Willson RK

TITLE JOURNAL COMMENT
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu

FEATURES
SOURCE This clone is available royalty-free through LUNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1275 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 228.
Location/Qualifiers
1..344
/organism="Homo sapiens"
/db_xref="GDB:5588193"
/db_xref="Laxson:9606"
/clone="IMAGE:651143"
/clone_lib="Stragatene NT2 neuronal precursor 937230"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"

```
/lab_host="SOLR (kanamycin resistant)"
/Note="Organ: Brain; Vector: pBluescript SK-; Site:1:
ECORI; Site:2: XhoI; Cloned unidirectionally. Primer:
0.190 dt. Uninduced, exponentially growing neuroepithelial
cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'."
BASE COUNT      65 a      92 c      115 g      66 t      6 others
ORIGIN

Query Match      30.4%; Score 143; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.3e-62;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 ttgattgccccctgaagacatcttcgacaaagtgtacaccagcagatgagtgatcgc 273
Db 1 tgcattgccccctgaagacatcttcgacaaagtgtacaccagcagatgagtgatcgc 60
QY 274 ttgggggtgctctcttgagatctctctctggggggcctcccgatccctgggggtcag 333
Db 61 ttgctgctctctctgagatctctctctggggggcctcccgatccctgggggtcag 120
QY 334 atcaatgaagatctgcagcagc 356
Db 121 atcaatgaagatctgcagcagc 143

RESULT 2
BE281514 687 bp mRNA linear EST 13-JUL-2000
LOCUS 601155083f1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138453 5'
DEFINITION mRNA sequence.
ACCESSION BE281514
VERSION BE281514.1 GI:9156534
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM103 row: f column: 22
High quality sequence stop: 590.
location/Qualifiers
1..687
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3138453"
/clone_1lb="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: Placenta; Vector: pOT87; Site:1: XhoI;
Site:2: EcorI; cDNA made by oligo-dt priming.
Directionally cloned into EcorI/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
BASE COUNT      167 a      183 c      214 g      123 t
ORIGIN

Query Match      14.2%; Score 67; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 3.4e-23;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 catacgcgcatactatcgaactcgtgcgcggaagcccaaggagagactcattc 464
Db 1 CATAGCCGCATCATGCTGACTGCTGCTGCGAGACCCCAAGCGACACCTGCATCTC 60
QY 465 ggaagctg 471
Db 61 GGAGCTG 67

RESULT 3
BE778623 920 bp mRNA linear EST 20-OCT-2000
LOCUS 601466167f1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869200 5'
DEFINITION mRNA sequence.
ACCESSION BE778623
VERSION BE778623.1 GI:10199821
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9618 row: f column: 17
High quality sequence stop: 716.
location/Qualifiers
1..920
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3869200"
/clone_1lb="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: eye; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
```

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BASE COUNT      236 a      240 c      268 g      176 t
ORIGIN

Query Match      11.5%; Score 54; DB 10; Length 920;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 atgcgaactctgtgcgagaccgaagcgagaccgtgacatctcggagctg 471
Db 1 ATGCTGAAGCTCTGCTGCGAGACCCCAAGCGACACCTGCATCTCGAGCTG 54

RESULT 4
BG815223 189 bp mRNA linear EST 22-MAY-2001
LOCUS gac02f10.y1 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4405795
DEFINITION 5' similar to TR-091897 Q91897 FIBROBLAST GROWTH FACTOR RECEPTOR
PRECURSOR. ;, mRNA sequence.
ACCESSION BG815223
```

```

VERSION      BG615223.1  GI:14186203
KEYWORDS     EST.
SOURCE       African clawed frog.
ORGANISM     Xenopus laevis
REFERENCE    Amphibia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Xenopodinae; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
              Xenopodinae; Xenopus.
              1 (bases 1 to 189)
              Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
              Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
              Waterston,R. and Wilson,R.
              Washu Xenopus EST project, 1999
              Unpublished (1999)
TITLE        JOURNAL
COMMENT      Contact: Sandy Clifton, Ph.D.
              Washu Xenopus EST project, 1999
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watsn.wustl.edu
              Library constructed by Life Technologies. DNA sequencing by:
              Washington University Genome Sequencing Center
              Clone distribution: Xenopus clones from this library are available
              through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov.
              Location/Qualifiers
                1..189
                /organism="Xenopus laevis"
                /db_xref="taxon:8355"
                /clone_image="4405795"
                /clone_lib="NICHD XCC Emb2"
                /tissue_type="embryo, stage 17/19"
                /lab_host="DH10B (phage-resistant)"
                /note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI;
                Cloned unidirectionally. Primer: Oligo dT. Average insert
                size 2.1 kb. Constructed by Life Technologies."
                size 2..189
                49 a 48 c 50 g 42 t

BASE COUNT
ORIGIN

Query Match      5.7% Score 27; DB 10; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 aaagtcacccacagagacctgctgc 95
|||||
DB 125 AAAGTCATCCACAGACCTGCTGC 151

RESULT 5
BG656884 514 bp mRNA linear EST 26-APR-2001
LOCUS     d125g11.y1 Wellcome CRC PRN3 SL10 5 Xenopus laevis cDNA clone
DEFINITION IMAGE:3558357 5' similar to TR:091897 091897 FIBROBLAST GROWTH
ACCESSION BG656884
VERSION    BG656884.1 GI:13796416
KEYWORDS   EST.
SOURCE     African clawed frog.
ORGANISM   Xenopus laevis
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
              Xenopodinae; Xenopus.
              1 (bases 1 to 514)
              Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
              Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
              Waterston,R. and Wilson,R.
              Washu Xenopus EST project, 1999
              Unpublished (1999)
TITLE      JOURNAL
COMMENT    Contact: Sandy Clifton, Ph.D.
              Washu Xenopus EST project, 1999

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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watsn.wustl.edu
Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.
Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington
University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 506.
Location/Qualifiers
  1..514
  /organism="Xenopus laevis"
  /db_xref="taxon:8355"
  /clone_image="3558357"
  /clone_lib="Wellcome CRC PRN3 SL10 5"
  /tissue_type="embryo, stage 10.5"
  /lab_host="DH10B (phage-resistant)"
  /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
  were oligo-dT primed and directionally cloned. Staging
  according to Neukoop and Faber. Library was constructed
  by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon
  (Wellcome/CRC Institute)."
  size 1..514
  148 a 110 c 141 g 114 t 1 others

BASE COUNT
ORIGIN

Query Match      5.7% Score 27; DB 10; Length 514;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 aaagtcacccacagagacctgctgc 95
|||||
DB 444 AAAGTCATCCACAGACCTGCTGC 470

RESULT 6
AA637964 525 bp mRNA linear EST 22-OCT-1997
LOCUS     vt30a02.r1 Barstead mouse myotubes MRLB5 Mus musculus cDNA clone
DEFINITION IMAGE:1122122 5' similar to gb:M44489 EXTRACELLULAR
ACCESSION AA637964
VERSION    AA637964.1 GI:2561552
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
              1 (bases 1 to 525)
              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
              Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
              Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
              Waterston,R.
              The Washu-HMI Mouse EST Project
              Unpublished (1996)
              Contact: Maria M/Mouse EST Project
              Washu-HMI Mouse EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: mouseest@watsn.wustl.edu
              This clone is available royalty-free through LLNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:611458
              Seg primer: -28m13 rev2 ET from Amersham
              High quality sequence stop: 313.
              Location/Qualifiers

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1. .525

```

/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:112212"
/clone_1b="Parsleed mouse myotubes MPLR85
/cell_line="C2C12"
/lab_host="DH10B"

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143 a	125 c	115 g	142 t
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Query Match	5.58;	Score 26;	DB 9;	Length 525;
Best Local Similarity	100.08;	Pred. No. 0.023;		
Matches	26;	Conservative 0.	Mismatches 0.	

5' - ATGACATTGGCCCTTGGCCG 257

RESULT	7	
LOCUS	AW911950	
DEFINITION	AW911950	542 bp mRNA
ACCESSION	U969603.1	NCI CGAP Mam6 Mus musculus cDNA clone IMAGE:3157468.5,
VERSION	similar to gb:X58712	Mouse MAPK mRNA for mitogen-activated protein kinase (MUSE).; mRNA sequence.
KEYWORDS	AW911950	
SOURCE	AW911950.1	GI:8077468
ORGANISM	EST.	
	Mus musculus	

Unpublished (1997)
Other_ESTs: ur89e03.x1

Email: cgabbs-remail.nih.gov
Tissue procurement: Jeffrey Green M.D.
cDNA library preparation: Life Technologies, Inc.
cDNA library arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
image.llnl.gov/image/html/resources.shtml

Seq primer: -40RP from Gibco
High quality sequence stop: 423
Location/Qualifiers
1. .542

```

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="IMAGE:3157468"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"

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/dev_stage="5 months"
/lab_host="DH10B"
/site_1:Organ: mammary: Vector: PCMW-SPORT6: Site:1: SalI
/site_2: NotI: Cloned unidirectionally. Primer: oligo dT
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH
150 a 133 c 113 g 145 t 1 others
BASE COUNT
ORIGIN

```

	Query Match	5.5%;	Score 26;	DB 9;	Length 542;
	Best Local Similarity	100.0%;	Pred. NO. 0.023;		
	Matches	26; Conservative	0; Mismatches	0; Indels	0;
Oy	130	aagatctgtagcttggtgcctgccga	155		
Db	98	AAGATCTGTGACTTGGCCTTGCCGC	123		

RESULT	8	
AZ645762/c		
LOCUS		
DEFINITION	AZ645762	589 bp DNA
	IM051IE24F Mouse 10kb plasmid UUGCJM library Mus musculus genomic	linear GSS 14-DEC-2000
ACCESSION	AZ645762	
VERSION	AZ645762.1	G1:I1775570
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 58)	Dunn, D., Aoyagi, A., Islam, H., Longacre, S., Mammad, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss

Location/Qualifiers
1. .589

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08C1M0511E2"
 /clone_lib="Mouse 10kb plasmid U08C1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD246; Purified genomic DNA from M.
 musculus C57BL/6J male; was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired at constant velocity. The sheared DNA
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 133 a 149 c 161 g 146 t

ORIGIN

Query Match 5.5%: Score 26; DB 12; Length 589;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 cccagagaccgtgctgcgcgaacat 104
|||||
Db 257 CACAGACACCTGCTCGGACACAT 232

RESULT 9
BC518797 748 bp mRNA linear EST 02-APR-2001
LOCUS 602578330F1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:3491663 5',
DEFINITION mRNA sequence.
ACCESSION BC518797
VERSION BC518797.1 GI:13514016
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 748)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8536 row: c column: 24
High quality sequence stop: 735.

FEATURES
Source Location/Qualifiers
1..748

/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:3491663"
/clone_1ib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
/lab_host="DH10B"
/note="Organ: lung; Vector: PCMV-SPORT6; Site:1; Salt: 1M; Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 215 a 180 c 156 g 197 t

ORIGIN

Query Match 5.5%: Score 26; DB 10; Length 748;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtacttgctgcgcg 155
|||||
Db 185 AACATCTGTACTTTGCCCTTCCCG 210

RESULT 10
B1158214 763 bp mRNA linear EST 26-JUN-2001
LOCUS 602899921F1 NCI_CGAP_Mam3 Mus musculus CDNA clone IMAGE:5029733 5',
DEFINITION mRNA sequence.
ACCESSION B1158214
VERSION B1158214.1 GI:14563147
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 763)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11083 row: j column: 06
High quality sequence stop: 761.

FEATURES
Source Location/Qualifiers
1..763

/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:5029733"
/clone_1ib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site:1; Salt: 1M; Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 222 a 179 c 159 g 203 t

ORIGIN

Query Match 5.5%: Score 26; DB 10; Length 763;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtacttgctgcgcg 155
|||||
Db 200 AACATCTGTACTTTGCCCTTCCCG 225

RESULT 11
B1158214 789 bp mRNA linear EST 05-JUL-2001
LOCUS 602920679F1 NIH_CGAP_Mam3 Mus musculus CDNA clone IMAGE:5060946 5',
DEFINITION mRNA sequence.
ACCESSION B1158214
VERSION B1158214.1 GI:14618215
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 789)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1164 row: n column: 19
High quality sequence start: 3
High quality sequence stop: 672.
Location/Qualifiers
1. 789
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_image="5060946"
/clone_lib="NIH_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert 2 kb. Library constructed by Life
Technologies, catalog #12017-018. Investigators providing
samples: Lochar Hennighausen/Chu-Xia Deng, NIH Reference
(1999). Note: this is a NCI-CGAP Library."
BASE COUNT 221 a 187 c 176 g 205 t
ORIGIN

Query Match 5.5%: Score 26; DB 10; Length 789;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgctgctgcgcg 155
Db 33 AAGATCTGTGACTTGGCTGCCGCCG 58
|||||

RESULT 12 827 bp mRNA linear EST 22-JUN-1999
A1746873 u108e07.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
LOCUS IMAGE:2076228 5' similar to gb:X58712 Mouse MAPK mRNA for
DEFINITION mitogen-activated protein kinase (MOUSE);, mRNA sequence.
A1746873
ACCESSION A1746873.1 GI:5125137
KEYWORDS EST.
VERSION house mouse.
KEYWORDS Mus musculus
SOURCE house mouse.
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 827)
Marrero, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterson, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
TITLE Other-ESTs: u108e07.x1
JOURNAL Contact: Maira M/WashU-NCI Mouse EST Project 1999
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:994664
Seq primer: custom primer used
High quality sequence stop: 510.
Location/Qualifiers

FEATURES

source

1. 827
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_image="2076228"
/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
/note="Vector: pME18-FL3; Site: 1: DraIII (CACTGCTG);
Site: 2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGCGCCCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTGGCTCACTG], digested and cloned into distinct DraIII
sites of the pME18-FL3 vector (5' site CACTGCTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTTAAGCTGCG and 3' end primer
CGACTGCACTGACGACGA."
BASE COUNT 199 a 226 c 223 g 179 t
ORIGIN

Query Match 5.5%: Score 26; DB 9; Length 827;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgctgctgcgcg 155
Db 698 AAGATCTGTGACTTGGCTGCCGCCG 723
|||||

RESULT 13 846 bp mRNA linear EST 13-JUL-2000
BE279830 601157156F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3140604 5',
LOCUS mRNA sequence.
DEFINITION BE279830.1 GI:9154825
ACCESSION BE279830
KEYWORDS EST.
VERSION human.
KEYWORDS Homo sapiens
SOURCE human.
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 846)
NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI08 row: p column: 13
High quality sequence stop: 85.
Location/Qualifiers
1. 846
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3140604"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pORF7; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAC(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by

FEATURES

source

Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 149 a 263 c 200 g 233 t 1 others

ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 846;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 436 ggaagccccaagggcgagacgtcattc 461
|||||
Db 32 GGACACCCCAAGCGACGACCTGCATT 57

RESULT 14
BC870441 869 bp mRNA linear EST 29-MAY-2001
LOCUS 602791353F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4922605 5',
DEFINITION mRNA sequence.
ACCESSION BC870441
VERSION BC870441 GI:14220981
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 869)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10842 row: 1 column: 14
High quality sequence stop: 709.

FEATURES
source Location/Qualifiers
1..869

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4922605"
/lab_host="NCI_CGAP_SG2"
/note="Organ: salivary gland; Vector: PCWV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 248 a 229 c 184 g 208 t
ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 869;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgagcctgcgcg 155
|||||
Db 482 AAGATCTGTGACTTTGGCTTGCCTGCCG 507

RESULT 15
BG923284 876 bp mRNA linear EST 05-JUN-2001
LOCUS 602825245F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4954067 5',
DEFINITION mRNA sequence.

ACCESSION BG923284
VERSION BG923284.1 GI:14303760
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 876)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10914 row: 1 column: 12
High quality sequence stop: 716.

FEATURES
source Location/Qualifiers
1..876

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4954067"
/lab_host="NCI_CGAP_Mam6"
/sex="female; virgin"
/tissue="infiltrating ductal carcinoma"
/dev_stage="5 months"
/note="Organ: mammary; Vector: PCWV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 219 a 250 c 224 g 183 t
ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 876;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgagcctgcgcg 155
|||||
Db 583 AAGATCTGTGACTTTGGCTTGCCTGCCG 608

RESULT 16
BF780935 916 bp mRNA linear EST 12-JAN-2001
LOCUS 602105450F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223556
DEFINITION 5', mRNA sequence.
ACCESSION BF780935
VERSION BF780935.1 GI:12085968
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE Mammalia: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 916)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9812 row: C Column: 13
 High quality sequence stop: 677.
 Location/Qualifiers
 1..916

FEATURES
 source
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4223556"
 /lab_host="NCI_CGAP_Kid14"
 /note="Organ: Kidney; Vector: pCMV-SPORT6; Site:1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.75 kb. Constructed by Life
 Technologies. Note: this is a NCI-CGAP library. 1"
 BASE COUNT 238 a 228 c 215 g 235 t
 ORIGIN

Query Match 5.3%; Score 26; DB 10; Length 916;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgacttgccctgccc 155
 |||||||||||||||||||||
 Db 158 AAGATCTGACTTTGGCCTTGCCG 183

RESULT 17
 BF140383 1002 bp mRNA linear EST 24-OCT-2000
 LOCUS 601787895F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015703 5',
 DEFINITION mRNA sequence.
 VERSION BF140383.1 GI:10979423
 ACCESSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgc.nci.nih.gov/
 1 (bases 1 to 1002)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9261 row: n column: 24
 High quality sequence start: 3
 High quality sequence stop: 556.
 Location/Qualifiers
 1..1002

FEATURES
 source
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:4015703"
 /lab_host="NCI_CGAP_Lu30"
 /clone="IMAGE:4015703"
 /lab_host="NCI_CGAP_Lu30"
 /note="Organ: Lung; Vector: pCMV-SPORT6; Site:1: NotI;
 Site_2: SalI; Transgenic model MMTV-1, expression driven by
 MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
 dt. Library constructed by Life Technologies.
 Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 287 a 245 c 231 g 239 t
 ORIGIN

Query Match 5.3%; Score 26; DB 10; Length 1002;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgacttgccctgccc 155
 |||||||||||||||||||||
 Db 79 AAGATCTGACTTTGGCCTTGCCG 104

RESULT 18
 BF320636 722 bp mRNA linear EST 29-DEC-2000
 LOCUS BF320636
 DEFINITION similar to SW:MK01_MOUSE P27703 MITOGEN-ACTIVATED PROTEIN KINASE 1
 ;, mRNA sequence.
 ACCESSION BF320636.1 GI:11269633
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgc.nci.nih.gov/
 1 (bases 1 to 722)
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 Other-ESTs: uz55b06.x1
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov/image/html/lresources.shtml
 MGI:1433715

FEATURES
 source
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:3672947"
 /clone="IMAGE:3672947"
 /sex="female, virgin"
 /tissue="mammary, infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 168 a 201 c 196 g 154 t
 ORIGIN

Query Match 5.3%; Score 25; DB 10; Length 722;
 Best Local Similarity 100.0%; Pred. No. 0.077;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 aagatctgacttgccctgccc 155
 |||||||||||||||||||||
 Db 685 AAGATCTGACTTTGGCCTTGCCG 709

RESULT 19
 BE030526 546 bp mRNA linear EST 09-JUL-2000
 LOCUS BE030526

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 1 T 1

RESULT 29
US-08-188-943-2
Sequence 2, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 4 T 4

RESULT 30
US-08-188-943-2/c
Sequence 2, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 3 t 3

RESULT 31
US-08-199-317-2
; Sequence 2, Application US/08199317
; Patent No. 5670316
; GENERAL INFORMATION:
; APPLICANT: Sena, Elissa P.
; APPLICANT: Calhoun, Cornelia J.
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Diagnostic Applications of Double D-loop
; TITLE OF INVENTION: Formation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,317
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,791
; FILING DATE: 09-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,462
; FILING DATE: 04-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520,321
; FILING DATE: 07-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 9150-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Cleavage site for Dpn I
; US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 3 t 3

Db 3 t 3

RESULT 32
US-08-199-317-2/c
; Sequence 2, Application US/08199317
; Patent No. 5670316
; GENERAL INFORMATION:
; APPLICANT: Sena, Elissa P.
; APPLICANT: Calhoun, Cornelia J.
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Diagnostic Applications of Double D-loop
; TITLE OF INVENTION: Formation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,317
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,791
; FILING DATE: 09-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,462
; FILING DATE: 04-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520,321
; FILING DATE: 07-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 9150-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Cleavage site for Dpn I
; US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 t 2

RESULT 33
US-08-393-219-11
; Sequence 11, Application US/08393219
; Patent No. 5689040

```

: GENERAL INFORMATION:
: APPLICANT: HARADA, John J.
: TITLE OF INVENTION: PLANT PROMOTER SEQUENCES USEFUL FOR GENE
: NUMBER OF INVENTION: EXPRESSION IN SEEDS AND SEEDLINGS
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Stewart Street Tower, 20th
: CITY: San Francisco
: STATE: California
: COUNTRY: US
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/393,219
: FILING DATE: 23-FEB-1995
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Baslian, Kevin L.
: REGISTRATION NUMBER: 34,774
: REFERENCE/DOCKET NUMBER: 2307E-581
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 543-9600
: TELEFAX: (415) 543-5043
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-393-219-11

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 3 t 3

RESULT 34
US-08-510-032A-9
: Sequence 9, Application US/08510032A
: Patent No. 5712126
: GENERAL INFORMATION:
: APPLICANT: Sherman Weissman and Yarlindra Prashar
: TITLE OF INVENTION: Analysis of Gene Expression By Display of 3'-
: NUMBER OF INVENTION: end Restriction Fragments of cDNA
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Yahwak & Associates
: STREET: 25 Skytop Drive
: CITY: Trumbull
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06611
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: Macintosh
: SOFTWARE: Microsoft Word 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/510,032A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: George M. Yahwak
: REGISTRATION NUMBER: 26,824
: REFERENCE/DOCKET NUMBER: Yale
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203)268-1951
: TELEFAX: (203)268-1951
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-510-032A-9

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 3 t 3

CLASSIFICATION: 435
```

```

: ATTORNEY/AGENT INFORMATION:
: NAME: George M. Yahwak
: REGISTRATION NUMBER: 26,824
: REFERENCE/DOCKET NUMBER: Yale
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203)268-1951
: TELEFAX: (203)268-1951
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-510-032A-9

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 3 t 3
```

```

RESULT 35
US-08-510-032A-9/c
: Sequence 9, Application US/08510032A
: Patent No. 5712126
: GENERAL INFORMATION:
: APPLICANT: Sherman Weissman and Yarlindra Prashar
: TITLE OF INVENTION: Analysis of Gene Expression By Display of 3'-
: NUMBER OF INVENTION: end Restriction Fragments of cDNA
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Yahwak & Associates
: STREET: 25 Skytop Drive
: CITY: Trumbull
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06611
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Microsoft Word 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/510,032A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: George M. Yahwak
: REGISTRATION NUMBER: 26,824
: REFERENCE/DOCKET NUMBER: Yale
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203)268-1951
: TELEFAX: (203)268-1951
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-510-032A-9

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 3 t 3
```

Db 2 T 2

RESULT 36

US-08-468-049-7/C
Sequence 7, Application US/08468049

Patent No. 5763171

GENERAL INFORMATION:

APPLICANT: Stefano, James E.

TITLE OF INVENTION: Nucleic Acid Structures with Catalytic

TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5763171val B. Galloway

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.

CITY: Naperville

STATE: IL

COUNTRY: USA

ZIP: 60563

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,049

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/630,288

FILING DATE: 17-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/370,218

FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/252,243

FILING DATE: 30-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: No. 5763171val B. Galloway

REGISTRATION NUMBER: 33,595

REFERENCE/DOCKET NUMBER: CN 581903

TELEPHONE: (708) 717-2443

TELEFAX: (708) 717-2430

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-468-049-7

Query Match

Best Local Similarity 100.0%; Score 1; DB 1; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1

Db 4 T 4

RESULT 37

US-08-468-049-11

Sequence 11, Application US/08468049

Patent No. 5763171

GENERAL INFORMATION:

APPLICANT: Stefano, James E.

TITLE OF INVENTION: Nucleic Acid Structures with Catalytic

TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5763171val B. Galloway

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.

CITY: Naperville

STATE: IL

COUNTRY: USA

ZIP: 60563

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,049

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/630,288

FILING DATE: 17-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/370,218

FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/252,243

FILING DATE: 30-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: No. 5763171val B. Galloway

REGISTRATION NUMBER: 33,595

REFERENCE/DOCKET NUMBER: CN 581903

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 717-2443

TELEFAX: (708) 717-2430

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-468-049-11

Query Match

Best Local Similarity 100.0%; Score 1; DB 1; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1

Db 3 T 3

RESULT 38

US-08-468-049-11/C

Sequence 11, Application US/08468049

Patent No. 5763171

GENERAL INFORMATION:

APPLICANT: Stefano, James E.

TITLE OF INVENTION: Nucleic Acid Structures with Catalytic

TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5763171val B. Galloway

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.

CITY: Naperville

STATE: IL

COUNTRY: USA

ZIP: 60563

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,049
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/630,288
FILING DATE: 17-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: No. 5763171val B. Galloway
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: CN 581903
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-468-049-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 t 1
Db 2 t 2

RESULT 39
US-08-468-049-34
Sequence 34, Application US/08468049
Patent No. 5763171
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5763171val B. Galloway
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,049
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/630,288
FILING DATE: 17-DEC-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: No. 5763171val B. Galloway
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: CN 581903
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-468-049-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 t 1
Db 1 u 1

RESULT 40
US-08-468-049-34/C
Sequence 34, Application US/08468049
Patent No. 5763171
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5763171val B. Galloway
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,049
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/630,288
FILING DATE: 17-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: No. 5763171val B. Galloway
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: CN 581903
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443

TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-468-049-34

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 3 t 3

RESULT 41
US-08-488-015B-5
; Sequence 5, Application US/08488015B
; Patent No. 5780272
; GENERAL INFORMATION:
; APPLICANT: Jarrell, Kevin A.
; TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
; NUMBER OF INVENTION: AND REAGENTS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,015B
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HUV-008.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-488-015B-5

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 2 u 2

RESULT 42

US-08-488-015B-12
; Sequence 12, Application US/08488015B
; Patent No. 5780272
; GENERAL INFORMATION:
; APPLICANT: Jarrell, Kevin A.
; TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
; NUMBER OF INVENTION: AND REAGENTS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,015B
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HUV-008.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-488-015B-12

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 t 1

RESULT 43
US-08-351-365-3
; Sequence 3, Application US/08351365
; Patent No. 5783681
; GENERAL INFORMATION:
; APPLICANT: Matusik, Robert J
; TITLE OF INVENTION: ANDROGEN REGULATION WITH DNA SEQUENCES
; NUMBER OF INVENTION: OF RAT PROBASTIN GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,365
; FILING DATE:

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1887-116 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-351-365-3
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Query Match          100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 t 1
Db       1 t 1
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RESULT 44
US-08-351-365-3/C
Sequence 3, Application US/08351365
Patent No. 5783681
GENERAL INFORMATION:
APPLICANT: Matusik, Robert J
TITLE OF INVENTION: ANDROGEN REGULATION WITH DNA SEQUENCES
NUMBER OF INVENTION: OF RAT PROBASIN GENE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,365
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1887-116 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-351-365-3
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```
Query Match          100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 t 1
Db       2 t 2
```

```
RESULT 45
US-08-351-365-4
Sequence 4, Application US/08351365
Patent No. 5783681
GENERAL INFORMATION:
APPLICANT: Matusik, Robert J
TITLE OF INVENTION: ANDROGEN REGULATION WITH DNA SEQUENCES
NUMBER OF INVENTION: OF RAT PROBASIN GENE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,365
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1887-116 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-351-365-4
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Query Match          100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 t 1
Db       2 t 2
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Search completed: July 15, 2002, 23:07:38
Job time: 22991 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:26 ; Search time 12941.8 Seconds

(without alignments)
1.672 Million cell updates/sec

Title: US-09-375-248-1_COPY_3150_3150

Perfect score: 1

Sequence: 1 t 1

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Searched: 21979536 seqs, 1081749327 residues

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Minimum DB seq length: 0

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2	100.0	1	2	US-08-392-180-271	Sequence 271, Appl		
3	100.0	1	13	US-08-964-265-271	Sequence 271, Appl		
4	100.0	1	15	US-09-172-826-15	Sequence 15, Appl		
5	100.0	1	2	US-09-227-782-16	Sequence 16, Appl		
6	100.0	1	2	US-09-387-777-1	Sequence 1, Appl		
7	100.0	1	2	US-09-387-777-2	Sequence 2, Appl		
8	100.0	1	2	US-09-387-777-3	Sequence 3, Appl		
9	100.0	1	2	US-09-387-777-4	Sequence 4, Appl		
10	100.0	1	2	US-09-387-777-5	Sequence 5, Appl		
11	100.0	1	2	US-09-387-777-8	Sequence 8, Appl		
12	100.0	1	2	US-09-387-777-9	Sequence 9, Appl		
13	100.0	1	2	US-09-387-777-12	Sequence 12, Appl		
14	100.0	1	2	US-09-387-777-13	Sequence 13, Appl		
15	100.0	1	2	US-09-387-777-14	Sequence 14, Appl		
16	100.0	1	2	US-09-387-777-15	Sequence 15, Appl		
17	100.0	1	2	US-09-472-035A-19	Sequence 19, Appl		
18	100.0	1	2	US-09-472-035A-20	Sequence 20, Appl		
19	100.0	1	2	US-09-634-306B-51869	Sequence 51869, A		
20	100.0	1	2	US-09-634-306B-52011	Sequence 52011, A		
21	100.0	1	2	US-09-634-306B-52015	Sequence 52015, A		
22	100.0	1	2	US-09-634-306B-52280	Sequence 52280, A		
23	100.0	1	2	US-09-634-306B-52357	Sequence 52357, A		
24	100.0	1	2	US-09-634-306B-53022	Sequence 53022, A		
25	100.0	1	2	US-09-634-306B-58305	Sequence 58305, A		
26	100.0	1	2	US-09-634-306B-58424	Sequence 58424, A		
27	100.0	1	2	US-09-634-306B-58424	Sequence 58424, A		
28	100.0	1	2	US-09-634-306B-58424	Sequence 58424, A		
29	100.0	1	2	US-09-634-306B-58424	Sequence 58424, A		
30	100.0	1	2	US-09-634-306B-58424	Sequence 58424, A		
31	100.0	1	2	US-09-634-306B-58424	Sequence 58424, A		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 35 1 100.0 2 24 US-09-634-306B-58520 Sequence 58520, A
C 36 1 100.0 2 24 US-09-634-306B-58520 Sequence 58520, A
C 37 1 100.0 2 24 US-09-634-306B-58578 Sequence 58578, A
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C 39 1 100.0 2 24 US-09-634-306B-58585 Sequence 58585, A
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C 41 1 100.0 2 24 US-09-634-306B-75814 Sequence 75814, A
C 42 1 100.0 2 24 US-09-634-306B-75842 Sequence 75842, A
C 43 1 100.0 2 24 US-09-634-306B-75889 Sequence 75889, A
C 44 1 100.0 2 24 US-09-634-306B-75902 Sequence 75902, A
C 45 1 100.0 2 24 US-09-634-306B-75923 Sequence 75923, A

ALIGNMENTS

RESULT 1
US-08-241-388-16/c
Sequence 16, Application US/08241388
GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
TITLE OF INVENTION: Tomita, Takashi
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,388
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEO ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Musca domestica
STRAIN: Learn-Pyr
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 1
US-08-241-388-16

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 T 2

RESULT 2
US-08-392-180-271
Sequence 271, Application US/08392180
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Deleage, Angelo M.
APPLICANT: Bills, Pamela Kay
APPLICANT: Pham, Mino Thu
TITLE OF INVENTION: SMALL INTESTINE CELL-DERIVED POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 1369
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,180
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PD-0023 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 855-0572
INFORMATION FOR SEO ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 232362
US-08-392-180-271

Query Match 100.0%; Score 1; DB 7; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 T 1
Db 1 T 1

RESULT 3
US-08-964-265-271
Sequence 271, Application US/08964265
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Deleage, Angelo M.
APPLICANT: Bills, Pamela Kay
APPLICANT: Pham, Mino Thu
TITLE OF INVENTION: SMALL INTESTINE CELL-DERIVED POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 1369
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE

CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,265
FILING DATE: 04-NOV-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,180
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PD-0023 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 855-0572
INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 232362
US-08-964-265-271

Query Match 100.0%; Score 1; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 1 t 1

RESULT 4
US-09-172-828-15
Sequence 15, Application US/09172828
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
APPLICANT: Klagsbrun, Michael
APPLICANT: Elenius, Klaus
APPLICANT: Corfas, Gabriel
TITLE OF INVENTION: Novel Human EGF Receptors and Use
TITLE OF INVENTION: Thereof
FILE REFERENCE: 47758-PCF
CURRENT APPLICATION NUMBER: US/09/172,828
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 2
TYPE: DNA
ORGANISM: mouse
US-09-172-828-15

Query Match 100.0%; Score 1; DB 15; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 2 t 2

RESULT 5
US-09-227-782-16
Sequence 16, Application US/09227782
GENERAL INFORMATION:
APPLICANT: Kawasaki, Andrew M
APPLICANT: Fraser, Allister S
APPLICANT: Manoharan, Muthiah
APPLICANT: Cook, Phillip D
APPLICANT: Prakash, Thazha P
TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
FILE REFERENCE: ISIS3335
CURRENT APPLICATION NUMBER: US/09/227,782
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 2
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(2)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-227-782-16

Query Match 100.0%; Score 1; DB 16; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 1 t 1

RESULT 6
US-09-387-777-1/c
Sequence 1, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-1

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 2 t 2

RESULT 7
US-09-387-777-2/c
Sequence 2, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: to an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-2

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

Db 1 t 1

RESULT 8
US-09-387-777-3/c
Sequence 3, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: to an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-3

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 1 t 1

RESULT 9
US-09-387-777-4
Sequence 4, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington

```

: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: twinhead* slimote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-4
:
: Query Match 100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Oy 1 t 1
: Db 2 t 2
:
: RESULT 10
: US-09-387-777-4/c
: Sequence 4; Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedmam c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: twinhead* slimote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-5
```

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: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-4
:
: Query Match 100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Oy 1 t 1
: Db 1 t 1
:
: RESULT 11
: US-09-387-777-5/c
: Sequence 5; Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedmam c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: twinhead* slimote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-5
```

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 t 2

RESULT 12
US-09-387-777-8
Sequence 8, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-8
Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
1
Db 2 t 2
RESULT 13
US-09-387-777-9/C
Sequence 9, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-9

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 t 2

RESULT 14
US-09-387-777-12
Sequence 12, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777

```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedmam, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-387-777-12
```

```
Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
```

```
Qy 1 t 1
    |
Db 2 T 2
```

```

RESULT 15
US-09-387-777-13
; Sequence 13, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedmam, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-387-777-13
```

```
Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
```

```
Qy 1 t 1
    |
Db 1 T 1
```

```

RESULT 16
US-09-387-777-13/C
; Sequence 13, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedmam, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-387-777-13
```

```
Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
```

```
Qy 1 t 1
    |
Db 2 T 2
```

```

RESULT 17
US-09-387-777-14
; Sequence 14, Application US/09387777
```



```

: GENERAL INFORMATION:
: APPLICANT: Hedar Klees
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: SOFTWARE: to an ASCII file
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-387-777-14

Query Match          100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 1 t 1

RESULT 18
US-09-387-777-15
: Sequence 15, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hedar Klees
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-387-777-15
```

```

: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: SOFTWARE: to an ASCII file
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-387-777-15

Query Match          100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 1 t 1

RESULT 19
US-09-387-777-16
: Sequence 16, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hedar Klees
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
```

TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-16

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 1 t 1

RESULT 20
US-09-472-035A-19
Sequence 19, Application US/09472035A
GENERAL INFORMATION:
APPLICANT: Yechezkel Kasht et al.
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472.035A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 74/77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-472-035A-19

Query Match 100.0%; Score 1; DB 18; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 1 t 1

DB 2 t 2

RESULT 21
US-09-472-035A-20
Sequence 20, Application US/09472035A
GENERAL INFORMATION:
APPLICANT: Yechezkel Kasht et al.
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472.035A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 74/77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-472-035A-20

Query Match 100.0%; Score 1; DB 18; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 1 t 1

RESULT 22
US-09-634-306B-51869
Sequence 51869, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218.006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198.676

```

; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-51869
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 1 t 1
```

```

RESULT 23
US-09-634-306B-52011
; Sequence 52011, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52011
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52011
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 1 t 1
```

```
RESULT 24
US-09-634-306B-52015
```

```

; Sequence 52015, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52015
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52015
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 1 t 1
```

```

RESULT 25
US-09-634-306B-52280/c
; Sequence 52280, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52280
```

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 1 t 1

RESULT 26
US-09-634-306B-52357
; Sequence 52357, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52357
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52357

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 1 t 1

RESULT 27
US-09-634-306B-53022/C
; Sequence 53022, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 53022
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-53022

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 2 t 2

RESULT 28
US-09-634-306B-58305
; Sequence 58305, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 58305
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58305

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 2 t 2

RESULT 29
US-09-634-306B-58424
; Sequence 58424, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006

```

: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 58424
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-58424
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
db 2 t 2
```

```
RESULT 30
: Sequence 58424, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 58424
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-58424
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
db 1 t 1
```

```
RESULT 31
: Sequence 58496, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 58496
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-58496
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
db 2 t 2
```

```
RESULT 32
: Sequence 58496, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 58496
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-58496
```

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 33
US-09-634-306B-58508

; Sequence 58508, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 58508
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58508

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 t 2

RESULT 34
US-09-634-306B-58508/C

; Sequence 58508, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 58508
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58508

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 35
US-09-634-306B-58520

; Sequence 58520, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 58520
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58520

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 t 2

RESULT 36
US-09-634-306B-58520/C

; Sequence 58520, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B

```

; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-3068-58520
```

```

Query Match          100.0%; Score 1: DB 24; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 t 1
```

```

RESULT 37
US-09-634-3068-58578
; Sequence 58578, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-3068-58578
```

```

Query Match          100.0%; Score 1: DB 24; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 2 t 2
```

```

RESULT 38
US-09-634-3068-58578/c
; Sequence 58578, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-3068-58578
```

```

Query Match          100.0%; Score 1: DB 24; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 t 1
```

```

RESULT 39
US-09-634-3068-75805/c
; Sequence 75805, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75805
; LENGTH: 2
; TYPE: DNA
```

ORGANISM: Human
US-09-634-306B-75805

Query Match
Best Local Similarity 100.0%; Score 1: DB 24; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 40
US-09-634-306B-75814/C

Sequence 75814, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 75814
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-75814

Query Match
Best Local Similarity 100.0%; Score 1: DB 24; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 41

US-09-634-306B-75842/C
Sequence 75842, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 75842
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-75842

Query Match
Best Local Similarity 100.0%; Score 1: DB 24; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 42

US-09-634-306B-75868/C
Sequence 75868, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 75868
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-75868

Query Match
Best Local Similarity 100.0%; Score 1: DB 24; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 43

US-09-634-306B-75889/C
Sequence 75889, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24


```
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75889
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-75889
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 1 t 1
```

```
RESULT 44
US-09-634-306B-75902/c
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75902
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-75902
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
```

```
Db 1 t 1
```

```
RESULT 45
US-09-634-306B-75923/c
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75923
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-75923
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 1 t 1
```

Search completed: July 16, 2002, 02:50:26
Job time: 31279 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:57:00 : Search time 808.35 Seconds
(without alignments)
2.105 Million cell updates/sec

Title: US-09-375-248-1-COPY_3150_3150

Perfect score: 1
Sequence: 1 t 1

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/plodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/plodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/plodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/plodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/plodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/plodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/plodata/2/pna/US60_NEW_COMB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1	100.0	2	6	US-10-027-632-51869
2	1	100.0	2	6	US-10-027-632-52011
3	1	100.0	2	6	US-10-027-632-52015
4	1	100.0	2	6	US-10-027-632-52280
5	1	100.0	2	6	US-10-027-632-52357
6	1	100.0	2	6	US-10-027-632-53022
7	1	100.0	2	6	US-10-027-632-53025
8	1	100.0	2	6	US-10-027-632-58424
9	1	100.0	2	6	US-10-027-632-58424
10	1	100.0	2	6	US-10-027-632-58496
11	1	100.0	2	6	US-10-027-632-58496
12	1	100.0	2	6	US-10-027-632-58508
13	1	100.0	2	6	US-10-027-632-58508
14	1	100.0	2	6	US-10-027-632-58520
15	1	100.0	2	6	US-10-027-632-58520
16	1	100.0	2	6	US-10-027-632-58520
17	1	100.0	2	6	US-10-027-632-58578
18	1	100.0	2	6	US-10-027-632-58578
19	1	100.0	2	6	US-10-027-632-75805
20	1	100.0	2	6	US-10-027-632-75814
21	1	100.0	2	6	US-10-027-632-75814
22	1	100.0	2	6	US-10-027-632-75868
23	1	100.0	2	6	US-10-027-632-75868
24	1	100.0	2	6	US-10-027-632-75889
25	1	100.0	2	6	US-10-027-632-75902
26	1	100.0	2	6	US-10-027-632-75928

c	27	1	100.0	2	6	US-10-027-632-175337	Sequence 175337,
	28	1	100.0	2	6	US-10-027-632-175354	Sequence 175354,
	29	1	100.0	2	6	US-10-027-632-175401	Sequence 175401,
	30	1	100.0	2	6	US-10-027-632-175403	Sequence 175403,
	31	1	100.0	2	6	US-10-027-632-175419	Sequence 175419,
	32	1	100.0	2	6	US-10-027-632-175419	Sequence 175419,
	33	1	100.0	2	6	US-10-027-632-175426	Sequence 175426,
	34	1	100.0	2	6	US-10-027-632-175433	Sequence 175433,
	35	1	100.0	2	6	US-10-027-632-176011	Sequence 176011,
	36	1	100.0	2	6	US-10-027-632-176011	Sequence 176011,
	37	1	100.0	2	6	US-10-027-632-176848	Sequence 176848,
	38	1	100.0	2	6	US-10-027-632-176849	Sequence 176849,
	39	1	100.0	2	6	US-10-027-632-176880	Sequence 176880,
	40	1	100.0	2	6	US-10-027-632-178008	Sequence 178008,
	41	1	100.0	2	6	US-10-027-632-178008	Sequence 178008,
	42	1	100.0	2	6	US-10-027-632-178104	Sequence 178104,
	43	1	100.0	2	6	US-10-027-632-178104	Sequence 178104,
	44	1	100.0	2	6	US-10-027-632-178114	Sequence 178114,
	45	1	100.0	2	6	US-10-027-632-178114	Sequence 178114,

ALIGNMENTS

```
RESULT 1
US-10-027-632-51869
; Sequence 51869, Application US/10027632
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51869

Query Match      100.0%  Score 1:  DB 6:  Length 2;
Best Local Similarity 100.0%:  Pred No. 0;
Matches 1;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 t 1
Db      1 t 1

RESULT 2
US-10-027-632-52011
; Sequence 52011, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52011
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52011
```

```
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52011
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52011
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
Db 1 t 1
```

```
RESULT 3
US-10-027-632-52015
; Sequence 52015, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52015
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52015
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
```

```
Db 1 t 1
RESULT 4
US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52280
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
Db 1 t 1
RESULT 5
US-10-027-632-52357
; Sequence 52357, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52357
```

```
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52357
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 1 t 1
```

```
RESULT 6
US-10-027-632-53022/C
; Sequence 53022, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53022
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-53022
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 2 t 2
```

```
RESULT 7
US-10-027-632-58305
; Sequence 58305, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58305
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58305
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 2 t 2
```

```
RESULT 8
US-10-027-632-58424
; Sequence 58424, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58424
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58424
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 2 t 2
```

```
RESULT 9
US-10-027-632-58424/C
; Sequence 58424, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58424
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-58424
```

```

Query Match          100.0%: Score 1: DB 6: Length 2:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
Oy      1 t 1
Db      1 T 1
```

```

RESULT 10
: US-10-027-632-58496
: Sequence 58496, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58496
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-58496
```

```

Query Match          100.0%: Score 1: DB 6: Length 2:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
Oy      1 t 1
Db      2 t 2
```

```

RESULT 11
: US-10-027-632-58496/c
: Sequence 58496, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58496
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-58496
```

```

Query Match          100.0%: Score 1: DB 6: Length 2:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
Oy      1 t 1
Db      1 T 1
```

```

RESULT 12
: US-10-027-632-58508
: Sequence 58508, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58508
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58508
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1 |
Db  2 t 2
```

```

RESULT 13
; Sequence 58508, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58508
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58508
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1 |
Db  1 t 1
```

```

RESULT 14
; Sequence 58520, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
```

```

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58520
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58520
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1 |
Db  2 t 2
```

```

RESULT 15
; Sequence 58520, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58520
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58520
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1 |
Db  1 t 1
```

```

RESULT 16
; Sequence 58578, Application US/10027632
```

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58578
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
         |
Db       2 t 2
```

```

RESULT 17
US-10-027-632-58578/c
; Sequence 58578, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58578
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
```

```

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
         |
Db       1 t 1
```

```

RESULT 18
US-10-027-632-75805/c
; Sequence 75805, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75805
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75805
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
         |
Db       1 t 1
```

```

RESULT 19
US-10-027-632-75814/c
; Sequence 75814, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
```



```

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75814
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75814
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 1 t 1
```

```
RESULT 20
US-10-027-632-75842/c
; Sequence 75842, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75842
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75842
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 1 t 1
```

```
RESULT 21
US-10-027-632-75868/c
; Sequence 75868, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```

; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75868
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75868
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 1 t 1
```

```
RESULT 22
US-10-027-632-75889/c
; Sequence 75889, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75889
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75889
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 1 t 1
```

RESULT 23

```
US-10-027-632-75902/C
; Sequence 75902, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75902
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75902
```

```
Query Match      100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
Db      1 t 1
```

```
RESULT 24
; Sequence 75923, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75923
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75923
```

```
Query Match      100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
Db      1 t 1
```

```
RESULT 25
; Sequence 75928, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75928
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75928
```

```
Query Match      100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
Db      1 t 1
```

```
RESULT 26
; Sequence 175312, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175312
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
    1
Db 2 t 2
```

```
RESULT 27
; Sequence 175337, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175337
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
    1
Db 2 t 2
```

```
RESULT 28
; Sequence 175354, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
```

```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175354
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
    1
Db 2 t 2
```

```
RESULT 29
; Sequence 175401, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
    1
Db 2 t 2
```

```
RESULT 30
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 2 t 2
```

```
RESULT 31
US-10-027-632-175415
; Sequence 175415, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
```

US-10-027-632-175415

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 2 t 2
```

```
RESULT 32
US-10-027-632-175419
; Sequence 175419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175419
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 2 t 2
```

```
RESULT 33
US-10-027-632-175426
; Sequence 175426, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
```

```

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426
```

```

Query Match          100.0%: Score 1: DB 6: Length 2:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
Oy 1 t 1
    1
Db  2 t 2
```

```

RESULT 34
US-10-027-632-175433
; Sequence 175433, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175433
```

```

Query Match          100.0%: Score 1: DB 6: Length 2:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
Oy 1 t 1
    1
Db  2 t 2
```

```

RESULT 35
US-10-027-632-176011
; Sequence 176011, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
```

```

; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 176011
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176011
```

```

Query Match          100.0%: Score 1: DB 6: Length 2:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
Oy 1 t 1
    1
Db  2 t 2
```

```

RESULT 36
US-10-027-632-176011/c
; Sequence 176011, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 176011
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176011
```

```

Query Match          100.0%: Score 1: DB 6: Length 2:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
Oy 1 t 1
    1
```

Db 1 T 1

RESULT 37

US-10-027-632-176848/c

: Sequence 176848, Application US/10027632

: GENERAL INFORMATION:

: APPLICANT: Wang, David G.

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

: FILE REFERENCE: 108827.129

: CURRENT APPLICATION NUMBER: US/10/027,632

: PRIOR FILING DATE: 2002-04-30

: PRIOR APPLICATION NUMBER: US 60/218,006

: PRIOR FILING DATE: 2000-07-12

: PRIOR APPLICATION NUMBER: US 60/198,676

: PRIOR FILING DATE: 2000-04-20

: PRIOR APPLICATION NUMBER: US 60/193,483

: PRIOR FILING DATE: 2000-03-29

: PRIOR APPLICATION NUMBER: US 60/185,218

: PRIOR FILING DATE: 2000-02-24

: PRIOR APPLICATION NUMBER: US 60/167,363

: PRIOR FILING DATE: 1999-11-23

: PRIOR APPLICATION NUMBER: US 60/156,358

: PRIOR FILING DATE: 1999-09-28

: PRIOR APPLICATION NUMBER: US 60/146,002

: NUMBER OF SEQ ID NOS: 325720

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 176848

: LENGTH: 2

: TYPE: DNA

: ORGANISM: Human

US-10-027-632-176848

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 T 1
Db 2 T 2

RESULT 38

US-10-027-632-176849/c

: Sequence 176849, Application US/10027632

: GENERAL INFORMATION:

: APPLICANT: Wang, David G.

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

: FILE REFERENCE: 108827.129

: CURRENT APPLICATION NUMBER: US/10/027,632

: PRIOR FILING DATE: 2002-04-30

: PRIOR APPLICATION NUMBER: US 60/218,006

: PRIOR FILING DATE: 2000-07-12

: PRIOR APPLICATION NUMBER: US 60/198,676

: PRIOR FILING DATE: 2000-04-20

: PRIOR APPLICATION NUMBER: US 60/193,483

: PRIOR FILING DATE: 2000-03-29

: PRIOR APPLICATION NUMBER: US 60/185,218

: PRIOR FILING DATE: 2000-02-24

: PRIOR APPLICATION NUMBER: US 60/167,363

: PRIOR FILING DATE: 1999-11-23

: PRIOR APPLICATION NUMBER: US 60/156,358

: PRIOR FILING DATE: 1999-09-28

: PRIOR APPLICATION NUMBER: US 60/146,002

: NUMBER OF SEQ ID NOS: 325720

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 176849

: LENGTH: 2

: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176849

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 T 1
Db 2 T 2

RESULT 39

US-10-027-632-176880/c

: Sequence 176880, Application US/10027632

: GENERAL INFORMATION:

: APPLICANT: Wang, David G.

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

: FILE REFERENCE: 108827.129

: CURRENT APPLICATION NUMBER: US/10/027,632

: PRIOR FILING DATE: 2002-04-30

: PRIOR APPLICATION NUMBER: US 60/218,006

: PRIOR FILING DATE: 2000-07-12

: PRIOR APPLICATION NUMBER: US 60/198,676

: PRIOR FILING DATE: 2000-04-20

: PRIOR APPLICATION NUMBER: US 60/193,483

: PRIOR FILING DATE: 2000-03-29

: PRIOR APPLICATION NUMBER: US 60/185,218

: PRIOR FILING DATE: 2000-02-24

: PRIOR APPLICATION NUMBER: US 60/167,363

: PRIOR FILING DATE: 1999-11-23

: PRIOR APPLICATION NUMBER: US 60/156,358

: PRIOR FILING DATE: 1999-09-28

: PRIOR APPLICATION NUMBER: US 60/146,002

: NUMBER OF SEQ ID NOS: 325720

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 176880

: LENGTH: 2

: TYPE: DNA

: ORGANISM: Human

US-10-027-632-176880

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 T 1
Db 2 T 2

RESULT 40

US-10-027-632-178008

: Sequence 178008, Application US/10027632

: GENERAL INFORMATION:

: APPLICANT: Wang, David G.

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

: FILE REFERENCE: 108827.129

: CURRENT APPLICATION NUMBER: US/10/027,632

: PRIOR FILING DATE: 2002-04-30

: PRIOR APPLICATION NUMBER: US 60/218,006

: PRIOR FILING DATE: 2000-07-12

: PRIOR APPLICATION NUMBER: US 60/198,676

: PRIOR FILING DATE: 2000-04-20

: PRIOR APPLICATION NUMBER: US 60/193,483

: PRIOR FILING DATE: 2000-03-29

: PRIOR APPLICATION NUMBER: US 60/185,218

```

; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178008
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178008
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 t 1
Db      2 t 2
```

```

RESULT 41
US-10-027-632-178008/c
; Sequence 178008, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178008
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178008
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 t 1
Db      1 t 1
```

```

RESULT 42
US-10-027-632-178104
; Sequence 178104, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178104
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178104
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 t 1
Db      2 t 2
```

```

RESULT 43
US-10-027-632-178104/c
; Sequence 178104, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178104
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178104
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 t 1
|
Db 1 t 1

RESULT 44
US-10-027-632-178114

; Sequence 178114, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178114
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178114

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 t 2

RESULT 45
US-10-027-632-178114/c

; Sequence 178114, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 178114
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178114

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 1 t 1

Search completed: July 16, 2002, 02:57:00
Job time: 24558 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 20:07:36 ; Search time 7067.1 Seconds
(without alignments)

1.910 Million cell updates/sec

Title: US-09-375-248-1_COPY_3150_3150

Perfect score: 1 c 1

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_esthm:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	1	2	HSM003817	A1039341 Homo sapi
2	100.0	1	2	HSM003931	A1039455 Homo sapi
3	100.0	1	2	HSM003931	A1039455 Homo sapi
4	100.0	1	2	HSM007187	A1042337 Homo sapi
5	100.0	1	2	HSM008709	A1043859 Homo sapi
6	100.0	1	2	HSM011919	A1047068 Homo sapi
7	100.0	1	10	B1817789	B1817789 G3-G22 Ax
8	100.0	1	2	C55081	C55081 C55081 Yuj1
9	100.0	1	2	A2463604	A2463604 1M0272J05
10	100.0	1	3	HSM003852	A1039376 Homo sapi
11	100.0	1	3	HSM003852	A1039376 Homo sapi
12	100.0	1	3	HSM007999	A1043149 Homo sapi
13	100.0	1	3	HSM008070	A1043220 Homo sapi
14	100.0	1	3	AW672605	AW672605 2XA Expla
15	100.0	1	3	A2438202	A2438202 1M0228108
16	100.0	1	3	A2438202	A2438202 1M0228108
17	100.0	1	4	BG926576	Bg926576 HNC56-1-A

C	18	1	100.0	4	2	BG926576	BG926576 HNC56-1-A
C	19	1	100.0	4	2	HSM003901	A1039425 Homo sapi
C	20	1	100.0	4	2	HSM010467	A1045617 Homo sapi
C	21	1	100.0	4	9	AW672622	AW672622 73C Expla
C	22	1	100.0	4	12	CNS004RB	AL054121 Drosophila
C	23	1	100.0	4	12	CNS004RB	AL054121 Drosophila
C	24	1	100.0	5	2	HSM007310	A1042460 Homo sapi
C	25	1	100.0	5	2	HSM007310	A1042460 Homo sapi
C	26	1	100.0	5	2	HSM007835	A1042985 Homo sapi
C	27	1	100.0	5	2	HSM011053	A1046203 Homo sapi
C	28	1	100.0	6	2	HSM011053	A1046203 Homo sapi
C	29	1	100.0	6	2	BG927410	BG927410 HNC1-1-C7
C	30	1	100.0	6	2	HSM003844	A1039368 Homo sapi
C	31	1	100.0	6	2	HSM003844	A1039368 Homo sapi
C	32	1	100.0	6	2	HSM004423	A1039947 Homo sapi
C	33	1	100.0	6	2	HSM004423	A1039947 Homo sapi
C	34	1	100.0	6	2	HSM007334	A1042484 Homo sapi
C	35	1	100.0	6	2	HSM007334	A1042484 Homo sapi
C	36	1	100.0	6	2	HSM007683	A1042833 Homo sapi
C	37	1	100.0	6	2	HSM007683	A1042833 Homo sapi
C	38	1	100.0	6	2	HSM008014	A1043164 Homo sapi
C	39	1	100.0	7	2	BG897546	BG897546 HOA14-1-H
C	40	1	100.0	7	2	BG897546	BG897546 HOA14-1-H
C	41	1	100.0	7	2	HSM007412	A1042562 Homo sapi
C	42	1	100.0	7	2	HSM007412	A1042562 Homo sapi
C	43	1	100.0	7	2	HSM007502	A1042652 Homo sapi
C	44	1	100.0	7	2	HSM007502	A1042652 Homo sapi
C	45	1	100.0	7	10	C58888	C58888 C58888 Yuj1

ALIGNMENTS

RESULT 1
ID HSM003817 standard: RNA: EST: 2 BP.
XX AL039341:
XX
SV AL039341.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA: EST DKFZp434F2010_r1 (from clone DKFZp434F2010)
XX
XX EST: expressed sequence tag.
KM
XX Homo sapiens (human)
OS Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia:
OC Eutheria: Primates: Catarrhini: Homnidae: Homo.
XX
XX [1]
RP 1-2
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.:
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MTPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH key Location/Qualifiers
FH
FT source 1..2
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434F2010"
FT /clone_11b="434 (synonym: htes3). Vector pSport1; host

FT DH10B: sites NotI + SalI*
 FT /dev_stage="adult"
 XX /tissue_type="testis"
 XX
 SO Sequence 2 BP; 0 A; 1 G; 0 C; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 t 1
 Db 1 T 1

RESULT 2
 HSM003931 ID HSM003931 standard; RNA; EST; 2 BP.
 AC AL039455;
 SV AL039455.1
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA: EST DKFZp434N0610_s1 (from clone DKFZp434N0610)
 DE EST; expressed sequence tag.
 KM Homo sapiens (human)
 XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 XX [1]
 RN RP 1-2
 KA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
 CC sequencing consortium of the German Genome Project
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 CC
 XX Key Location/Qualifiers
 FH source
 FT 1..2
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434N0610"
 FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SO Sequence 2 BP; 1 A; 0 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 t 1
 Db 1 T 1
 RESULT 3

HSM003931/C
 ID HSM003931 standard; RNA; EST; 2 BP.
 AC AL039455;
 SV AL039455.1
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA: EST DKFZp434N0610_s1 (from clone DKFZp434N0610)
 DE EST; expressed sequence tag.
 KM Homo sapiens (human)
 XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 XX [1]
 RN RP 1-2
 RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
 CC sequencing consortium of the German Genome Project
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 CC
 XX Key Location/Qualifiers
 FH source
 FT 1..2
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434N0610"
 FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SO Sequence 2 BP; 1 A; 0 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 t 1
 Db 2 T 2

RESULT 4
 HSM007187 ID HSM007187 standard; RNA; EST; 2 BP.
 AC AL042337;
 SV AL042337.1
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA: EST DKFZp434O0820_r1 (from clone DKFZp434O0820)
 DE EST; expressed sequence tag.
 KM Homo sapiens (human)
 XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.

```

XX RN [1]
RP 1-2
RA Oltenswelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
KI MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Medigenomix within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..2
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
SO Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 1 t 1

RESULT 5
HSM008709 standard; RNA; EST; 2 BP.
XX
XX AL043859;
XX
SV AL043859.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434B2128_r1 (from clone DKFZp434B2128)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
FH [1]
FH 1-2
FH Bioecker H., Boecker M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
FH ;
FH Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
FH MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by GBF within the cDNA
CC sequencing consortium of the German Genome Project
CC s1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..2
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
SO Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

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FT source 1..2
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
SO Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 1 t 1

RESULT 6
HSM011919 standard; RNA; EST; 2 BP.
XX
XX AL047069;
XX
SV AL047069.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp586P0517_r1 (from clone DKFZp586P0517)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
FH [1]
FH 1-2
FH Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
FH ;
FH Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
FH MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..2
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="586 (synonym: hute1). Vector pSport1; host
FT DH10B; sites NotI + SalI/MluI"
FT /dev_stage="adult"
FT /tissue_type="uterus"
SO Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

```

Db 1 t 1

RESULT 7

B1817789

LOCUS C3-G22 Axolotl Lambda zap library Ambystoma mexicanum cDNA similar
DEFINITION to Putative ribosomal protein S2, mRNA sequence.

ACCESSION B1817789

VERSION B1817789.1 GI:15951401

KEYWORDS EST.

SOURCE axolotl.

ORGANISM Ambystoma mexicanum

REFERENCE 1 (bases 1 to 2)

AUTHORS Voss,S.R., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,

TITLE JOURNAL

COMMENT

Expressed sequence tags from an axolotl limb regeneration library
Unpublished (2001)
Contact: Voss SR
Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel: 970 491 4869
Fax: 970 491 0649
Email: sross@amar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate = 5%). Trace file available:
sross@amar.colostate.edu.

FEATURES

source

1..2
Location/Qualifiers

BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 2 T 2

RESULT 8

C55081/c

LOCUS C55081 2 bp mRNA linear EST 16-SEP-1997
DEFINITION C55081 Yujl Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone YK350C9 3', mRNA sequence.

ACCESSION C55081

VERSION C55081.1 GI:2399682

KEYWORDS EST.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans.

REFERENCE 1 (bases 1 to 2)

AUTHORS Kohara,Y., Motolashvili,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano

TITLE JOURNAL

COMMENT

Expression map of the C. elegans genome
Unpublished (1996)
Contact: Yujl Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

FEATURES

source

1..2
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"

ACCESSION

VERSION C55081

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 2)

AUTHORS

TITLE

COMMENT

Expressed sequence tags from an axolotl limb regeneration library
Unpublished (2001)
Contact: Voss SR
Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel: 970 491 4869
Fax: 970 491 0649
Email: sross@amar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate = 5%). Trace file available:
sross@amar.colostate.edu.

FEATURES

source

1..2
Location/Qualifiers

BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 2 T 2

RESULT 9

A2463604

LOCUS A2463604 2 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0272J05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0272J05 R, DNA sequence.

ACCESSION A2463604

VERSION A2463604.1 GI:10621729

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 2)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

TITLE JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: J column: 05
Seq primer: CACACGGAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 451.
Location/Qualifiers

FEATURES

source

1..2
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0272J05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydromatically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (914732114191AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 2 T 2

RESULT 10
HSM003852 standard; RNA; EST; 3 BP.

AC AL039376;
XX AL039376.1

DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp43412010_r1 (from clone DKFZp43412010)
KW EST: expressed sequence tag.

XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.

XX [1]
RN 1-3

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPs, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX [1]

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers
FH source

FT 1..3
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp43412010"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"

Sequence 3 BP: 1 A; 0 C; 0 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 2 T 2

RESULT 11
HSM003852/C
ID HSM003852 standard; RNA; EST; 3 BP.

AC AL039376;
XX AL039376.1

DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp43412010_r1 (from clone DKFZp43412010)
KW EST: expressed sequence tag.

XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.

XX [1]
RN 1-3

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPs, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX [1]

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers
FH source

FT 1..3
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp43412010"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"

Sequence 3 BP: 1 A; 0 C; 0 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 1 T 1

RESULT 12
HSM007999
ID HSM007999 standard; RNA; EST; 3 BP.

AC AL043149;
XX AL043149.1

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XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434E1923_r1 (from clone DKFZp434E1923)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-3
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RT MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1..3
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434E1923"
XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX Sequence 3 BP; 0 A; 0 C; 0 G; 2 T; 1 other;
SQ

```

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 t 1
DB 1 T 1

```

RESULT 13
HSM008070/c standard; RNA; EST; 3 BP.
XX
AC AL043220;
XX
SV AL043220.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434I1923_r1 (from clone DKFZp434I1923)
XX
KW EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-3
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL

```

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1..3
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434I1923"
XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX Sequence 3 BP; 2 A; 0 C; 0 G; 0 T; 1 other;
SQ

```

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 t 1
DB 3 T 3

```

RESULT 14
AM672605/c
LOCUS
DEFINITION
2Xa Explanted metanephric mesenchyme induced to differentiate into
epithelial structures of the nephron ex vivo. Rattus norvegicus
CDNA similar to: gp1AFC022811.11AFC022811 Mus musculus
cornichon mRNA, mRNA sequence.
ACCESSION
AM672605
VERSION
AM672605.1 GI:7541085
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 3)
REFERENCE
Pilisov S.Y., Ivanov S.V., Yoshino K., Dove L.F., Pilisova T.M.,
Higginbotham K.G., Karavanova I., Lerman M. and Perantoni A.O.
Mesenchymal-epithelial transition in the developing metanephric
kidney: gene expression study by differential display
Genes 27 (1), 22-31 (2000)
20321327
CONTACT: Pilisov S.Y.
Laboratory of Comparative Carcinogenesis
National Cancer Institute
FCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA
Tel: 301 846 1242
Fax: 301 846 4956
Email: pilisov@mail.ncifcrf.gov
PCR Primers
FORWARD: ctgaagcttcgcgc
BACKWARD: ttaagcttttttttc
Insert Length: 350 Std Error: 0.00
Seq primer: SP6
High quality sequence stop: 261.
Location/Qualifiers
1..3
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone_lib="Explanted metanephric mesenchyme induced to
differentiate into epithelial structures of the nephron ex

vivo."
 /tissue_type="Metanephric mesenchyme"
 /cell_type="Mesenchymal/Epithelial"
 /dev_stage="13 dpc-1dpc"
 /lab_host="JM109"
 /note="Organ: Kidney; Vector: pCEM-TEasy (Promega); Restriction Enzymes 1: ApaI, AclI, SphI, NcoI, BstXI, NotI, SacI, and EcoRI SpeI, EcoRI, NotI, BstXI, SalI, NdeI, SacI, BstXI, and NsiI. CDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pCEM-TEasy (Promega); Its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."

BASE COUNT

1 a 0 c 2 g 0 t

Query Match 100.0%; Score 1; DB 9; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 t 1
 Db 2 T 2

RESULT 15

AZ438202 3 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0228108F Mouse 10kb plasmid UUCG1M library Mus musculus genomic

DEFINITION clone UUCG1M0228108 F, DNA sequence.

ACCESSION AZ438202

VERSION AZ438202.1 GI:10562215

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, R., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0228 row: 1 column: 08
 Seq primer: CGTTGTAAACGACGCCGACT
 Class: plasmid ends
 High quality sequence stop: 302.
 Location/Qualifiers
 1..3
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0228108"
 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

BASE COUNT
 ORIGIN 1 a 1 c 0 g 1 t

Query Match 100.0%; Score 1; DB 12; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
 Db 3 T 3

RESULT 16

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, R., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0228 row: 1 column: 08
 Seq primer: CGTTGTAAACGACGCCGACT
 Class: plasmid ends
 High quality sequence stop: 302.
 Location/Qualifiers
 1..3
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0228108"
 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321149b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 2 T 2

RESULT 17

BC926576 standard; RNA; EST; 4 BP.

AC BC926576;

SV BC926576.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

DE EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RP 1-4 MEDLINE: 21482651.

RX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,

Sathe G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.,

"Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries";

RT Osteoarthritis Cartilage 9(7):641-653(2001).

RL Osteoarthritis Cartilage 9(7):641-653(2001).

CC Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay_kumar-1@sk.com

CC Seq primer: T7.

XX Key

XX Location/Qualifiers

XX source 1..4

XX /db_xref="taxon:9606"

XX /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

FT Directional"
FT /organism="Homo sapiens"
FT /clone_lib="HNC (Human Normal Cartilage)"
FT /tissue_type="cartilage"
FT /lab_host="E.coli DH10 B"
XX

SO Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 T 1

RESULT 18

BC926576/C standard; RNA; EST; 4 BP.

AC BC926576;

SV BC926576.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

DE EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RP 1-4 MEDLINE: 21482651.

RX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,

Sathe G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.,

"Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries";

RT Osteoarthritis Cartilage 9(7):641-653(2001).

RL Osteoarthritis Cartilage 9(7):641-653(2001).

CC Contact: Sanjay Kumar

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CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay_kumar-1@sk.com

CC Seq primer: T7.

XX Key

XX Location/Qualifiers

XX source 1..4

XX /db_xref="taxon:9606"

XX /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

XX Directional"

XX /organism="Homo sapiens"

XX /clone_lib="HNC (Human Normal Cartilage)"

XX /tissue_type="cartilage"

XX /lab_host="E.coli DH10 B"

XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

XX Query Match

XX 100.0%; Score 1; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 2 t 2

RESULT 19
HSM003901/c standard; RNA; EST; 4 BP.
ID HSM003901
XX AL039425;
XX AL039425.1
XX SV
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434L0810_s1 (from clone DKFZp434L0810)
XX XX
XX KM
XX CC EST: expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX CC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX XX
XX RN
XX RP 1-4
XX RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
XX RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX XX

CC Clone from S. Wiemann, sequenced by Olagen within the cDNA
CC sequencing consortium of the German Genome Project
CC r1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX XX
XX FH Key Location/Qualifiers
XX FH source 1..4
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp434L0810"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1, host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SO Sequence 4 BP; 2 A; 0 C; 1 G; 0 T; 1 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 3 t 3

RESULT 20
HSM010467 standard; RNA; EST; 4 BP.
ID HSM010467
XX AC AL045617;
XX AL045617.1
XX SV
XX DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX XX
XX DE Homo sapiens mRNA; EST DKFZp434O245_r1 (from clone DKFZp434O245)
XX XX
XX KM EST: expressed sequence tag.
XX XX

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX CC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX XX

RN
RP 1-4
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX XX

CC Clone from S. Wiemann, sequenced by Olagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX XX
XX FH Key Location/Qualifiers
XX FH source 1..4
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp434O245"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1, host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SO Sequence 4 BP; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 3 t 3

RESULT 21
AM672622/c 4 bp mRNA linear EST 26-SEP-2001
LOCUS
DEFINITION
73C Explanted metanephric mesenchyme induced to differentiate into
epithelial structures of the nephron ex vivo. Rattus norvegicus
CDNA similar to: emb|AL049970.1|HSM800317 Homo sapiens
mRNA; CDNA DKFZp564B102 (from clone DKFZp564B102);, mRNA sequence.
AM672622
AM672622.1 GI:7541102

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
1 (bases 1 to 4)
Plisov,S.Y., Ivanov,S.V., Yoshino,K., Dove,L.F., Plisova,T.M.,
Higginbotham,K.G., Karavanova,I., Lerman,M., and Perantoni,A.O.,
Mesenchymal-epithelial transition in the developing metanephric
kidney: gene expression study by differential display
20321327
Contact: Plisov S.Y.
Laboratory of Comparative Carcinogenesis
National Cancer Institute
FCRDC, Bldg.538, Room 205, Frederick, MD 21702, USA

Tel: 301 846 1242
 Fax: 301 846 4956
 Email: plisov@mail.ncifcrf.gov
 PCR primers
 FORWARD: ctgcagctccgctc
 BACKWARD: ttaagctttttttt
 Insert Length: 262 Std Error: 0.00
 Seq primer: SP6
 High quality sequence stop: 262
 PolyA-yes

FEATURES

source

1. .4
 /location/Qualifiers
 /db_xref="taxon:10116"
 /clone_lib="Explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo"
 /tissue_type="Metanephric mesenchyme"
 /cell_type="Mesenchymal/Epithelial"
 /dev_stage="13 dpc-16dpc"
 /lab_host="JM109"
 /note="Organ: Kidney; Vector: pGEM-Teasy (Promega); Restriction Enzymes: 1: ApaI, AatII, SphI, NcoI, BstXI, NotI, SacI, and EcoRI SpeI, EcoRI, NotI, BstXI, PstI, SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pGEM-Teasy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."
 BASE COUNT
 ORIGIN
 1 a 0 c 3 g 0 t

Query Match
 Best Local Similarity 100.0%; Score 1; DB 9; Length 4;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
 Db 3 t 3

RESULT 22
 CDS004RB
 LOCUS
 DEFINITION
 CDS004RB 4 bp DNA linear GSS 03-JUN-1999
 Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 AL054121
 AL054121.1 GI:4931932
 GSS.
 SOURCE
 ORIGINISM
 fruit fly.
 Drosophila melanogaster
 Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
 Pterygota: Neoptera: Endopterygota: Diptera: Brachycera:
 Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.
 1 (bases 1 to 4)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's

PI and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1. .4
 /location/Qualifiers
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR10A06"
 /note="end : TET3"
 BASE COUNT
 ORIGIN
 1 a 1 c 0 g 2 t

Query Match
 Best Local Similarity 100.0%; Score 1; DB 12; Length 4;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
 Db 1 t 1

RESULT 23
 CDS004RB/c
 LOCUS
 DEFINITION
 CDS004RB 4 bp DNA linear GSS 03-JUN-1999
 Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 AL054121
 AL054121.1 GI:4931932
 GSS.
 SOURCE
 ORIGINISM
 fruit fly.
 Drosophila melanogaster
 Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
 Pterygota: Neoptera: Endopterygota: Diptera: Brachycera:
 Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.
 1 (bases 1 to 4)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 pl and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 location/Qualifiers
 1. .4
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR10A06"
 /note="end : TET3"
 BASE COUNT
 ORIGIN
 1 a 1 c 0 g 2 t

Query Match
 Best Local Similarity 100.0%; Score 1; DB 12; Length 4;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 DB 3 T 3

RESULT 24
 HSM007310 standard; RNA; EST: 5 BP.
 AC AL042460;
 XX AL042460.1

12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

Homo sapiens mRNA: EST DKFZP434E1821_r1 (from clone DKFZP434E1821)
 DE EST: expressed sequence tag.

OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
 RP 1-5
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX

CC Clone from S. Wiemann, sequenced by LMU within the CDNA
 CC sequencing consortium of the German Genome Project
 CC No st sequence available

CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..5
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone_id="DKFZP434E1821"
 FT DH10B: sites NotI + SalI
 FT /dev_stage="adult"
 FT /tissue_type="testis"

SO Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 DB 4 T 4

RESULT 25
 HSM007310/c standard; RNA; EST: 5 BP.
 ID HSM007310
 AC AL042460;
 XX AL042460.1

12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA: EST DKFZP434E1821_r1 (from clone DKFZP434E1821)
 XX EST: expressed sequence tag.

OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
 RP 1-5
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX

CC Clone from S. Wiemann, sequenced by LMU within the CDNA
 CC sequencing consortium of the German Genome Project
 CC No st sequence available

CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..5
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone_id="DKFZP434E1821"
 FT DH10B: sites NotI + SalI
 FT /dev_stage="adult"
 FT /tissue_type="testis"

SO Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 DB 3 T 3

RESULT 26
 HSM007835/c standard; RNA; EST: 5 BP.
 ID HSM007835
 AC AL042985;
 XX AL042985.1

12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

Homo sapiens mRNA: EST DKFZP434N1522_r1 (from clone DKFZP434N1522)

DE EST: expressed sequence tag.

OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
 RP 1-5
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX

CC Clone from S. Wiemann, sequenced by LMU within the CDNA
 CC sequencing consortium of the German Genome Project

```

CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH key location/Qualifiers
FH
FT source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434N152"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 5 BP; 2 A; 1 C; 0 G; 0 T; 2 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 2 T 2

RESULT 27
HSM011053 standard; RNA; EST; 5 BP.
ID HSM011053
AC AL046203;
XX
SV AL046203.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DL 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434D137_r1 (from clone DKFZp434D137)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-5
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH key location/Qualifiers
FH
FT source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434D137"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 3 T 3

RESULT 29
BG927410 standard; RNA; EST; 6 BP.
ID BG927410
AC BG927410;
XX

```

```

SV      BG927410.1
XX
DT      09-JUN-2001 (Rel. 68, Created)
DT      14-NOV-2001 (Rel. 69, Last updated, Version 2)
XX
DE      HNC1-1-C7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
XX
XX      EST.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX      [1]
XX      MEDLINE: 21482651.
XX      PUBMED: 11597177.
XX      Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
XX      Sahle G.M., Hui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
XX      Identification and Initial Characterization of 5000 expressed sequenced
XX      tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
XX      libraries";
XX      Osteoarthritis Cartilage 9(7):641-653(2001).
XX
XX      Contact: Sanjay Kumar
XX      CC      UN2109
XX      CC      GlaxoSmithKline
XX      CC      709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
XX      CC      Tel: 610-270-7245
XX      CC      Fax: 610-270-5598
XX      CC      Email: sanjay_kumar-1@gsk.com
XX      CC      Seq primer: T7.
XX
FH      Key      Location/Qualifiers
FH
FT      source      1..6
FT      /db_xref="taxon:9606"
FT      /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
FT      Directional"
FT      /organism="Homo sapiens"
FT      /clone_lib="HNC (Human Normal Cartilage)"
FT      /tissue_type="cartilage"
FT      /lab_host="E.coli DH10 B"
FT
SO      Sequence 6 BP: 0 A; 5 C; 0 G; 1 T; 0 other:

Query Match      100.0%; Score 1: DB 2: Length 6:
Best Local Similarity 100.0%; Pred. No. 0:
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

OY      1 t 1
        |
DB      3 t 3

RESULT 30
HSM003844
ID      HSM003844 standard; RNA: EST: 6 BP.
XX
AC      AL039368:
XX
SV      AL039368.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX
XX      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

```

```

OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX      [1]
XX      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX      sequencing consortium of the German Genome Project
XX      CC      No s1 sequence available
XX      CC      This clone is available at the RZPD in Berlin
XX      CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key      Location/Qualifiers
FH
FT      source      1..6
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone_lib="DKFZp434I0110"
FT      /clone_lib="434 (synonym: htes3). Vector pSPORT1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
FT
SO      Sequence 6 BP: 2 A; 0 C; 2 G; 2 T; 0 other:

Query Match      100.0%; Score 1: DB 2: Length 6:
Best Local Similarity 100.0%; Pred. No. 0:
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

OY      1 t 1
        |
DB      5 T 5

RESULT 31
HSM003844/C
ID      HSM003844 standard; RNA: EST: 6 BP.
XX
AC      AL039368:
XX
SV      AL039368.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX
XX      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX      [1]
XX      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX      sequencing consortium of the German Genome Project
XX      CC      No s1 sequence available
XX      CC      This clone is available at the RZPD in Berlin
XX      CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key      Location/Qualifiers
FH

```

```

FH source 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J0110"
FT /clone_id="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SO Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

```

```

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 t 1
Db 4 T 4

```

```

RESULT 32
ID HSM004423 standard; RNA; EST; 6 BP.
XX AL039947;
XX AL039947.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX
XX EST: expressed sequence tag.
XX
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1..6
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434J0112"
XX /clone_id="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX
XX Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

```

```

OY 1 t 1
Db 5 T 5

```

```

RESULT 33
ID HSM004423/C standard; RNA; EST; 6 BP.
XX AL039947;
XX AL039947.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX
XX EST: expressed sequence tag.
XX
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1..6
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434J0112"
XX /clone_id="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX
XX Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

```

```

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 t 1
Db 4 T 4

```

```

RESULT 34
ID HSM007334 standard; RNA; EST; 6 BP.
XX AL042484;
XX AL042484.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434F0321_r1 (from clone DKFZp434F0321)

```

```
XX EST: expressed sequence tag.
KM Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
CC
FH Key Location/Qualifiers
FH
FT source
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434f0321"
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 5 T 5

RESULT 35
HSM007334/C
ID HSM007334 standard; RNA; EST; 6 BP.
XX
AC AL042484;
XX
SV AL042484.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434f0321_r1 (from clone DKFZp434f0321)
XX
XX EST: expressed sequence tag.
XX
KW Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
```

```
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
CC
FH Key Location/Qualifiers
FH
FT source
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434f0321"
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 4 T 4

RESULT 36
HSM007683
ID HSM007683 standard; RNA; EST; 6 BP.
XX
AC AL042833;
XX
SV AL042833.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX
XX EST: expressed sequence tag.
XX
KW Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
CC
FH Key Location/Qualifiers
FH
FT source
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434G1622"
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
XX
SQ Sequence 6 BP; 2 A; 2 C; 0 G; 2 T; 0 other;
```


Query Match 100.0%; Score 1; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 3 t 3

RESULT 37
 HSM007683/C
 ID HSM007683 standard; RNA; EST; 6 BP.

XX AL042833;
 AC AL042833.1
 SV
 XX

12-MAR-1999 (Rel. 59, Created)
 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)

XX EST; expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.

XX

11
 1-6
 RP Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

PH key Location/Qualifiers

FT source 1..6

FT /db_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434G1622"

FT /clone_11b="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev_stage="adult"

FT /tissue_type="testis"

FT

XX

SO

Sequence 6 BP; 2 A; 2 C; 0 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 2 t 2

RESULT 38
 HSM008014
 ID HSM008014 standard; RNA; EST; 6 BP.

XX AL043164;
 AC AL043164.1
 SV

XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 DE Homo sapiens mRNA; EST DKFZp434F1123_s1 (from clone DKFZp434F1123)

XX EST; expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.

XX

11

1-6

RP Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

PH key Location/Qualifiers

FT source 1..6

FT /db_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434F1123"

FT /clone_11b="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev_stage="adult"

FT /tissue_type="testis"

FT

XX

SO

Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 1 t 1

RESULT 39
 HSM008014/C
 ID HSM008014 standard; RNA; EST; 6 BP.

XX AL043164;
 AC AL043164.1
 SV

12-MAR-1999 (Rel. 59, Created)
 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 DE Homo sapiens mRNA; EST DKFZp434F1123_s1 (from clone DKFZp434F1123)

XX EST; expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.

XX

11

1-6

RP Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

KL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
 CC Clone from S. Wiemann, sequenced by LMU within the CCNA
 CC sequencing consortium of the German Genome Project
 CC rl sequencing also available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 FH Key Location/Qualifiers
 FT source 1..6
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone_lib="434 (synonym: htes3). Vector pSPORT1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 SO Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 t 1
 1
 Db 3 T 3

RESULT 40
 BC897546 Standard: RNA; EST; 7 BP.
 AC BC897546;
 XX BC897546.1
 SV BC897546.1
 XX 09-JUN-2001 (Rel. 68, Created)
 DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)
 XX
 DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA
 DE sequence.
 DE
 XX
 XX EST.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX
 RN [1]
 RP 1-7
 RX MEDLINE: 21482651.
 RX PUBMED: 11597177.
 RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
 RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.,
 RT "Identification and initial characterization of 5000 expressed sequenced
 RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
 RT libraries";
 RL Osteoarthritis Cartilage 9(7):641-653(2001).
 XX
 XX
 CC Contact: Sanjay Kumar
 CC UW2109
 CC GlaxoSmithKline
 CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 CC Tel: 610-270-7245
 CC Fax: 610-270-5598
 CC Email: sanjay.kumar-1@gsk.com
 CC Seq primer: T7.
 CC
 XX
 XX
 FH Key Location/Qualifiers

FH source 1..7
 FT /db_xref="taxon:9606"
 FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 FT Directional"
 FT /organism="Homo sapiens"
 FT /clone_lib="HOA (Human Osteoarthritic Cartilage)"
 FT /tissue_type="Cartilage"
 FT /lab_host="E.coli DH10 B"
 XX
 XX
 SO Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 t 1
 1
 Db 2 T 2

RESULT 41
 BC897546/C Standard: RNA; EST; 7 BP.
 ID BC897546
 XX BC897546;
 AC BC897546.1
 SV BC897546.1
 XX 09-JUN-2001 (Rel. 68, Created)
 DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)
 XX
 DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA
 DE sequence.
 DE
 XX
 XX EST.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX
 RN [1]
 RP 1-7
 RX MEDLINE: 21482651.
 RX PUBMED: 11597177.
 RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
 RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.,
 RT "Identification and initial characterization of 5000 expressed sequenced
 RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
 RT libraries";
 RL Osteoarthritis Cartilage 9(7):641-653(2001).
 XX
 XX
 CC Contact: Sanjay Kumar
 CC UW2109
 CC GlaxoSmithKline
 CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 CC Tel: 610-270-7245
 CC Fax: 610-270-5598
 CC Email: sanjay.kumar-1@gsk.com
 CC Seq primer: T7.
 CC
 XX
 XX
 FH Key Location/Qualifiers
 FT source 1..7
 FT /db_xref="taxon:9606"
 FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 FT Directional"
 FT /organism="Homo sapiens"
 FT /clone_lib="HOA (Human Osteoarthritic Cartilage)"
 FT /tissue_type="Cartilage"
 FT /lab_host="E.coli DH10 B"
 XX
 XX

Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1: DB 2; Length 7;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 4 T 4

RESULT 42

HS0007412
ID HSM007412 standard; RNA; EST; 7 BP.

AC AL042562;

SV AL042562.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)

KW EST; expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP 1-7

KA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopsterspitz 18a D-82152 Martinsried, GERMANY

XX

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC No s1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

XX

FT Key Location/Qualifiers

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

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FT

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FT

FT

FT

FT

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SV

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DT

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DT

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DE

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AL042562.1

12-MAR-1999 (Rel. 59, Created)

12-MAR-1999 (Rel. 59, Last updated, Version 1)

Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)

EST; expressed sequence tag.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

Eutheria; Primates; Catarrhini; Homiidae; Homo.

[1]

1-7

Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

MIPS, Am Klopsterspitz 18a D-82152 Martinsried, GERMANY

Clone from S. Wiemann, sequenced by LMU within the CDNA

sequencing consortium of the German Genome Project

No s1 sequence available

This clone is available at the RZPD in Berlin

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

Location/Qualifiers

1. .7

/db_xref="taxon:9606"

/organism="Homo sapiens"

/clone="DKFZp434J1721"

/DH0B; s1:es NotI + Salt"

/dev-stage="adult"

/tissue-type="testis"

Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 1: DB 2; Length 7;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

DB 5 T 5

RESULT 44

HS0007502

ID HSM007502 standard; RNA; EST; 7 BP.

AC AL042562;

SV AL042562.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434J1921_r1 (from clone DKFZp434J1921)

EST; expressed sequence tag.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

Eutheria; Primates; Catarrhini; Homiidae; Homo.

[1]

1-7

Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
KL MIPS, Am Klopferstr. 18a D-82152 Martinsried, GERMANY
XX
CC (clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No. 51 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434N1921"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other:

Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
1
Db 4 T 4

RESULT 45
LOCUS C58888 7 bp mRNA linear EST 22-SEP-1997
DEFINITION C58888 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
ACCESSION C58888
VERSION C58888.1 GI:2417593
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 7)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
TITLE Expression map of the C. elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1..7
source
/organism="Caenorhabditis elegans"
/strain="CBI489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="YK383a7"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT 2 a 0 c 1 g 3 t 1 others
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
1
Db 4 T 4

Search completed: July 15, 2002, 20:07:36
Job time: 14494 sec

Run on: July 15, 2002, 20:07:35 ; Search time 7067.1 Seconds

1.910 Million cell updates/sec

Title: US-09-375-248-1_COPY_3360_3360
perfect score: 1

Sequence:

Scoring table: OLIGO_NUC

Capop 60.0 , Capext 60.0

searched: 13736207 seqs, 6748477542 residues

Word size :

Total number of hits satisfying chosen parameters: 27472414

Maximum DB seq length:	20000000000
------------------------	-------------

Post-processing: Listing first 45 summaries

Database :

```

1:  em_estba:*
2:  em_esthum:*
3:  em_estlm:*
4:  em_estlm:*
5:  em_estlm:*
6:  em_estlp:*
7:  em_estro:*
8:  em_hlc:*
9:  gb_estl:*
10: gb_estc:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1	100.0	2	2	HSMM03817	A1039341 Homo sapi
2	1	100.0	2	2	HSMM007187	A1043237 Homo sapi
3	1	100.0	2	2	HSMM008709	A1043859 Homo sapi
4	1	100.0	2	2	HSMM011919	A1047069 Homo sapi
5	1	100.0	2	10	B1817789	G3-G327
6	1	100.0	2	10	C55081	C55081 C55081
7	1	100.0	2	10	BE351920	BE351920 89405300
8	1	100.0	2	12	A2463604	A2463604 1M027230
9	1	100.0	3	9	AM672605	AM672605 2Xa ExptA
C 9	1	100.0	3	12	CNS00KCV	A2438202 1M0228102
C 11	1	100.0	3	12	A2438202	A1077515 Drosophila
C 12	1	100.0	4	2	BG936576	B9926576 HNC56-1-A
C 13	1	100.0	4	2	BG926576	B9926576 HNC56-1-A
C 14	1	100.0	4	2	HSMM003901	A1039425 Homo sapi
C 15	1	100.0	4	2	HSMM010467	A1045617 Homo sapi
C 16	1	100.0	4	2	HSMM010467	A1045617 Homo sapi
C 17	1	100.0	4	9	AM672622	AM672622 73c ExptA

18	1	100.0	4	12	CNS004RB
C 19	1	100.0	5	2	HSM007310
C 20	1	100.0	5	2	HSM007835
C 21	1	100.0	5	2	HSM011053
C 22	1	100.0	6	2	BG927410
C 23	1	100.0	6	2	HSM003864
C 24	1	100.0	6	2	HSM004423
C 25	1	100.0	6	2	HSM007334
C 26	1	100.0	6	2	HSM007663
C 27	1	100.0	6	2	HSM008014
C 28	1	100.0	6	2	HSM010918
C 29	1	100.0	6	2	HSM010918
C 30	1	100.0	6	10	BE726686
C 31	1	100.0	6	10	BE726686
C 32	1	100.0	7	2	BG897546
C 33	1	100.0	7	2	BG897546
C 34	1	100.0	7	2	HSM007412
C 35	1	100.0	7	2	HSM007412
C 36	1	100.0	7	2	HSM007502
C 37	1	100.0	7	2	HSM007502
C 38	1	100.0	7	10	C58888
C 39	1	100.0	8	2	HSM001420
C 40	1	100.0	8	2	HSM001743
C 41	1	100.0	8	2	HSM004451
C 42	1	100.0	8	2	HSM004451
C 43	1	100.0	8	2	HSM007277
C 44	1	100.0	8	2	HSM007277
C 45	1	100.0	8	2	HSM007323
					AL054121 Drosophila
					AL042460 Homo sapi
					AL042985 Homo sapi
					AL045203 Homo sapi
					Bg927410 HNC1-1-G7
					AL033368 Homo sapi
					AL039947 Homo sapi
					AL042484 Homo sapi
					AL042833 Homo sapi
					AL043164 Homo sapi
					AL046068 Homo sapi
					AL046068 Homo sapi
					BE726686 894095D11
					BE726686 894095D11
					Bg897546 HOA14-1-H
					Bg897546 HOA14-1-H
					AL042562 Homo sapi
					AL042562 Homo sapi
					AL042562 Homo sapi
					C58888 C58888 Yuj1
					AL037095 Homo sapi
					AL037413 Homo sapi
					AL039975 Homo sapi
					AL039975 Homo sapi
					AL042427 Homo sapi
					AL042427 Homo sapi
					AL042473 Homo sapi

ALIGNMENTS

RESULT 1
HSM003817

standard; RNA; EST; 2 BP.

AC AL039341;

SV AL039341.1
yy

DT 12-MAR-1999 (Rel. 59, Created)

12 MAR 1999 (REL. 59, Last updated, Version 1)
XX

XX sapiens mRNA; EST DKFZp434F2010_r1 (from clone DKFZp434F2010)

EST; expressed sequence tag.

OS Homo sapiens (human)

Eutheria; Primates; Catarrhini; Hominoidea; Homo

XX
RN
(1)

RP 1-2

RT : Gassenhuber J., Wleemann S.,
RT : Gassenhuber J., Wleemann S.,

Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
MIPS, Am Klopfersnitz 18a D-82165 Matriedl, Germany.
RL

XX - not considered, German

sequencing consortium of the German Genotox Project

CC No SI sequence available
CC This clone is available

Please contact the RZPD: Ressourcenzentrum. H

cc Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
xx

FH FH	Key	Location/Qualifiers
----------	-----	---------------------

FT source

ET ET

ET

3.1

```
/crlone_id=434 (synonym: htes3). Vector pSport1; host
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FT DH10B: sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
 DB 2 C 2

RESULT 2
 HSM007187 standard; RNA; EST; 2 BP.

AC AL042337;
 XX
 SV AL042337.1
 XX
 UT 12-MAR-1999 (Rel. 59, Created)
 UT 12-MAR-1999 (Rel. 59, last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp43400820_r1 (from clone DKFZp43400820)
 XX
 EST: expressed sequence tag.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 XX
 FN 111
 RP 1-2
 RA Ottenaeider B., Obermaier B., Neues W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX

CC Clone from S. Wiemann, sequenced by Medigenomix within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No st sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX

FN Key Location/Qualifiers

FT source 1..2
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp43400820"
 FT /clone_1b="434 (synonym: htcs3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX

SQ Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
 DB 2 C 2

RESULT 3

HSM008709 standard; RNA; EST; 2 BP.

AC AL043859;
 XX
 SV AL043859.1
 XX

DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp434B2128_r1 (from clone DKFZp434B2128)
 XX
 EST: expressed sequence tag.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 XX

FN 111
 RP 1-2
 RA Bloeker H., Boecker M., Brandt P., Neues W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX

CC Clone from S. Wiemann, sequenced by GBF within the cDNA
 CC sequencing consortium of the German Genome Project
 CC s1 sequence also available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX

FN Key Location/Qualifiers

FT source 1..2
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434B2128"
 FT /clone_1b="434 (synonym: htcs3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX

SQ Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
 DB 2 C 2

RESULT 4
 HSM011919 standard; RNA; EST; 2 BP.

AC AL047069;
 XX
 SV AL047069.1
 XX

DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp586P0517_r1 (from clone DKFZp586P0517)
 XX
 EST: expressed sequence tag.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 XX

```

XX      (1)
RN      1-2
RP      Koehler K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT      :
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by BMFZ within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the KZPD in Berlin
CC      Please contact the KZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
PH      Key      Location/Qualifiers
FT      source      1..2
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZps86P0517"
FT      /clone_1lb="586 (synonym: hute1). Vector pSport1; host
FT      DH10B; sites NotI + SalI/MluI"
FT      /dev_stage="adult"
FT      /tissue_type="uterus"
XX
SQ      Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other:
Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 c 1
DB      2 C 2

RESULT 5
BI817789
LOCUS      2 bp      mRNA      linear      EST 04-OCT-2001
DEFINITION      G3-G22 Axolotl Lambda zap Library Ambystoma mexicanum cDNA similar
ACCESSION      BI817789
VERSION      BI817789.1 GI:15951401
KEYWORDS      EST.
SOURCE      axolotl.
ORGANISM      Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomidae;
Ambystoma.
1 (bases 1 to 2)
Voss,S.R., Kling,D., Maness,N., Smith,J.J., Rondel,M., Bryant,S.V.,
Gardiner,D.M. and Parichy,D.M.
Expressed sequence tags from an axolotl limb regeneration library
Unpublished (2001)
Contact: Voss SR
Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel: 970 491 4869
Fax: 970 491 0649
Email: svoss@lamar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate = 5%). Trace file available:
svoss@lamar.colostate.edu.
Location/Qualifiers
1..2
/organism="Ambystoma mexicanum"
/db_xref="taxon:8296"
/clone_1lb="Axolotl Lambda zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

FEATURES
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/db_xref="taxon:8296"
/clone_1lb="Axolotl Lambda zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

BASE COUNT      0 a      1 c      0 g      1 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 1; DB 10; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 c 1
DB      2 C 2

RESULT 7
BE351920
LOCUS      2 bp      mRNA      linear      EST 18-JUL-2000
DEFINITION      894053D07.y1 C. reinhardtii CC-1690, normalized, Lambda zap II
ACCESSION      BE351920
VERSION      BE351920.1 GI:9263773
KEYWORDS      EST.
SOURCE      Chlamydomonas reinhardtii.
ORGANISM      Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
1 (bases 1 to 2)

```


AUTHORS Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J. P., Silligow, C., Stern, D. and Surzycki, R.

TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants: Project Phase 2

JOURNAL Unpublished (2000)

COMMENT Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu

FEATURES
source
1..2
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 219r"
/db_xref="taxon:3055"
/clone_11b="C. reinhardtii CC-1690, normalized, lambda Zap II"

BASE COUNT
ORIGIN 0 a 0 c 2 g 0 t

Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1
|
Db 2 c 2

RESULT 8
A2463604 2 bp DNA linear GSS 04-OCT-2000
LOCUS J00272205R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone A2463604
ACCESSION A2463604
VERSION A2463604.1 GI:10621729
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

JOURNAL
COMMENT

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: J column: 05
Seq primer: CACACAGCAAAACACGATACAC
Class: plasmid ends
High quality sequence stop: 451.

FEATURES
source
1..2
/organism="Mus musculus"
/strain="C57Bl/6j"
/db_xref="taxon:10090"
/clone="UUCG1M027205"
/clone_11b="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57Bl/6j (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (911473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN 0 a 0 c 1 g 1 t

Query Match 100.0%; Score 1; DB 12; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1
|
Db 1 c 1

RESULT 9
AW672605 3 bp mRNA linear EST 26-SEP-2001
LOCUS AW672605
DEFINITION 2Xa explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo. Rattus norvegicus
CDNA similar to: gb|AF022811.1|AF022811 Mus musculus
corinchnon mRNA, mRNA sequence.
ACCESSION AW672605
VERSION AW672605.1 GI:7541085
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 3)
Pilsnov, S.Y., Ivanov, S.V., Yoshino, K., Dove, L.F., Pilsnova, T.M., Higginbotham, K.G., Karavanova, I., Lerman, M. and Perantoni, A.O.
Mesenchymal-epithelial transition in the developing metanephric kidney: gene expression study by differential display
Genetics 27 (1), 22-31 (2000)
20321327
Contact: Pilsnov S.Y.
Laboratory of Comparative Carcinogenesis
National Cancer Institute
FCRDC, Bldg.538, Room 205, Frederick, MD 21702, USA

JOURNAL
COMMENT

Tel: 301 846 1242
 Fax: 301 846 4956
 Email: pliso@mail.ncifcrf.gov
 PCR Primers
 FORWARD: ctcgagctccgc
 REVERSE: ttaagcttttttttc
 Insert Length: 350 Std Error: 0.00
 Seq primer: Sp6
 High quality sequence stop: 261.

FEATURES

source

1..3
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /clone_lib="Explanated metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo."
 /tissue_type="Metanephric mesenchyme"
 /cell_type="Mesenchymal/epithelial"
 /dev_stage="13 dpc-16dpc"
 /lab_host="JM109"
 /note="Organ: Kidney; Vector: pGEM-Teasy (Promega).; Restriction Enzymes: I, AclI, AclII, SphI, NcoI, BstXI, NotI, SacII, and EcoRI SpeI, EcoRI, NotI, BstXI, PstI, SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pGEM-Teasy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."

BASE COUNT

1 a 0 c 2 g 0 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 1; DB 9; Length 3;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1

Db 3 c 3

RESULT 10

A2438202

LOCUS A2438202 3 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0228108F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0228108 F, DNA sequence.

ACCESSION A2438202

VERSION A2438202.1 GI:10562215

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 3)

REFERENCE

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0228 row: 1 column: 08

Seq primer: CGTTGTAAACGACGCCACT

Class: plasmid ends

High quality sequence stop: 302.

Location/Qualifiers

1..3

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="UUGC1M0228108"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (911473211419b1AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

1 a 1 c 0 g 1 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 1; DB 12; Length 3;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1

Db 1 c 1

RESULT 11

CNS00RCV/c

LOCUS CNS00RCV/c 3 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence Tref3 end of BAC:
 BACR17D19 of RPiC-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION AL077515

VERSION AL077515.1 GI:4956992

KEYWORDS GSS.

SOURCE fruit fly.

Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; 1 (bases 1 to 3)

REFERENCE

AUTHORS

TITLE Direct Submission

Genoscope.

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazuo Osoegawa and

Aaron Mammose in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPiC-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain yz; cn bw sp, the same strain used for the BDGP's

Db 4 C 4

RESULT 14

HSMD03901/c standard; RNA: EST; 4 BP.

XX AL039425;

SV AL039425.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434L0810_s1 (from clone DKFZp434L0810)

DE EST: expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia:

XX Eutheria: Primates: Catarrhini: Homiidae: Homo.

XX [1]

KA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

KL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Kioferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA

CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

XX source

XX 1..4

XX /db_xref="taxon:9606"

XX /organism="Homo sapiens"

XX /clone_lib="434 (synonym: htes3). Vector pSport1; host

XX DH10B; sites NotI + SalI"

XX /dev_stage="adult"

XX /tissue_type="testis"

XX Sequence 4 BP; 2 A; 0 C; 1 G; 0 T; 1 other;

XX Query Match 100.0%; Score 1; DB 2; Length 4;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 4 C 4

XX RESULT 15

XX HSM010467 standard; RNA: EST; 4 BP.

XX AL045617;

SV AL045617.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434O245_r1 (from clone DKFZp434O245)

KW EST: expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia:

XX Eutheria: Primates: Catarrhini: Homiidae: Homo.

XX [1]

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Kioferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA

CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

XX source

XX 1..4

XX /db_xref="taxon:9606"

XX /organism="Homo sapiens"

XX /clone="DKFZp434O245"

XX /clone_lib="434 (synonym: htes3). Vector pSport1; host

XX DH10B; sites NotI + SalI"

XX /dev_stage="adult"

XX /tissue_type="testis"

XX Sequence 4 BP; 0 A; 2 C; 1 G; 1 T; 0 other;

XX Query Match 100.0%; Score 1; DB 2; Length 4;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 C 1

XX RESULT 16

XX HSM010467/c standard; RNA: EST; 4 BP.

XX AL045617;

SV AL045617.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434O245_r1 (from clone DKFZp434O245)

DE EST: expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia:

XX Eutheria: Primates: Catarrhini: Homiidae: Homo.

XX [1]

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Kioferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA

CC sequencing consortium of the German Genome Project

CC No s1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX Key Location/Qualifiers
 FH source 1..4
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone_lib="OKF2p4340245"
 FT /clone_lib="434 (synonym: h10s). Vector pSport1: host
 FT /dev_stage="adult"
 FT /issue_type="testis"
 XX
 SO Sequence 4 bp; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
 Db 4 C 4

RESULT 17
 LOCUS AM672622/c 4 bp mRNA linear EST 26-SEP-2001
 DEFINITION 73C Explaned metanephric mesenchyme induced to differentiate into
 epithelial structures of the nephron ex vivo. Rattus norvegicus
 cDNA similar to: emb1AL049970.1|HSM800317 Homo sapiens
 mRNA: CDNA DKF2p5648102 (from clone DKF2p5648102); mRNA sequence.
 AM672622.1 GI:7541102
 EST.
 VERSION AM672622.1 GI:7541102
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 4)
 Pilsov,S.Y., Ivanov,S.V., Yoshino,K., Dove,L.F., Pilsova,T.M.,
 Higginbotham,K.G., Karavanova,I., Lerman,M., and Perantonis,A.O.,
 Kidney: gene expression study by differential display
 Genests 27 (1), 22-31 (2000)
 20321327
 COMMENT Contact: Pilsov S.Y.
 Laboratory of Comparative Carcinogenesis
 National Cancer Institute
 PCRDC, Bldg.538, Room 205, Frederick, MD 21702, USA
 Tel: 301 846 1242
 Fax: 301 846 4956
 Email: pilsov@mail.ncifcrf.gov
 PCR Primers
 FORWARD: ctgagctccgctc
 BACKWARD: cttaagctttcttcttg
 Insert Length: 262 Std Error: 0.00
 Seq primer: SP6
 High quality sequence stop: 262
 POLYA=yes.

FEATURES
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 Location/Qualifiers
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 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /clone_lib="Explaned metanephric mesenchyme induced to
 differentiate into epithelial structures of the nephron ex
 vivo."
 /issue_type="metanephric mesenchyme"
 /cell_type="Mesenchymal/Epithelial"
 /dev_stage="13 dpc-16dpc"
 /lab_host="JMI09"

/note="Organ: Kidney; Vector: pGEM-Teasy (Promega).";
 Restriction Enzymes 1: AclI, AatII, SphI, NcoI, BstXI,
 NotI, SacII, and EcoRI SpeI, EcoRI, NcoI, BstXI, PstI,
 SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment
 PCR-amplified in mRNA differential display analysis:
 cloned in pGEM-Teasy (Promega); its expression is
 developmentally regulated during mesenchymal-epithelial
 conversion in the metanephric kidney."

BASE COUNT 1 a 0 c 3 g 0 t
 ORIGIN

Query Match 100.0%; Score 1; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
 Db 4 C 4

RESULT 18
 LOCUS CNS004RB 4 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TERT3 end of BAC #
 BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL054121
 AL054121.1 GI:4931932
 GSS.
 VERSION
 KEYWORDS
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 4)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;
 BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
 - Web: www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 PL and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library,
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

FEATURES

source

1..4
 Location/Qualifiers
 1..4
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR10A06"
 /note="end : TERT3"
 BASE COUNT 1 a 1 c 0 g 2 t
 ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
 Db 4 C 4

Db 4 C 4

RESULT 19

HSM007310/c
ID HSM007310 standard; RNA: EST: 5 BP.

XX AL042460:

XX AL042460.1

SV 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434E1821_r1 (from clone DKFZp434E1821)

XX EST: expressed sequence tag.

CS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
UC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

KA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FH source 1..5

FT /db_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone_lib="434 (synonym: hres3). Vector psportl: host

FT DH10B: sites NotI + SalI"

FT /dev_stage="adult"

FT /tissue_type="testis"

FT Sequence 5 BP: 2 A: 0 C: 1 G: 2 T: 0 other;

SQ

Query Match 100.0%; Score 1; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1

Db 1 C 1

RESULT 20

HSM007835 standard; RNA: EST: 5 BP.

XX AL042985:

SV AL042985.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434N1522_r1 (from clone DKFZp434N1522)

XX EST: expressed sequence tag.

XX

Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

UC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

KA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FH source 1..5

FT /db_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone_lib="434 (synonym: hres3). Vector psportl: host

FT DH10B: sites NotI + SalI"

FT /dev_stage="adult"

FT /tissue_type="testis"

FT Sequence 5 BP: 2 A: 1 C: 0 G: 0 T: 2 other;

SQ

Query Match 100.0%; Score 1; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1

Db 5 C 5

RESULT 21

HSM011053/c standard; RNA: EST: 5 BP.

XX AL046203:

SV AL046203.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434D137_r1 (from clone DKFZp434D137)

XX EST: expressed sequence tag.

CS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
UC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

KA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by BMFZ within the CDNA

CC sequencing consortium of the German Genome Project

CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

```

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: hhes3). Vector pSPORT1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SO Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 22
HG927410 standard; RNA; EST; 6 BP.
XX
AC HG927410;
XX
SV HG927410.1
XX
SV 09-JUN-2001 (Rel. 68, Created)
XX 14-NOV-2001 (Rel. 69, Last updated, Version 2)
XX
DE HNC1-1-C7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
XX
XX EST.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX [1]
XX 1-6
XX MEDLINE: 21482651.
XX PUBMED: 11597177.
XX
RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
RA Salhe G.H., Mut P., Agarwal P., Badger A.M., Lee J.C., Gonen M., Lark M.W.:
RT "Identification and initial characterization of 5000 expressed sequenced
RT tags (ESTs) each from adult human normal and osteoarthritis cartilage cDNA
RT libraries";
RL Osteoarthritis Cartilage 9(7):641-653(2001).
XX
XX Contact: Sanjay Kumar
XX UW2109
XX GlaxoSmithKline
XX 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
XX Tel: 610-270-7245
XX Fax: 610-270-5598
XX Email: sanjay_kumar-1@gsk.com
XX Seq primer: T7.
XX
FH Key Location/Qualifiers
FH
FT source 1..6
FT /db_xref="taxon:9606"
FT /note="Vector: pSPORT 1; site_1: SalI; site_2: NotI;
FT directional"
FT /organism="Homo sapiens"
FT /clone_lib="HNC (Human Normal Cartilage)"
FT /tissue_type="Cartilage"
FT

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FT /lab_host="E.coli DH10 B"
XX
SO Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 23
HSM003844/C standard; RNA; EST; 6 BP.
XX
ID HSM003844
XX
AC AL039368;
XX
SV AL039368.1
XX
SV 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX
XX EST: expressed sequence tag.
XX
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX [1]
XX 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Cloned from S. Wiemann, sequenced by Qiagen within the cDNA
XX sequencing consortium of the German Genome Project
XX No sl sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="DKFZp434I0110"
FT /clone_lib="434 (synonym: hhes3). Vector pSPORT1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
XX Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 2 C 2

RESULT 24
HSM004423/C standard; RNA; EST; 6 BP.
ID HSM004423

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XX AC AL039947;
XX SV AL039947.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX KW EST: expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX RN [1]
XX RP 1-6
XX RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key
XX FH Location/Qualifiers
XX FT source
XX FT 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp434J0112"
XX FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SO Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 2 C 2

RESULT 25
HSM007334/C standard; RNA; EST; 6 BP.
XX ID HSM007334
XX AC AL042484;
XX SV AL042484.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434F0321_r1 (from clone DKFZp434F0321)
XX KW EST: expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX RN [1]

```

```

RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the CDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key
XX FH Location/Qualifiers
XX FT source
XX FT 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp434F0321"
XX FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SO Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 2 C 2

RESULT 26
HSM007683 standard; RNA; EST; 6 BP.
XX ID HSM007683
XX AC AL042833;
XX SV AL042833.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX KW EST: expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX RN [1]
XX RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the CDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key
XX FH Location/Qualifiers
XX FT source
XX FT 1..6
XX FT /db_xref="taxon:9606"

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FT      /organism="Homo sapiens"
FT      /clone="DKFzp434G1622"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
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XX
XX
SO      Sequence 6 BP; 2 A; 2 C; 0 G; 2 T; 0 other;

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Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 C 1
DB      5 C 5

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RESULT 27
HSM008014 standard; RNA; EST; 6 BP.
XX
XX      AL043164;
XX      SV
XX      AL043164.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFzp434F1123_s1 (from clone DKFzp434F1123)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX      [1]
XX      source      1.6
XX      FT      /db_xref="taxon:9606"
XX      FT      /organism="Homo sapiens"
XX      FT      /clone="DKFzp434F1123"
XX      FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX      FT      DH10B; sites NotI + SalI"
XX      FT      /dev_stage="adult"
XX      FT      /tissue_type="testis"
XX
XX      Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 other;

```

```

PH      key      location/Qualifiers
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FH      source      1.6
FH      FT      /db_xref="taxon:9606"
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FH      FT      DH10B; sites NotI + SalI"
FH      FT      /dev_stage="adult"
FH      FT      /tissue_type="testis"
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XX
XX
SO      Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 other;

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Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 C 1
DB      2 C 2

```

```

RESULT 28
HSM010918 standard; RNA; EST; 6 BP.
XX
XX      HSM010918 standard; RNA; EST; 6 BP.
XX
XX      AL046068;
XX
XX      AL046068.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFzp434F1672_r1 (from clone DKFzp434F1672)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX      [1]
XX      source      1.6
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XX      FT      /organism="Homo sapiens"
XX      FT      /clone="DKFzp434F1672"
XX      FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX      FT      DH10B; sites NotI + SalI"
XX      FT      /dev_stage="adult"
XX      FT      /tissue_type="testis"
XX
XX      Sequence 6 BP; 0 A; 2 C; 2 G; 0 T; 2 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 C 1
DB      4 C 4

```

```

RESULT 29
HSM010918/C standard; RNA; EST; 6 BP.
XX
XX      HSM010918 standard; RNA; EST; 6 BP.
XX
XX      AL046068;
XX
XX      AL046068.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFzp434F1672_r1 (from clone DKFzp434F1672)
XX
XX      EST; expressed sequence tag.
XX
XX
XX

```

```

DE      Homo sapiens mRNA; EST DKFzp434F1672_r1 (from clone DKFzp434F1672)
XX
XX      EST; expressed sequence tag.
XX
XX
XX

```

OS	Homo sapiens (human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Hominoideae; Homo.				
XX					
RN	[1]				
RP	1-6				
RA	Pousluka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;				
RT	; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.				
RL	MIPS. Am Klopferplatz 18a D-82152 Martinsried, GERMANY				
CC	Clone from S. Wiemann, sequenced by DKFZ within the CDNA				
CC	sequencing consortium of the German Genome Project				
CC	No s1 sequence available				
CC	This clone is available at the RZPD in Berlin				
CC	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059				
CC	Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de				
XX					
FH	Key				
FH	Location/Qualifiers				
FT	source				
FT	1..6				
FT	/db_xref="taxon:9606"				
FT	/organism="Homo sapiens"				
FT	/clone="DKFPd434P1672"				
FT	/clone_lib="434 (synonym: htes3). Vector pSport1, host				
FT	DH10B; slices NotI + SalI"				
FT	/dev_stage="adult"				
FT	/tissue_type="testis"				
XX					
SQ	Sequence 6 BP; 0 A; 2 C; 2 G; 0 T; 2 other;				
Query Match					
Best Local Similarity		100.0%;	Score 1;	DB 2;	Length 6;
Matches 1:		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 c 1				
DB	6 C 6				
RESULT 30					
BE726686					
LOCUS	BE726686	6 bp	mRNA	linear	EST 14-SEP-2000
DEFINITION	BE726686	894095D11.y1 C. reinhardtii CC-1690, normalized, Lambda zap II			
ACCESSION	BE726686	Chlamydomonas reinhardtii cDNA, mRNA sequence.			
VERSION	BE726686.1	GI:10128110			
KEYWORDS	EST.				
SOURCE	Chlamydomonas reinhardtii.				
ORGANISM	Chlamydomonas reinhardtii				
REFERENCE	Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;				
AUTHORS	Chlamydomonadaceae; Chlamydomonas.				
TITLE	1 (bases 1 to 6)				
JOURNAL	Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,				
COMMENT	Modermott,J.P., Silflow,C., Stern,D. and Surzycki,R.				
	Analyses of the Chlamydomonas reinhardtii Genome: A Model,				
	Intracellular System for Analyzing Gene Function and Regulation in				
	Vascular Plants: project phase 2				
	Unpublished (2000)				
	Contact: Charles Hauser				
	DCMB Box 91000				
	Duke University				
	Durham, NC 27708-1000				
	Tel: 919 613 8159				
	Fax: 919 613 8177				
	Email: chauser@duke.edu.				
	1..6				
FEATURES	Location/Qualifiers				
SOURCE	1..6				
	/organism="Chlamydomonas reinhardtii"				
	/strain="CC-1690 wild type mt+ 21gr"				
	/db_xref="taxon:3055"				
	/clone_1ib="C. reinhardtii CC-1690, normalized, Lambda zap				

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"II"
/!note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermost, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
POLYA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned and cDNA
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phase. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT      0 a
ORIGIN           1 c      5 g      0 t

Oy      1 c 1
        |
Db       2 c 2

Query Match      100.0%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31
BE726686/c      6 bp      mRNA      linear      EST 14-SEP-2000
DEFINITION      894095D11.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
ACCESSION      BE726686
VERSION        BE726686
KEYWORDS       BE726686.1 GI:10128110
SOURCE         EST.
ORGANISM       Chlamydomonas reinhardtii.
                Chlamydomonas reinhardtii.
                Eukaryote; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                Chlamydomonadaceae; Chlamydomonas.
REFERENCE       1 (bases 1 to 6)
AUTHORS        Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
                McDermost,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE          Analyses of the Chlamydomonas reinhardtii Genome: A Model,
                Unicellular System for Analyzing Gene Function and Regulation in
                Vascular Plants: project phase 2
JOURNAL        Unpublished (2000)
COMMENT        Contact: Charles Hauser
                DCMB Box 91000
                Duke University
                Durham, NC 2708-1000
                Tel: 919 613 8159
                Fax: 919 613 8177
                Email: chauser@duke.edu.

FEATURES
    source
        1..6
            /organism="Chlamydomonas reinhardtii"
            /strain="CC-1690 wild type mt+ 21gr"
            /db_xref="taxon:3055"
            /clone_11b="C. reinhardtii CC-1690, normalized, Lambda Zap
            II"
            /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
            XhoI; This library, constructed by John Davies and Jeffrey
            McDermost, combines cDNAs from CC-1690 cells grown to
            mid-log phase in TAP (acetate-containing) medium in the
            light, TAP medium in the dark, HS (minimal) medium in
            ambient levels of CO2 and HS medium bubbled with 5% CO2.
            POLYA mRNA was purified from each sample, pooled and cDNA
            synthesized. The cDNA was directionally cloned into lambda
            ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
            pBluescript II SK- plasmids were excised from the lambda
            ZAP clones by superinfection with Exassist (Stratagene)
            phase. The library was normalized using method 4 described
            in Bonaldo et al (1996) Genome Research 6: 791-806."

```



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XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434J172L_r1 (from clone DKFZp434J1721)
DE EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-7
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1..7
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434J1721"
XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:
XX
XX Query Match 100.0%; Score 1; DB 2; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 C 1
XX 1 C 1
XX
XX RESULT 35
XX HSM007412/C
XX ID HSM007412 standard; RNA; EST; 7 BP.
XX
XX AL042562;
XX
XX AL042562.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434J172L_r1 (from clone DKFZp434J1721)
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-7
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

```

```

XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1..7
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434J1721"
XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
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XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:
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XX Query Match 100.0%; Score 1; DB 2; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 C 1
XX 3 C 3
XX
XX RESULT 36
XX HSM007502
XX ID HSM007502 standard; RNA; EST; 7 BP.
XX
XX AL042652;
XX
XX AL042652.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434N192L_r1 (from clone DKFZp434N1921)
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-7
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1..7
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434N1921"
XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"

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FT /dev_stage="adult"
XX /tissue_type="testis"
SO Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 C 1
DB 1 C 1

RESULT 37
HSM007502/c
ID HSM007502 standard; RNA; EST; 7 BP.
AC AL042652;
SV AL042652.1

XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA: EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
DE EST: expressed sequence tag.
XX

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX

CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No. 51 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX

XX Key Location/Qualifiers
FH 1.7
FT source

FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI
FT /dev_stage="adult"
FT /tissue_type="testis"
XX

SO Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 C 1
DB 7 C 7

RESULT 38
CS8888/c

LOCUS CS8888 7 bp mRNA linear EST 22-SEP-1997
DEFINITION C58888 Yuj1 Kohara unpublished CDNA Caenorhabditis elegans CDNA
clone YK383a7 3', mRNA sequence.
ACCESSION C58888
VERSION C58888
KEYWORDS C58888.1 GI:2417593
SOURCE EST.
ORGANISM Caenorhabditis elegans.
Caenorhabditis elegans.

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 7)
AUTHORS Kohara,Y., Motobashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
COMMENT Contact: Yuj1 Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1.7
Location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="YK383a7"
/clone_lib="Yuj1 Kohara unpublished CDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT 2 a 1 g 3 t 1 others
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 C 1
DB 7 C 7

RESULT 39
HSM001420

ID HSM001420 standard; RNA; EST; 8 BP.
XX
AC AL037095;
SV AL037095.1

XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX

DE Homo sapiens mRNA: EST DKFZp564L2064_r1 (from clone DKFZp564L2064)
XX
XX EST: expressed sequence tag.
XX

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX

CC Clone from S. Wiemann, sequenced by QIAGEN within the CDNA
CC sequencing consortium of the German Genome Project


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Query Match Similarity      100.0%; Score 1; DB 2; Length 8;
Best Local Similarity      100.0%; Pred. No. 0;
Matches      1; Conservative 0; Mismatches      0; Indels      0; Gaps      0;
Oy      1 c 1
          |
          2 c 2
Db

RESULT 43
HSM007277
ID      HSM007277      standard; RNA; EST; 8 Bp.
XX      AC
XX      AL042427;
XX      SV
XX      AL042427.1
XX      DE
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX      Homo sapiens mRNA: EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX      EST: expressed sequence tag.
XX      Homo sapiens (human)
XX      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX      RN
XX      11
XX      1-8
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      IT

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				Gaps
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AC	AL042427;	
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SV	AL042427.1	
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DT	12-MAR-1999 (Rel. 59, Created)	
DT	12-MAR-1999 (Rel. 59, Last updated, Version 1)	
DE		
XX	Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)	
XX		
KM	EST; expressed sequence tag.	
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OS	Homo sapiens (human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;	
XX	Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
XX		
RN	[1]	
RP	1-8	
RA	Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;	
RT		
RL	Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.	
CC	MIS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY	
XX		
CC	Clone from S. Wiemann, sequenced by LMU within the CDNA	
CC	sequencing consortium of the German Genome Project	
CC	No sl sequence available	
CC	This clone is available at the RZPD in Berlin	
CC	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059	
CC	Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de	
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Search completed: July 15, 2002, 20:07:36
Job time: 14494 sec

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 1 C 1
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Db 2 C 2

RESULT 45
HSM007323

1D HSM007323 standard: RNA: EST: 8 BP.

AC AL042473:

XX AL042473.1

SV 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA: EST DKFZp434F0121_f1 (from clone DKFZp434F0121)

XX EST: expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

RP Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the cDNA

CC sequencing consortium of the German Genome Project

CC No s1 sequence available
CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..8

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FT /organism="Homo sapiens"

FT /clone_lib="434 (synonym: htest). Vector pSPORT1; host

FT DH10B; sites NotI + SalI"

FT /dev_stage="adult"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 1 C 1
1
Db 7 C 7

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:28:08 ; Search time 9532.94 Seconds
(Without alignments)
2.195 Million cell updates/sec

Title: US-09-375-248-1_COPY_3164_3164

Perfect score: 1
Sequence: 1 g 1

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
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22: em_ov:*
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30: em_hlg_hum:*
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32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C	1	100.0	2	6	AX092441	AX092441 Sequence
C	2	100.0	2	6	AX092442	AX092442 Sequence
C	3	100.0	2	6	AX092443	AX092443 Sequence
C	4	100.0	2	6	AX092444	AX092444 Sequence
C	5	100.0	2	6	AX092445	AX092445 Sequence
C	6	100.0	2	6	AX092446	AX092446 Sequence
C	7	100.0	2	6	AX092447	AX092447 Sequence
C	8	100.0	2	6	AX092448	AX092448 Sequence
C	9	100.0	2	6	AX092449	AX092449 Sequence
C	10	100.0	2	6	AX092450	AX092450 Sequence
C	11	100.0	2	6	AX092451	AX092451 Sequence
C	12	100.0	2	6	AX092452	AX092452 Sequence
C	13	100.0	2	6	AX092453	AX092453 Sequence
C	14	100.0	2	6	AX092454	AX092454 Sequence
C	15	100.0	2	6	AX092455	AX092455 Sequence
C	16	100.0	2	6	AX092456	AX092456 Sequence
C	17	100.0	2	6	AX092457	AX092457 Sequence
C	18	100.0	2	6	AX092458	AX092458 Sequence
C	19	100.0	2	6	AX092459	AX092459 Sequence
C	20	100.0	2	6	AX092460	AX092460 Sequence
C	21	100.0	2	6	AX092461	AX092461 Sequence
C	22	100.0	2	6	AX092462	AX092462 Sequence
C	23	100.0	2	6	AX092463	AX092463 Sequence
C	24	100.0	2	6	AX092464	AX092464 Sequence
C	25	100.0	2	6	AX092465	AX092465 Sequence
C	26	100.0	2	6	AX092466	AX092466 Sequence
C	27	100.0	2	6	AX092467	AX092467 Sequence
C	28	100.0	2	6	AX092468	AX092468 Sequence
C	29	100.0	2	6	AX092469	AX092469 Sequence
C	30	100.0	2	6	AX092470	AX092470 Sequence
C	31	100.0	2	6	AX092471	AX092471 Sequence
C	32	100.0	2	6	AX092472	AX092472 Sequence
C	33	100.0	2	6	AX092473	AX092473 Sequence
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C	35	100.0	2	6	AX092475	AX092475 Sequence

ALIGNMENTS

RESULT 1 AX092441 2 bp DNA PAT 21-MAR-2001
LOCUS AX092441 Sequence 2 from Patent WO0116366.
DEFINITION AX092441
ACCESSION AX092441
VERSION AX092441.1 GI:13444536
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2)
AUTHORS
TITLE
JOURNAL
FEATURES
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/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 0 g 0 t

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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
DB 2 C 2

RESULT 2

AX092442
LOCUS AX092442 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 3 from Patent WO0116366.
ACCESSION AX092442
VERSION AX092442.1 GI:13444537
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 3 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
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OY 1 g 1
1
DB 2 C 2

RESULT 3

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LOCUS AX092444 2 bp DNA linear PAT 23-MAR-2001
DEFINITION Sequence 5 from Patent WO0116366.
ACCESSION AX092444
VERSION AX092444.1 GI:13444539
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 5 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
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/db_xref="taxon:32644"
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BASE COUNT 1 a 1 c 0 g 0 t
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1
DB 1 C 1

RESULT 4

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LOCUS AX092445 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 6 from Patent WO0116366.
ACCESSION AX092445
VERSION AX092445.1 GI:13444540
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 6 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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BASE COUNT 0 a 2 c 0 g 0 t
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DB 2 G 2

RESULT 5

AX092446
LOCUS AX092446 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 7 from Patent WO0116366.
ACCESSION AX092446
VERSION AX092446.1 GI:13444541
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 7 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX092446 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 7 from Patent WO0116366.
ACCESSION AX092446
VERSION AX092446.1 GI:13444541
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 7 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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Best Local Similarity 100.0%; Pred. No. 0;
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Db 1 G 1

RESULT 7
LOCUS AX092447/c 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 8 from Patent WO0116366.
ACCESSION AX092447
VERSION AX092447.1 GI:13444542
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 8 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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Db 1 G 1

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DEFINITION Sequence 9 from Patent WO0116366.
ACCESSION AX092448
VERSION AX092448.1 GI:13444543
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 9 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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Best Local Similarity 100.0%; Pred. No. 0;
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Db 1 G 1

RESULT 9
LOCUS AX092449 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 10 from Patent WO0116366.
ACCESSION AX092449
VERSION AX092449.1 GI:13444544
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 10 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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RESULT 10
AX092449/c 2 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 10 from Patent WO0116366.
DEFINITION AX092449
ACCESSION AX092449
VERSION AX092449.1 GI:13444544
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 10 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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BASE COUNT
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ORIGIN

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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
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Db 2 G 2

RESULT 11
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LOCUS Sequence 11 from Patent WO0116366.
DEFINITION AX092450
ACCESSION AX092450
VERSION AX092450.1 GI:13444545
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 11 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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/db_xref="taxon:32644"
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BASE COUNT
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ORIGIN

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Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1
Db 2 G 2

RESULT 12
AX092451 2 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 12 from Patent WO0116366.
DEFINITION AX092451
ACCESSION AX092451.1 GI:13444546
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 12 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
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Location/Qualifiers
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BASE COUNT
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ORIGIN

Query Match
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 G 2

RESULT 13
AX092453/c 2 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 14 from Patent WO0116366.
DEFINITION AX092453
ACCESSION AX092453
VERSION AX092453.1 GI:13444548
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 14 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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BASE COUNT
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1
Db 2 G 2

RESULT 14
AX092454 2 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 15 from Patent WO0116366.
DEFINITION AX092454
ACCESSION AX092454
VERSION AX092454.1 GI:13444549

RESULT 14
AX092454 2 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 15 from Patent WO0116366.
DEFINITION AX092454
ACCESSION AX092454
VERSION AX092454.1 GI:13444549

KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 15 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
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BASE COUNT 0 a 0 c 1 g 1 t
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
DB 2 c 2

RESULT 15
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LOCUS AX092528 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 89 from Patent WO0116366.
ACCESSION AX092528
VERSION AX092528.1 GI:13444623
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 89 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
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Location/Qualifiers
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BASE COUNT 1 a 1 c 0 g 0 t
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 c 1

RESULT 16
AX092529/c
LOCUS AX092529 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 90 from Patent WO0116366.
ACCESSION AX092529
VERSION AX092529.1 GI:13444624
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE unclassified.
AUTHORS 1 (bases 1 to 2)
Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 90 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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BASE COUNT 0 a 2 c 0 g 0 t
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
DB 2 c 2

RESULT 17
AX092530
LOCUS AX092530 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 91 from Patent WO0116366.
ACCESSION AX092530
VERSION AX092530.1 GI:13444625
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 91 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
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BASE COUNT 1 a 0 c 1 g 0 t
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Best Local Similarity 100.0%; Pred. No. 0;
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QY 1 g 1
DB 2 c 2

RESULT 18
AX092538
LOCUS AX092538 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 99 from Patent WO0116366.
ACCESSION AX092538
VERSION AX092538.1 GI:13444633
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 98-08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN /note="synthetic oligonucleotide;"

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 19
AX175286 2 bp DNA linear PAT 03-JUL-2001
LOCUS AX175286
DEFINITION Sequence 50 from Patent WO0144465.
ACCESSION AX175286
VERSION AX175286.1 GI:14598654
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 2)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 50 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
source Location/Qualifiers
1..2
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 20
AX175287 2 bp DNA linear PAT 03-JUL-2001
LOCUS AX175287
DEFINITION Sequence 51 from Patent WO0144465.
ACCESSION AX175287
VERSION AX175287.1 GI:14598655
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 2)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 51 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
source Location/Qualifiers
1..2
/organism="synthetic construct"

BASE COUNT 0 a /db_xref="taxon:32630"
ORIGIN 0 c 1 g 1 t

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 g 2

RESULT 21
BD009609 2 bp DNA linear PAT 31-JAN-2002
LOCUS BD009609/c
DEFINITION Probes, methods and kits for detection and typing of Helicobacter pylori, nucleic acids in biological samples.
ACCESSION BD009609
VERSION BD009609.1 GI:18637982
KEYWORDS JP 2001502536-A/201.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Quint,W. and Doorn,L.J.V.
TITLE Probes, methods and kits for detection and typing of Helicobacter pylori, nucleic acids in biological samples
JOURNAL Patent: JP 2001502536-A 201 27-FEB-2001;
INNOGENETICS NV, DDL BV

COMMENT OS unidentified
PN JP 2001502536-A/201
PD 27-FEB-2001
PR 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
PC C1201/68,C07K14/205,C12N15/11
CC
FH Key
FT source
FT Location/Qualifiers

FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 0 a 1 c 0 g 0 t 1 others
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 g 2

RESULT 22
CNS01C99 2 bp mRNA linear PLN 02-SEP-1999
LOCUS CNS01C99
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ACCESSION AL115237
VERSION AL115237.1 GI:5829856
KEYWORDS cDNA library; nitrogen deprivation.
SOURCE Botryotinia fuckeliana.
ORGANISM Botryotinia fuckeliana.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

REFERENCE 1 (bases 1 to 2)
AUTHORS Bilton,F., Lewis,C., Fortin,D., Pradier,J.M. and Brygoo,Y.

TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
76026 Versailles, France
REFERENCE 2 (bases 1 to 2)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT The cDNA library to be analyzed within the framework of this
project was created using a Boticella cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
vector.

FEATURES

source Location/Qualifiers
1..2
/organism="Botryotinia fuckeliana"
/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : M04F091"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 8; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 23

AC079635 3 bp DNA linear HTG 14-AUG-2001
LOCUS Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC079635
ACCESSION AC079635.3 GI:14647267
VERSION HTG: HTGS PHASED.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS 1 (bases 1 to 3)
McCombie,W.R., Baker,J.P., Bahret,A., Yang,C., Balija,V.,
Dedhia,N.N., de la Bastide,M., Kuhl,K., King,L., Kirchoff,K.A.,
Miller,B., Nasclmento,L.O., O'Shaughnessy,A.L., Preston,R.R.,
Rodriguez,S., Santos,L., Shah,R.S., Spiegel,L.A., Palmer,L.,
Vill,M.D. and Zlatavern,T.
COMMENT Mouse genomic sequence
Unpublished
2 (bases 1 to 3)
McCombie,W.R.
JOURNAL Direct Submission
TITLE Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing
AUTHORS Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Habor, NY 11724, USA
JOURNAL On Jul 10, 2001 this sequence version replaced gi:14595773.
COMMENT * NOTE: This record contains 1 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
3: contig of 3 bp in length.
This entry has been temporarily removed. An update for RP23-152L20

will be submitted as soon as it becomes available.

FEATURES Location/Qualifiers
source 1..3
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-152L20"

BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 24

CHKNCAMC5 3 bp DNA linear VRT 17-JUL-2000
LOCUS Chicken cardiac neural cell adhesion (NCAM) gene, exon 12D.
DEFINITION M23994 J04140
ACCESSION M23994.1 GI:212442
VERSION 5 of 6
KEYWORDS chicken.
SEGMENT
SOURCE
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 3)
Prediger,E.A., Hoffman,S., Edelman,G.M. and Cunningham,B.A.
Four exons encode a 93-base-pair insert in three neural cell
adhesion molecule mRNAs specific for chicken heart and skeletal
muscle.
Proc. Natl. Acad. Sci. U.S.A. 85 (24), 9616-9620 (1988)
JOURNAL 89071747
MEDLINE 3200847
PUBMED
COMMENT Exon 12D represents a very small exon.
LOCATION/Qualifiers
1..3
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pc101B"
/tissue-type="cardiac muscle"
/dev-stage="day 10 embryo"
1..3
/gene="NACM"
/number=12
BASE COUNT 2 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 3 g 3

RESULT 25
LOCUS A97991 3 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 21 from Patent W09914366.
ACCESSION A97991
VERSION A97991.1 GI:5781229
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified

REFERENCE 1 (bases 1 to 3)
AUTHORS Pongers-Willense,M.J. and Van,D.J.
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)
FEATURES
source 1..3
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 1 c 2 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 g 2

RESULT 26
A97991/c
LOCUS A97991 3 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 21 from Patent WO9914366.
ACCESSION A97991
VERSION A97991.1 GI:6781229
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Pongers-Willense,M.J. and Van,D.J.
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)
FEATURES
source 1..3
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 1 c 2 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 1 g 1

RESULT 27
AX092457/c
LOCUS AX092457 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 18 from Patent WO0116366.
ACCESSION AX092457
VERSION AX092457.1 GI:13444552
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 18 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar (IL)
FEATURES
source Location/Qualifiers

source 1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 3 g 3

RESULT 28
AX092458
LOCUS AX092458 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 19 from Patent WO0116366.
ACCESSION AX092458
VERSION AX092458.1 GI:13444553
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 19 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar (IL)
FEATURES
source Location/Qualifiers

BASE COUNT 2 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 3 g 3

RESULT 29
AX092460/c
LOCUS AX092460 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 21 from Patent WO0116366.
ACCESSION AX092460
VERSION AX092460.1 GI:13444555
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 21 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar (IL)
FEATURES
source Location/Qualifiers

BASE COUNT 1..3
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 c 2

RESULT 30
LOCUS AX092461 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 22 from Patent WO0116366.
ACCESSION AX092461
VERSION AX092461.1 GI:13444556
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 22 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 3 c 3

RESULT 31
LOCUS AX092462 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 23 from Patent WO0116366.
ACCESSION AX092462
VERSION AX092462.1 GI:13444557
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 23 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 3 c 3

RESULT 32
LOCUS AX092462 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 23 from Patent WO0116366.
ACCESSION AX092462
VERSION AX092462.1 GI:13444557
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 23 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 c 2

RESULT 33
LOCUS AX092463 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 24 from Patent WO0116366.
ACCESSION AX092463
VERSION AX092463.1 GI:13444558
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 24 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
|
Db 2 G 2

RESULT 34
LOCUS AX092464 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 25 from Patent WO0116366.
ACCESSION AX092464
VERSION AX092464.1 GI:13444559
KEYWORDS
SOURCE . unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 25 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 2 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
|
Db 2 G 2

RESULT 35
LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS
SOURCE . unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 26 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 2 G 2

RESULT 36
LOCUS AX092465/c 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS
SOURCE . unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 26 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
|
Db 3 G 3

RESULT 37
LOCUS AX092466 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 27 from Patent WO0116366.
ACCESSION AX092466
VERSION AX092466.1 GI:13444561
KEYWORDS
SOURCE . unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 27 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 2 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
|
Db 2 G 2

RESULT 38
AX092467
LOCUS AX092467 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 28 from Patent WO0116366.
ACCESSION AX092467
VERSION AX092467.1 GI:13444562
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES
source
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN
1 a 0 c 1 g 1 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 G 2

RESULT 39
AX092469
LOCUS AX092469 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 30 from Patent WO0116366.
ACCESSION AX092469
VERSION AX092469.1 GI:13444564
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES
source
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN
1 a 1 c 0 g 1 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 3 G 3

RESULT 40

AX092470
LOCUS AX092470 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 31 from Patent WO0116366.
ACCESSION AX092470
VERSION AX092470.1 GI:13444565
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES
source
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN
1 a 0 c 1 g 1 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 3 G 3

RESULT 41
AX092472
LOCUS AX092472 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 33 from Patent WO0116366.
ACCESSION AX092472
VERSION AX092472.1 GI:13444567
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES
source
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN
2 a 1 c 0 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 G 1

RESULT 42
AX092473
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 34 from Patent WO0116366.

ACCESSION AX092473
VERSION AX092473.1 GI:13444568
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 34 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 3 G 3

RESULT 43
AX092474
LOCUS AX092474 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 35 from Patent WO0116366.
ACCESSION AX092474
VERSION AX092474.1 GI:13444569
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 35 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t
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Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 3 G 3

RESULT 44
AX092474/c
LOCUS AX092474 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 35 from Patent WO0116366.
ACCESSION AX092474
VERSION AX092474.1 GI:13444569
KEYWORDS

SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 35 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 1 G 1

RESULT 45
AX092475/c
LOCUS AX092475 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 36 from Patent WO0116366.
ACCESSION AX092475
VERSION AX092475.1 GI:13444570
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 36 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 1 G 1

Search completed: July 15, 2002, 23:28:08
Job time: 24541 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:10:11 : Search time 932.4 seconds
(without alignments)
1.841 Million cell updates/sec

Title: US-09-375-248-1_COPY_3164_3164

Perfect score: 1
Sequence: 1 g 1

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	3	17	AAT33326	CAPL trinucleotide
2	100.0	3	17	AAT33326	CAPL trinucleotide
3	100.0	3	21	AAAG4655	Human TUB gene pro
4	100.0	3	22	AAAL20244	Human breast cance
5	100.0	4	16	AAO81664	bcrf binding oligo
6	100.0	4	16	AAO81664	bcrf binding oligo
7	100.0	4	16	AAO81665	bcrf binding oligo
8	100.0	4	16	AAO81665	bcrf binding oligo
9	100.0	4	18	AAT86385	Probe for target n

C	10	1	100.0	4	18	AAT86385	Probe for target n
C	11	1	100.0	4	18	AAT77252	Immunostimulatory
C	12	1	100.0	4	18	AAT77252	Immunostimulatory
C	13	1	100.0	4	22	AAI17191	Human breast cancer
C	14	1	100.0	4	22	AAI17191	Human breast cancer
C	15	1	100.0	4	22	AAI17191	Human breast cancer
C	16	1	100.0	4	22	AAI17191	Human breast cancer
C	17	1	100.0	4	22	AAI17191	Human breast cancer
C	18	1	100.0	4	22	AAI17191	Human breast cancer
C	19	1	100.0	4	22	AAI17191	Human breast cancer
C	20	1	100.0	4	22	AAI17191	Human breast cancer
C	21	1	100.0	4	22	AAI17191	Human breast cancer
C	22	1	100.0	4	22	AAI17191	Human breast cancer
C	23	1	100.0	4	22	AAI17191	Human breast cancer
C	24	1	100.0	4	22	AAI17191	Human breast cancer
C	25	1	100.0	4	22	AAI17191	Human breast cancer
C	26	1	100.0	4	22	AAI17191	Human breast cancer
C	27	1	100.0	4	22	AAI17191	Human breast cancer
C	28	1	100.0	4	22	AAI17191	Human breast cancer
C	29	1	100.0	4	22	AAI17191	Human breast cancer
C	30	1	100.0	4	22	AAI17191	Human breast cancer
C	31	1	100.0	4	22	AAI17191	Human breast cancer
C	32	1	100.0	4	22	AAI17191	Human breast cancer
C	33	1	100.0	4	22	AAI17191	Human breast cancer
C	34	1	100.0	4	22	AAI17191	Human breast cancer
C	35	1	100.0	4	22	AAI17191	Human breast cancer
C	36	1	100.0	4	22	AAI17191	Human breast cancer
C	37	1	100.0	4	22	AAI17191	Human breast cancer
C	38	1	100.0	4	22	AAI17191	Human breast cancer
C	39	1	100.0	4	22	AAI17191	Human breast cancer
C	40	1	100.0	4	22	AAI17191	Human breast cancer
C	41	1	100.0	4	22	AAI17191	Human breast cancer
C	42	1	100.0	4	22	AAI17191	Human breast cancer
C	43	1	100.0	4	22	AAI17191	Human breast cancer
C	44	1	100.0	4	22	AAI17191	Human breast cancer
C	45	1	100.0	4	22	AAI17191	Human breast cancer

ALIGNMENTS

RESULT	1
AAT33326	standard; RNA; 3 BP.
AC	AAT33326;
XX	12-NOV-1996 (first entry)
DT	
DE	CAPL trinucleotide.
XX	
KW	CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
KW	osteosarcoma; therapy; ss.
XX	
OS	Synthetic.
XX	
PN	W09625499-A1.
XX	
FD	22-AUG-1996.
XX	
PF	16-FEB-1996; 96MO-US02108.
XX	
PR	17-FEB-1995; 95US-0391375.
XX	
PA	(HYBR-) HYBRID INC.
PA	(NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
PI	Agrawal S, Engebraten O, Fodstad O, Hovig E, Maeldandsmo GJ;
PI	Von Hofe E;
XX	
DR	WPI; 1996-393400/39.
XX	
PT	Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -

PT useful to inhibit metastatic cancer, partic. osteosarcoma
 XX
 PS Claim 2: Page 56; 70pp; English.
 XX
 CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5'
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.
 XX
 SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 g 1
 Db 3 g 3

RESULT 2
 AAT33326/C
 ID AAT33326 standard; RNA: 3 BP.
 XX
 AC AAT33326;
 XX
 DT 12-NOV-1996 (first entry)
 XX
 ME CAPL trinucleotide.
 NE
 KW CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
 KW osteosarcoma; therapy; ss.
 XX
 OS Synthetic.
 OS
 PN MO9625499-A1.
 XX
 PD 22-AUG-1996.
 XX
 PF 16-FEB-1996; 96MO-US02108.
 XX
 PR 17-FEB-1995; 95US-0091375.
 XX
 PA (HYBR-) HYBRIDON INC.
 PA (MORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.
 XX
 PI Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandmo GJ;
 PI Von Hofe E;
 XX
 DR WPI: 1996-393400/39.
 XX
 PT Synthetic oligonucleotide(s) inhibiting CAPL gene expression -
 PT useful to inhibit metastatic cancer, partic. osteosarcoma
 XX
 PS Claim 2: Page 56; 70pp; English.
 XX
 CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5'
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.
 XX
 SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 g 1
 Db 1 g 1

RESULT 3
 AAA94655
 ID AAA94655 standard; DNA: 3 BP.
 XX
 AC AAA94655;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Human TUB gene probe #2.
 XX
 KW Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;
 KW TUB; ss.
 XX
 OS Homo sapiens.
 OS
 PN US6114502-A.
 XX
 PD 05-SEP-2000.
 XX
 PF 27-FEB-1998; 98US-0032365.
 XX
 PR 22-AUG-1996; 96US-0701380.
 PR 04-SEP-1996; 96US-0706292.
 PR 10-APR-1996; 96US-0630592.
 PR 17-SEP-1996; 96US-0714991.
 PR 30-APR-1997; 97US-0850218.
 PR 01-AUG-1997; 97US-0904699.
 PR 17-SEP-1997; 97US-0932306.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI North M, Nishina P, Noben-Trauth K, Naggett J;
 XX
 DR WPI: 2000-586483/55.
 XX
 PT Mammalian proteins expressed in retina and brain, useful for producing
 PT antibodies and for diagnosing neurosensory defects including cochlear
 PT degeneration, peripheral retinal degeneration and cone-rod retinal
 PT dystrophy -
 XX
 PS Disclosure; Columns 81-82; 61pp; English.
 XX
 CC The present invention relates to human and murine cDNAs from a
 CC neurosensory defect associated gene family. The novel cDNAs are mouse
 CC tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB
 CC form 6 (see AAA94632), human TUB form 1 (see AAA94633), human TULP1 (see
 CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
 CC immunogens to raise antibodies that specifically identify TUB/TULP
 CC expressing cells and in drug screening assays directed at neurosensory
 CC defects. The novel proteins encoded by the present sequence can be used
 CC for the treatment of neurosensory degenerative conditions e.g. retinal
 CC dystrophies. The present sequence is a probe used to isolate the novel
 CC genes of the present invention.
 XX
 SO Sequence 3 BP: 0 A; 0 C; 3 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 g 1
 Db 1 g 1


```

RESULT 4
AA020244/C
ID AAL20244 standard: cDNA: 3 BP.
XX
AC AAL20244:
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 12701.
XX
KW Human; breast cancer; cell marker; cytosolic; ss.
XX
OS Homo sapiens.
XX
PM WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 25-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steilmann K;
XX
DR WPI: 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS Claim 1: Page 2245; 3695pp; English.
XX
XX
The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytosolic
CC activity.
XX
SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other:

```

```

Query Match      100.0%; Score 1; DB 22; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 g 1
   1
Db 2 G 2

```

```

RESULT 5
AA081664
ID AAO81664 standard: RNA: 4 BP.
XX
AC AAO81664:
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
XX
OS Synthetic.
XX
PM WO9500528-A.
XX

```

```

KW Inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PM WO9500528-A.
XX
PD 05-JAN-1995.
XX
PF 17-JUN-1994; 94WO-US06884.
XX
PR 18-JUN-1993; 93US-0079677.
PR 07-JAN-1994; 94US-0179491.
XX
PA (PHAR-) PHARMAGENICS INC.
XX
PI Beutel BA, Joesten ME;
XX
DR WPI: 1995-051992/07.
XX

```

```

PT New oligo-nucleotide(s) that bind to basic fibroblast growth
factor - modulating, esp. inhibiting, its activity, useful in
treating cancer, preventing metastasis, and diagnosis.
XX
PS Claim 3: Page 25; 44pp; English.
XX

```

```

CC The sequences given in AA081642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AA081664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC gene therapy.
XX
SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other:

```

```

Query Match      100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 g 1
   1
Db 1 g 1

```

```

RESULT 6
AA081664/C
ID AAO81664 standard: RNA: 4 BP.
XX
AC AAO81664:
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX

```

```

KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
XX
OS Synthetic.
XX
PM WO9500528-A.
XX

```


PT factor - modulating, esp. inhibiting, its activity, useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS

Claim 3; Page 25; 44pp; English.

CC The sequences given in AA081642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AA081644-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC with its receptor and heparin. These oligonucleotides may inhibit
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX

Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 4 C 4

RESULT 9
 AAT86385
 ID AAT86385 standard; DNA: 4 BP.

AC AAT86385;

XX 23-APR-1998 (first entry)

DE Probe for target nucleic acid sequence P0.

KW Point mutation detection; nucleic acid sequence analysis; probe;
 KM viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /note= "C-5' phosphate"

PN WO9718131-A1.

PD 16-OCT-1997.

PF 11-APR-1996; 96WO-RU00087.

PR 11-APR-1996; 96WO-RU00087.

PA (DYMS/) DYMSHITS G M.
 PA (IVAN/) IVANOVA E M.
 PA (KRIV/) KRIVENKO A A.
 PA (KULI/) KULIKOVA V F.
 PA (LOKH/) LOKHOV S G.
 PA (PYSH/) PYSHNY D V.

PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
 PI Likhov SG, Pyshny DV;

WP1: 1997-512737/47.

PT Detection of target nucleic acid sequence - based on ligation of
 PT hybridised short probe to flanking target-complementary sequences
 XX
 PS

Example; Page 4; 15pp; Russian.

CC This sequence represents a probe for the target sequence P0 (shown in
 CC AAT86376). This sequence was used to test the method of the invention.
 CC The method of the invention is for detecting a nucleic acid sequence to
 CC be analysed, and comprises hybridisation of an oligonucleotide probe
 CC complementary to the sequence to be analysed and bearing a reporter
 CC group, the novelty is that detection of a sequence is based on the
 CC ligation of a short oligonucleotide (with a length of 4-6 units) with
 CC flanking oligonucleotide sequences (or their derivatives bearing
 CC polycyclic aromatic groups). The method is especially useful for
 CC detecting point mutations. Diagnosis of viral, genetic and other
 CC diseases is also mentioned.
 XX

Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 3 g 3

RESULT 10
 AAT86385/C
 ID AAT86385 standard; DNA: 4 BP.

AC AAT86385;

XX 23-APR-1998 (first entry)

DE Probe for target nucleic acid sequence P0.

KW Point mutation detection; nucleic acid sequence analysis; probe;
 KM viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /note= "C-5' phosphate"

PN WO9738131-A1.

PD 16-OCT-1997.

PF 11-APR-1996; 96WO-RU00087.

PR 11-APR-1996; 96WO-RU00087.

PA (DYMS/) DYMSHITS G M.
 PA (IVAN/) IVANOVA E M.
 PA (KRIV/) KRIVENKO A A.
 PA (KULI/) KULIKOVA V F.
 PA (LOKH/) LOKHOV S G.
 PA (PYSH/) PYSHNY D V.

PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
 PI Likhov SG, Pyshny DV;

WP1: 1997-512737/47.

PT Detection of target nucleic acid sequence - based on ligation of
 PT hybridised short probe to flanking target-complementary sequences
 XX
 PS

Example; Page 4; 15pp; Russian.

XX This sequence represents a probe for the target sequence P0 (shown in
 CC AAT86376). This sequence was used to test the method of the invention.
 CC The method of the invention is for detecting a nucleic acid sequence
 CC be analysed, and comprises hybridisation of an oligonucleotide probe
 CC complementary to the sequence to be analysed and bearing a reporter
 CC group, the novelty is that detection of a sequence is based on the
 CC ligation of a short oligonucleotide (with a length of 4-6 units) with
 CC flanking oligonucleotide sequences (or their derivatives bearing
 CC polycyclic aromatic groups). The method is especially useful for
 CC detecting point mutations. Diagnosis of viral, genetic and other
 CC diseases is also mentioned.

SO Sequence 4 BP; 1 A; 2 G; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 g 1
 Db 4 G 4

RESULT 11

AA77252
 ID AAT77252 standard; DNA; 4 BP.

AC AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome; vaccine;
 KW immune response; antigen; naked gene expression vector; IgE;
 KM antibody; immunotherapy; ss.

XX Synthetic.

OS WO9728259-A1.

PN 07-AUG-1997.

PD 28-JAN-1997; 97WO-US01277.

PF 30-JAN-1996; 96US-0593554.

PR (REGC) UNIV CALIFORNIA.

PA Carson DA, Raz E;

PI WP1: 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic

PT polynucleotide - useful for selectively enhancing the TH1 immune

PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide
 CC (ISP) comprised of at least one strand of a palindrome, which includes
 CC at least one dinucleotide consisting of adjacent, unethylated cytosine
 CC and guanine residues. ISP's could be used in vaccination methods
 CC for enhancing the immune response of a host to an antigen. Administration
 CC of naked gene expression vectors which encode antigens or their
 CC immunostimulatory fragments suppresses IgE antibody production
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.
 CC Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
 Db 3 g 3

RESULT 12

AA77252/C
 ID AAT77252 standard; DNA; 4 BP.

AC AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome; vaccine;
 KW immune response; antigen; naked gene expression vector; IgE;
 KM antibody; immunotherapy; ss.

XX Synthetic.

OS WO9728259-A1.

PN 07-AUG-1997.

PD 28-JAN-1997; 97WO-US01277.

PF 30-JAN-1996; 96US-0593554.

PR (REGC) UNIV CALIFORNIA.

PA Carson DA, Raz E;

PI WP1: 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic

PT polynucleotide - useful for selectively enhancing the TH1 immune

PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide
 CC (ISP) comprised of at least one strand of a palindrome, which includes
 CC at least one dinucleotide consisting of adjacent, unethylated cytosine
 CC and guanine residues. ISP's could be used in vaccination methods
 CC for enhancing the immune response of a host to an antigen. Administration
 CC of naked gene expression vectors which encode antigens or their
 CC immunostimulatory fragments suppresses IgE antibody production
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.
 CC Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
 Db 2 G 2

RESULT 13

AA17191
 ID AAL17191 standard; cDNA; 4 BP.

AC AAL17191;

DT 07-DEC-2001 (first entry)

XX New peptide useful as a marker for the diagnosis of breast cancer -
 PS Claim 1: Page 3087; 3695pp; English.

CC The invention relates to human breast cancer expressed polynucleotides
 CC (AA07544-AA026789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterizing, treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity.

SO Sequence 4 BP; 0 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1: DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 Db 3 G 3

RESULT 16

AA061450 ID AA061450 standard; RNA; 4 BP.

XX AA061450;

DT 18-JUN-2001 (first entry)

DE Cyclin binding hammerhead ribozyme 3' catalytic fragment SEQ ID 19.

KM Hammerhead ribozyme; cyclin E; restenosis; catalytic; angioplasty;

KW cyclin E2P1; vasotrophic; gene therapy; cell cycle arrest; ss.

OS Synthetic.

PN WO200121789-A1.

PD 29-MAR-2001.

PP 22-SEP-1999; 99WO-EP07049.

PR 22-SEP-1999; 99WO-EP07049.

PA (UUTU-) UNIV TUEBINGEN EBERHARD-KARLS.

PJ Grassl G, Kuhn AC, Kandolf R;

DR WPI: 2001-257985/26.

PT New catalytically acting RNA molecule comprising hammerhead ribozyme
 PT directed against mRNA molecules encoding cyclin E or E2P1, useful for
 PT inhibiting vascular smooth muscle cell proliferation and restenosis -
 PS Claim 12; Page 28; 40pp; German.

CC This invention describes a novel catalytic RNA molecule which is directed
 CC against mRNA molecules (11) which encode the cell-relevant protein cyclin
 CC E or E2P1. The products of the invention have vasotrophic activity and can
 CC be used for gene therapy. The use of (11), or a DNA molecule or a plasmid
 CC for the invention is claimed for obtaining a vector for gene therapy and
 CC for inhibiting restenosis of blood vessel after angioplasty; therapeutic
 CC compositions containing these components are also claimed. (11)
 CC efficiently induces cell cycle arrest by combined inactivation of cyclin
 CC E and E2P1.

SO Sequence 4 BP; 2 A; 0 C; 1 G; 0 U; 1 other;

Query Match 100.0%; Score 1: DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 Db 2 g 2

RESULT 17

AA093676/c ID AA093676 standard; DNA; 5 BP.

XX AA093676;

DT 24-JUN-1990 (first entry)

DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber
 DE variant (HSV-c) and HSV grape variant (HSV-g).

KM Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.

OS Hop growth retarding viroid.

PN JP01040000-A.

PD 10-FEB-1989.

PF 05-AUG-1987; 87JP-0194377.

PR 05-AUG-1987; 87JP-0195377.

PA (YUKI) YUKI GOSHI YAKUHIN.

DR WPI: 1989-089715/12.

PT Fractionating and detecting hop growth retarding viroids -
 PT using synthetic DNA probe contg. specific base sequence

PS Disclosure; page 3; 5pp; Japanese.

CC The synthetic probes is complementary to the RNA of HSV-g bases 53-59.
 CC HSV, HSV-c and HSV-g are fractionated and detected using the synthetic
 CC probe. The probe is 15-25mer. The probe can be used to diagnose HSV
 CC infections in plants.

SO Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1: DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 Db 5 G 5

RESULT 18

AA068752 ID AA068752 standard; DNA; 5 BP.

XX AA068752;

DT 22-FEB-1995 (first entry)

DE CHA255 heavy chain CDR1 clone 3.3.3. coding sequence.

KM Polymerase chain reaction; primer; PCR; amplify; heavy; light;
 KW chain; complementarity determining region; CDR; variable; constant;
 KW region; monoclonal antibody; Mab; binding affinity; EDTA; DOTA;

KW tumour; cancer; colorectal; breast; metal chelate; hapten; ss.
XX
XX Synthetic.

OS
XX
PN AU9350602-A.

XX
XX
PD 26-MAY-1994.

XX
PF 10-NOV-1993; 93AU-0050602.

XX
PK 12-NOV-1992; 92US-0975230.

XX
PA (HYBR-) HYBRITTECH INC.

XX
PI Ahnweiler PM, Moore MD;

XX
DR WPI: 1994-209063/26.

XX
PT P-PSDB; AAR54150.

PT Polypeptide used in imaging and treatment of carcinomas and
XX tumours - comprising substd antibody CDR having binding affinity
XX for metal chelate of EDTA or DETA or analogues

PS Claim 25; Fig 3A: 61pp; English.

XX
XX The sequences given in AA068747-57 encode the wild type and mutagenised
CC versions of the complementarity determining region 1 (CDR1) of the
CC antibody designated CHA255. CHA255 is a murine monoclonal antibody
CC (Mab) which is capable of binding complexes. Mutagenesis of these
CC CDRs, causes the production of polypeptides with a particularly
CC high binding affinity for EDTA or DETA metal complexes. CDR1 and -3
CC of the heavy chain, and CDR2 and -3 of the light chain were targeted
CC for mutagenesis. Five residues of both CDR1 and -3 of the CHA255
CC heavy chain, five of seven residues of light chain CDR and six of
CC nine light chain CDR3 residues were specifically targeted for
CC codon-based mutagenesis. The mutagenised MAB's can be used in
CC compositions for in vivo imaging of malignant tissues or tumours. They
CC are also useful for the treatment of malignant tissues or tumours. eg.
CC colorectal or breast cancer. Both methods involve the use of
CC radiolabelled antibodies which bind to metal chelates or haptens which are
CC specifically delivered to the target site by a targeting molecule. CDR
CC derived peptides may be used to construct bi-functional antibodies.
CC having dual specificities, or as donor or recipients of CDR sequences.

XX
S0 Sequence 5 BP; 0 A; 0 C; 1 G; 1 T; 3 Other;

Query Match 100.0%; Score 1; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
1 g 1

RESULT 19
AA081667/c
ID AA081667 standard; RNA; 5 BP.

XX
AC AA081667;

XX
DT 29-SEP-1995 (first entry)

XX
DE bFGF binding oligomer core sequence #4.

XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;

KW bubble structure; pseudoknot; receptor; heparin; competition;

KM inhibition; enhance; neovascularisation; solid tumour; cancer;

KM metastasis; diagnosis; gene therapy; ss.

OS Synthetic.

PN WO9500528-A.

XX
XX 05-JAN-1995.

XX
PF 17-JUN-1994; 94WO-US06884.

XX
PK 18-JUN-1993; 93US-0079677.

XX
PR 07-JAN-1994; 94US-0179491.

XX
PA (PHAR-) PHARMAGENICS INC.

XX
PI Beutel BA, Joesten ME;

XX
DR WPI: 1995-051992/07.

PT New oligo-nucleotide(s) that bind to basic fibroblast growth
XX factor - modulating, esp. inhibiting, its activity, useful in
XX treating cancer, preventing metastasis, and diagnosis.

PS Claim 3; Page 25; 44pp; English.

XX
XX The sequences given in AA081642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AA081664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
XX gene therapy.

XX
S0 Sequence 5 BP; 2 A; 2 C; 0 G; 1 U; 0 Other;

Query Match 100.0%; Score 1; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
5 G 5

RESULT 20
AAT12043/c
ID AAT12043 standard; RNA; 5 BP.

XX
AC AAT12043;

XX
DT 17-JUL-1996 (first entry)

XX
DE Cleavable replicable-inhibiting sequence.

XX
KW Ribozyme; hairpin; hammerhead; probe; MDV-1; multidomain-1;

KM replication; cleavage; ss.

XX
OS Synthetic.

XX
PN US5472840-A.

XX
PD 05-DEC-1995.

XX
PF 30-SEP-1988; 88US-0252243.

XX
PR 17-DEC-1990; 90US-0630288.

XX
PR 30-SEP-1988; 88US-0252243.

XX
PR 22-JUN-1989; 89US-0370218.

XX (STAD) AMOCO CORP.
PA
XX
PI Stefano JF.
XX
DR WPI: 1996-029807/03.
XX
PT Ribozyme-forming nucleic acid probes - contg. MDV-1 sequence and
XX cleavable replicable-inhibiting sequence.
PS
XX Claim 4: Column 62; 43pp: English.
XX
CC A composition comprises RNA of formula P4-P1-P2-P3 (1a), a nucleic
CC acid of formula R1-R2 (111), where (1a) and (111) bind to a target
CC nucleic acid of formula X2-X1-X3 (11) to form a hammerhead ribozyme,
CC where P1 is a MDV-1 sequence capable of autocatalytic replication in
CC the absence of P3; P2 is a sequence (AA112042 or AA112044) that binds
CC to (11) and forms a cleavage site between P1 and P3; P3 (AA112043)
CC is an inhibitory element that binds to X2 and interacts with a
CC region of P1 corresp. to nucleotides 81-126 of MDV-1; P4 contributes
CC nucleotides to form the ribozyme with X1 and P2, or is the terminal
CC nucleotide of P1; X1 is a target region of (11); X2 and X3 are
CC terminal nucleotides or second or third target regions of (11); R1
CC is a ribozyme-forming area of (111); and R2 is a terminal nucleotide
CC of R1 or an area of (111) that binds to (11). X1 and R1 are
CC mutually exclusive and are represented by the sequences of AA112040 and
CC AA112041. For hairpin ribozymes, P2 is AA112045 and R1 is AA112046.
CC Probes bearing ribozymes are produced in a single step by transcription
CC of DNA of appropriate sequence, thereby reducing costs. The ribozymes
CC produce specific cleavage events, leading to a product RNA with
CC defined replication properties.
XX
SQ Sequence 5 BP: 0 A; 1 C; 0 G; 2 U; 2 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 17; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 5 G 5

RESULT 21
AAV61663
ID AAV61663 standard; DNA: 5 BP.
XX
AC AAV61663;
XX
DT 03-DEC-1998 (first entry)
XX
DE Fusarium sp. 18S rRNA DNA fragment #7.
XX
KW 18S rRNA: detection; identification; fungus; ss.
XX
OS Fusarium sp.
XX
PN JP10234380-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-0062104.
XX
PR 28-FEB-1997; 97JP-0062104.
XX
PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
XX
DR WPI: 1998-535034/46.
XX
PT Use of oligo:nucleotide for detecting and identification of fungus
PT of Fusarium genus - as primer or probe to detect or identify
PT microbes rapidly and exactly

XX
PS Claim 1: Page 7; 20pp: Japanese.
XX
CC AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are
CC used in a method for the detection and identification of a fungus of
CC Fusarium genus. The process can be used to detect or identify microbes
CC rapidly and exactly.
XX
SQ Sequence 5 BP: 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 19; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 5 G 5

RESULT 22
AAV61663/C
ID AAV61663 standard; DNA: 5 BP.
XX
AC AAV61663;
XX
DT 03-DEC-1998 (first entry)
XX
DE Fusarium sp. 18S rRNA DNA fragment #7.
XX
KW 18S rRNA: detection; identification; fungus; ss.
XX
OS Fusarium sp.
XX
PN JP10234380-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-0062104.
XX
PR 28-FEB-1997; 97JP-0062104.
XX
PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
XX
DR WPI: 1998-535034/46.
XX
DE Use of oligo:nucleotide for detecting and identification of fungus
PT of Fusarium genus - as primer or probe to detect or identify
PT microbes rapidly and exactly
XX
PS Claim 1: Page 7; 20pp: Japanese.
XX
CC AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are
CC used in a method for the detection and identification of a fungus of
CC Fusarium genus. The process can be used to detect or identify microbes
CC rapidly and exactly.
XX
SQ Sequence 5 BP: 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 19; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 5 G 5

RESULT 23
AAV62299
ID AAV62299 standard; DNA: 5 BP.
XX


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AC  AA196299;
XX
XX  08-APR-1998  (first entry)
XX
XX  Fungal telomeric nucleic acid sequence.
XX
XX  Detection: eukaryotic pathogen: telomeric nucleic acid sequence;
XX  telomerase activity; diagnosis: fungal infection; fungus: fungi;
XX  malarial infection; malaria: ss.
XX
XX  Saccharomyces cerevisiae.
XX
XX  US5695932-A.
XX
XX  09-DEC-1997.
XX
XX  13-MAY-1993: 93US-0060952.
XX
XX  13-MAY-1993: 93US-0060952.
XX  13-MAY-1992: 92US-0862438.
XX  24-MAR-1993: 93US-0038766.
XX
XX  (REGC ) UNIV CALIFORNIA.
XX  (TEXA ) UNIV TEXAS SYSTEM.
XX
XX  Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;
XX  WPI: 1998-041292/04.
XX
XX  Detection of eukaryotic pathogens, especially fungal or Plasmodium
XX  spp. - by detecting telomerase activity
XX
XX  Claim 5: Columns 81-82: 82pp: English.
XX
XX  The present sequence can be used in a novel method for detecting a
XX  eukaryotic pathogen in a patient. The method comprises obtaining a
XX  sample of somatic tissue or cells from the patient, determining if
XX  telomerase activity is present and correlating this with the
XX  presence of the pathogen. The method is useful for diagnosis of
XX  fungal infections, especially a fungus of the genus Candida,
XX  Kluyveromyces, Saccharomyces, Sporobolus, Coccidioides,
XX  Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,
XX  Aspergillus, Mucor or Rhizopus, or malarial infections, especially
XX  Plasmodium vivax, P. ovale, P. malariae or P. falciparum.
XX
XX  Sequence 5 BP: 0 A; 0 C; 3 G; 2 T; 0 other:

Query Match          100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 g 1
    1
Db  2 g 2

RESULT 24
AA10695
ID  AA210695 standard; DNA: 5 BP.
XX
XX  AA210695;
XX
XX  23-NOV-1999  (first entry)
XX
XX  Oligonucleotide sequence that increases p53 activity in a cell.
XX
XX  p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
XX  UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX  atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
XX  skin cancer; ss.
XX
XX  Synthetic.
OS

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XX
XX  GB2336157-A.
XX
XX  13-OCT-1999.
XX
XX  24-MAR-1999: 99GB-0006758.
XX
XX  26-MAR-1998: 98US-0048927.
XX
XX  (UYBO-) UNIV BOSTON.
XX
XX  Gilchrist BA, Yaar M, Eller M;
XX  WPI: 1999-543520/46.
XX
XX  DNA fragments useful for increasing p53 activity in a cell and reducing
XX  susceptibility to UV-induced hyperproliferative diseases -
XX
XX  Claim 11: Page 30; 44pp: English.
XX
XX  AA210692-97 represent DNA fragments that are used for increasing p53
XX  activity in a cell. The oligonucleotides are UV mimetics and
XX  protect cells against subsequent exposure to UV-irradiation or
XX  chemicals. The oligonucleotides are useful for increasing p53 activity
XX  in a cell, reducing the susceptibility to UV-induced hyperproliferative
XX  diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
XX  rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
XX  and reducing susceptibility to skin cancer.
XX
XX  Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other:

Query Match          100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 g 1
    1
Db  1 g 1

RESULT 25
AA210696/C
ID  AA210696 standard; DNA: 5 BP.
XX
XX  AA210696;
XX
XX  23-NOV-1999  (first entry)
XX
XX  Oligonucleotide sequence that increases p53 activity in a cell.
XX
XX  p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
XX  UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX  atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
XX  skin cancer; ss.
XX
XX  Synthetic.
OS
XX
XX  GB2336157-A.
XX
XX  13-OCT-1999.
XX
XX  24-MAR-1999: 99GB-0006758.
XX
XX  26-MAR-1998: 98US-0048927.
XX
XX  (UYBO-) UNIV BOSTON.
XX
XX  Gilchrist BA, Yaar M, Eller M;
XX  WPI: 1999-543520/46.
XX
XX  DNA fragments useful for increasing p53 activity in a cell and reducing

```


Db 5 C 5

RESULT 28

AAV72347/C

ID AAV72347 standard; DNA; 5 BP.

XX AAV72347;

XX 28-JUL-1999 (first entry)

XX US5908745 primer #4.

DE DNA sequencing; disease-associated allele; polyacrylamide matrix;
 KW continuous/contiguous stacking hybridization technique; detection;
 KM mutation; diagnosis; primer; ss.

XX Synthetic.

XX US5908745-A.

XX 01-JUN-1999.

XX 16-JAN-1996; 96US-0587332.

XX 16-JAN-1996; 96US-0587332.

XX (UYCH-) UNIV CHICAGO.

XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

XX Parinov SV, Yershov GM;

XX WPI; 1999-347002/29.

PT Detecting disease-associated alleles using continuous/contiguous
 PT stacking hybridization as a diagnostic tool

XX Example 1; Column 9; 16pp; English.

CC This invention describes novel methods for sequencing and analysing DNA
 CC samples to detect disease-associated alleles, by continuous/contiguous
 CC stacking hybridization techniques (utilizing universal bases) with
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
 CC be used to detect multiple DNA base mutations which are specific for
 CC certain diseases. The methods of the invention provide accurate and
 CC efficient and sensitive methods for diagnosing disease by detecting
 CC multiple mutation sequences in patient DNA. The method require the
 CC minimum number of oligonucleotides and few stacking hybridization steps
 CC than prior art methods. The methods are also efficient enough to
 CC discriminate between perfect and imperfect duplexes. The methods also
 CC obviate the need for the fabrication and array placement of large numbers
 CC of immobilized oligomers.

SQ Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1

Db 5 C 5

RESULT 29

AAV72348

ID AAV72348 standard; DNA; 5 BP.

XX AAV72348;

XX 28-JUL-1999 (first entry)

XX

DE US5908745 primer #5.

KW DNA sequencing; disease-associated allele; polyacrylamide matrix;
 KW continuous/contiguous stacking hybridization technique; detection;
 KM mutation; diagnosis; primer; ss.

XX Synthetic.

XX US5908745-A.

XX 01-JUN-1999.

XX 16-JAN-1996; 96US-0587332.

XX 16-JAN-1996; 96US-0587332.

XX (UYCH-) UNIV CHICAGO.

XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

XX Parinov SV, Yershov GM;

XX WPI; 1999-347002/29.

PT Detecting disease-associated alleles using continuous/contiguous
 PT stacking hybridization as a diagnostic tool

XX Example 1; Column 9; 16pp; English.

CC This invention describes novel methods for sequencing and analysing DNA
 CC samples to detect disease-associated alleles, by continuous/contiguous
 CC stacking hybridization techniques (utilizing universal bases) with
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
 CC be used to detect multiple DNA base mutations which are specific for
 CC certain diseases. The methods of the invention provide accurate and
 CC efficient and sensitive methods for diagnosing disease by detecting
 CC multiple mutation sequences in patient DNA. The method require the
 CC minimum number of oligonucleotides and few stacking hybridization steps
 CC than prior art methods. The methods are also efficient enough to
 CC discriminate between perfect and imperfect duplexes. The methods also
 CC obviate the need for the fabrication and array placement of large numbers
 CC of immobilized oligomers.

SQ Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1

Db 2 g 2

RESULT 30

AAV72348/C

ID AAV72348 standard; DNA; 5 BP.

XX AAV72348;

XX 28-JUL-1999 (first entry)

XX US5908745 primer #5.

DE DNA sequencing; disease-associated allele; polyacrylamide matrix;
 KW continuous/contiguous stacking hybridization technique; detection;
 KM mutation; diagnosis; primer; ss.

XX Synthetic.

XX US5908745-A.

XX 01-JUN-1999.

XX 16-JAN-1996; 96US-0587332.
XX 16-JAN-1996; 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX Parinov SV, Yershov GM;
XX WPI: 1999-347002/29.
XX
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9, 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
XX
XX Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
DB 5 G 5

RESULT 31
AAV72349/c
ID AAV72349 standard; DNA: 5 BP.
XX
XX AAV72349;
XX
XX 28-JUL-1999 (first entry)
XX
XX US5908745 primer #6.
XX
XX
XX DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer; ss.
XX
XX Synthetic.
XX
XX US5908745-A.
XX
XX 01-JUN-1999.
XX
XX 16-JAN-1996; 96US-0587332.
XX
XX 16-JAN-1996; 96US-0587332.
XX
XX (UYCH-) UNIV CHICAGO.
XX
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX Parinov SV, Yershov GM;
XX WPI: 1999-347002/29.
XX
XX

XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9, 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
XX
XX Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
DB 5 G 5

RESULT 32
AAV72350/c
ID AAV72350 standard; DNA: 5 BP.
XX
XX AAV72350;
XX
XX 28-JUL-1999 (first entry)
XX
XX US5908745 primer #7.
XX
XX
XX DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer; ss.
XX
XX Synthetic.
XX
XX US5908745-A.
XX
XX 01-JUN-1999.
XX
XX 16-JAN-1996; 96US-0587332.
XX
XX 16-JAN-1996; 96US-0587332.
XX
XX (UYCH-) UNIV CHICAGO.
XX
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX Parinov SV, Yershov GM;
XX WPI: 1999-347002/29.
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XX stacking hybridization as a diagnostic tool
XX
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XX
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XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for

CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method requires the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.

SO Sequence 5 BP: 3 A: 2 C: 0 G: 0 U: 0 other:

Query Match 100.0%; Score 1: DB 20: Length 5:
Best Local Similarity 100.0%; Pred. No. 0:

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1
DB 5 G 5

RESULT 33

AA56964
ID AAX56964 standard: DNA: 5 BP.

AC AAX56964:

DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
cell growth inhibitor; treatment; cancer; ras protein; ss.

US Synthetic.

XX MO9922772-A1.

PN 14-MAY-1999.

PF 28-OCT-1998: 98WO-US22821.

PR 31-OCT-1997: 97US-0961469.

PS (ISIS-) ISIS PHARM INC.

PI Geary RS, Hardee GE, Howard R, Levin A, Mehra RC;
Templin MV;

DR WPI: 1999-313181/26.

PT Liposome-encapsulated oligonucleotides useful for treating or
preventing cancers associated with ras gene activation
Example 1: Page 107; 120pp; English.

CC This invention describes novel compositions comprising oligonucleotides
CC (AAX56957-X57017), entrapped within liposomes, that hybridize
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
CC ras protein. The products of the invention have anticancer activity and
CC specifically bring about the antisense inhibition of ras genes or mRNA.
CC The products of the invention are used to modulate expression of a ras
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
CC growth and especially to treat or prevent cancers associated with
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
CC rate at which it is cleared from the blood when compared with
CC non-encapsulated material, and the oligonucleotides become distributed to
CC practically all parts of the body.

SO Sequence 5 BP: 1 A: 2 C: 2 G: 0 U: 0 other:

Query Match 100.0%; Score 1: DB 20: Length 5:

Best Local Similarity 100.0%; Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1
DB 2 g 2

RESULT 34

AA56964/c
ID AAX56964 standard: DNA: 5 BP.

AC AAX56964:

DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
cell growth inhibitor; treatment; cancer; ras protein; ss.

OS Synthetic.

PN MO9922772-A1.

PD 14-MAY-1999.

PF 28-OCT-1998: 98WO-US22821.

PR 31-OCT-1997: 97US-0961469.

PS (ISIS-) ISIS PHARM INC.

PI Geary RS, Hardee GE, Howard R, Levin A, Mehra RC;
Templin MV;

DR WPI: 1999-313181/26.

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preventing cancers associated with ras gene activation
Example 1: Page 107; 120pp; English.

CC This invention describes novel compositions comprising oligonucleotides
CC (AAX56957-X57017), entrapped within liposomes, that hybridize
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
CC ras protein. The products of the invention have anticancer activity and
CC specifically bring about the antisense inhibition of ras genes or mRNA.
CC The products of the invention are used to modulate expression of a ras
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
CC growth and especially to treat or prevent cancers associated with
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
CC rate at which it is cleared from the blood when compared with
CC non-encapsulated material, and the oligonucleotides become distributed to
CC practically all parts of the body.

SO Sequence 5 BP: 1 A: 2 C: 2 G: 0 U: 0 other:

Query Match 100.0%; Score 1: DB 20: Length 5:
Best Local Similarity 100.0%; Pred. No. 0:

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1
DB 4 G 4

RESULT 35

AA56964
ID AAX21608 standard: DNA: 5 BP.

AC AAX21608:

XX 14-MAY-1999 (first entry)
 DT
 XX
 DE Mutant H-ras specific antisense oligo ISIS #2563.
 XX
 XX Human: N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
 KW diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.
 XX
 US Synthetic.
 XX
 XX WO9902732-A1.
 PN
 XX
 XX 21-JAN-1999.
 PD
 XX
 XX 06-JUL-1998: 98WO-US13966.
 PF
 XX
 XX 08-JUL-1997: 97US-0889296.
 PK
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX
 PI Cowsett LM, Manoharan M, Monia BP;
 P1
 XX
 XX WPI: 1999-120932/10.
 DR
 XX
 XX New oligonucleotide targeting human N-ras nucleic acid - is
 PT capable of inhibiting human N-ras expression, useful for preventing
 PT or treating conditions arising from the activation of a human N-ras
 PT oncogene
 XX
 PS Disclosure; Page 22: 97pp; English.
 XX
 XX The invention relates to oligonucleotides, which target a nucleic acid
 CC encoding human N-ras, and are capable of inhibiting human N-ras
 CC expression. The antisense oligonucleotides form a pharmaceutical
 CC composition, which is useful for modulating the expression of human
 CC N-ras, inhibiting the proliferation of cancer cells, and preventing or
 CC treating conditions arising from the activation of a human N-ras
 CC oncogene. The oligonucleotides are also useful in diagnostics,
 CC therapeutics, and as research reagents and kits. The oligonucleotides
 CC enable the specific modulation of activated human N-ras expression,
 CC which is associated with tumour formation. Sequences AAX21601-619
 CC represent antisense oligonucleotides targeted to mutant H-ras.
 CC
 SO Sequence 5 BP: 1 A: 2 C: 2 G: 0 U: 0 other;

Query Match 100.0%; Score 1: DB 20: Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1
 |
 Db 2 g 2

RESULT 36
 AAX21608/C
 ID AAX21608 standard: DNA: 5 BP.
 XX
 AC AAX21608;
 XX
 XX 14-MAY-1999 (first entry)
 DT
 XX
 XX Mutant H-ras specific antisense oligo ISIS #2563.
 DE
 XX
 XX Human: N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
 KW diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.
 XX
 OS Synthetic.
 XX
 XX WO9902732-A1.
 PN
 XX
 PD 21-JAN-1999.

XX 06-JUL-1998: 98WO-US13966.
 PF
 XX
 XX 08-JUL-1997: 97US-0889296.
 PR
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX
 PI Cowsett LM, Manoharan M, Monia BP;
 P1
 XX
 XX WPI: 1999-120932/10.
 DR
 XX
 XX New oligonucleotide targeting human N-ras nucleic acid - is
 PT capable of inhibiting human N-ras expression, useful for preventing
 PT or treating conditions arising from the activation of a human N-ras
 PT oncogene
 XX
 PS Disclosure; Page 22: 97pp; English.
 XX
 XX The invention relates to oligonucleotides, which target a nucleic acid
 CC encoding human N-ras, and are capable of inhibiting human N-ras
 CC expression. The antisense oligonucleotides form a pharmaceutical
 CC composition, which is useful for modulating the expression of human
 CC N-ras, inhibiting the proliferation of cancer cells, and preventing or
 CC treating conditions arising from the activation of a human N-ras
 CC oncogene. The oligonucleotides are also useful in diagnostics,
 CC therapeutics, and as research reagents and kits. The oligonucleotides
 CC enable the specific modulation of activated human N-ras expression,
 CC which is associated with tumour formation. Sequences AAX21601-619
 CC represent antisense oligonucleotides targeted to mutant H-ras.
 CC
 SO Sequence 5 BP: 1 A: 2 C: 2 G: 0 U: 0 other;

Query Match 100.0%; Score 1: DB 20: Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1
 |
 Db 4 G 4

RESULT 37
 AAA56981
 ID AAA56981 standard: cDNA: 5 BP.
 XX
 AC AAA56981;
 XX
 XX 14-NOV-2000 (first entry)
 DT
 XX
 XX Human colon cancer cell cDNA sequence #109.
 DE
 XX
 XX Human: arbitrary primer: cDNA synthesis; contig sequence construction;
 KW open reading frame; ORF; low stringency; cDNA sequencing; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200031299-A2.
 PN
 XX
 XX 02-JUN-2000.
 PD
 XX
 XX 19-NOV-1999: 99WO-US27430.
 PF
 XX
 XX 20-NOV-1998: 98US-0196716.
 PR
 XX
 XX (LUDWIG) LUDWIG INST CANCER RES.
 PA
 XX
 PI Simpson AG, Dias Neto E, Brentani RR;
 P1
 XX
 XX WPI: 2000-400100/34.
 DR
 XX
 XX Method for determining open reading frames of the genome of an organism
 PT using primers at low stringency conditions, useful in the construction

PT of contigs or constructs of sequenced nucleic acid molecules -
XX
PS Example 6; Page 47; 113pp; English.
XX
CC The present sequence is a cDNA sequence obtained using a method for
CC determining open reading frames (ORFs) of the genome of an
CC organism. An aliquot of mRNA from human colon cancer cells was mixed
CC with a single, arbitrary primer, Moloney murine leukemia virus reverse
CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
CC incubated under low stringency conditions to yield single stranded
CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
CC than providing nucleotide sequence information from the non-coding
CC terminal of nucleic acid molecules, the method provides information on
CC the more interesting and relevant internal portions, such as ORFs. The
CC method also permits the construction of contigs of sequenced nucleic
CC acid molecules.
SQ Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other:
Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
DB 3 g 3
RESULT 38
ID AAA56981/C
XX AAA56981 standard; cDNA; 5 BP.
AC
XX
AC AAA56981;
XX
DT 14-NOV-2000 (first entry)
XX
DE Human colon cancer cell cDNA sequence #109.
XX
XX
KW Human: arbitrary primer; cDNA synthesis; contig sequence construction;
XX open reading frame; ORF; low stringency; cDNA sequencing; ss.
OS Homo sapiens.
XX
PN WO200031299-A2.
XX
PD 02-JUN-2000.
XX
PF 19-NOV-1999; 99WO-US27430.
XX
PR 20-NOV-1998; 98US-0196716.
XX
PA (LUDM-) LUDMIG INST CANCER RES.
XX
PI Simpson AJG, Dias Neto E, Brentani RR;
XX
DR WPI: 2000-400100/34.
XX
PT Method for determining open reading frames of the genome of an organism
PT using primers at low stringency conditions, useful in the construction
PT of contigs or constructs of sequenced nucleic acid molecules -
XX
XX Example 6; Page 47; 113pp; English.
XX
CC The present sequence is a cDNA sequence obtained using a method for
CC determining open reading frames (ORFs) of the genome of an
CC organism. An aliquot of mRNA from human colon cancer cells was mixed
CC with a single, arbitrary primer, Moloney murine leukemia virus reverse
CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
CC incubated under low stringency conditions to yield single stranded
CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
CC than providing nucleotide sequence information from the non-coding
CC terminal of nucleic acid molecules, the method provides information on

CC the more interesting and relevant internal portions, such as ORFs. The
CC method also permits the construction of contigs of sequenced nucleic
CC acid molecules.
SQ Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other:
Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
DB 5 g 5
RESULT 39
ID AA293601
XX AA293601 standard; DNA; 5 BP.
AC
XX
AC AA293601;
XX
DT 24-JUL-2000 (first entry)
XX
DE Transcription factor binding site of tobacco gene promoter sequence.
XX
XX
KW Regulatory sequence; meristem; genetic engineering;
KW gene expression; crop protection; transgenic plant; resistance;
KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.
OS Synthetic.
XX
OS Nicotiana glauca.
XX
PN WO200012713-A1.
XX
PD 09-MAR-2000.
XX
PF 26-AUG-1999; 99WO-AU00692.
XX
PR 26-AUG-1998; 98AU-0005498.
XX
PA (UYQU) UNIV QUEBENS LAND.
XX
PI Mudge SR, Birch RG;
XX
DR WPI: 2000-237875/20.
XX
PT Meristem-expressible nucleic acid sequences, useful for producing
PT transgenic plants with improved characteristics such as resistance to
PT pathogens
XX
PS Example 9; Page 51; 102pp; English.
XX
CC Isolated regulatory sequences of plants that are operable in
CC dividing cells. In particular the meristem cells of plants are useful
CC in the genetic engineering of plants. The regulatory sequences can
CC be used to control the expression of foreign genes placed under their
CC control. Such methods are useful for producing transgenic plants with
CC altered shape and/or size. The sequences are also useful for
CC producing transgenic plants capable of rapid regeneration following
CC harvest or plants having improved resistance to pathogens. This
CC sequence has been shown to bind a factor involved in the activation
CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three
CC times in the meristem regulatory sequence of Tobacco described in
CC GENSSEQ record AA293567.
XX
SQ Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other:
Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
|
DB 5 9 5

RESULT 40
AA293601/C
ID AA293601 standard; DNA: 5 BP.

AC AA293601;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KW gene expression; crop protection; transgenic plant; resistance;

KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

XX Synthetic.

OS Nicotiana acuminata.

XX WO200012713-A1.

PN 09-MAR-2000.

PI 26-AUG-1999; 99WO-AU00692.

XX 26-AUG-1998; 98AU-0005498.

DR (UYOU) UNIV QUEENSLAND.

XX Mudge SR, Birch RG;

PI WPI: 2000-237875/20.

XX Meristem-expressible nucleic acid sequences, useful for producing

PT transgenic plants with improved characteristics such as resistance to

PT pathogens

XX Example 9; Page 51; 102pp; English.

PS Isolated regulatory sequences of plants that are operable in

XX dividing cells, in particular the meristem cells of plants are useful

CC in the genetic engineering of plants. The regulatory sequences can

CC be used to control the expression of foreign genes placed under their

CC control. Such methods are useful for producing transgenic plants with

CC altered shape and/or size. The sequences are also useful for

CC producing transgenic plants capable of rapid regeneration following

CC harvest or plants having improved resistance to pathogens. This

CC sequence has been shown to bind a factor involved in the activation

CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three

CC times in the meristem regulatory sequence of Tobacco described in

CC GENESQ record AA293567.

XX Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
|
DB 4 G 4

RESULT 41

AA293602/C

ID AA293602 standard; DNA: 5 BP.

AC AA293602;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KW gene expression; crop protection; transgenic plant; resistance;

KW tobacco; transcription factor; N1R2; nitrate; ss.

XX Synthetic.

OS Nicotiana acuminata.

XX WO200012713-A1.

PN 09-MAR-2000.

PI 26-AUG-1999; 99WO-AU00692.

XX 26-AUG-1998; 98AU-0005498.

DR (UYOU) UNIV QUEENSLAND.

XX Mudge SR, Birch RG;

PI WPI: 2000-237875/20.

XX Meristem-expressible nucleic acid sequences, useful for producing

PT transgenic plants with improved characteristics such as resistance to

PT pathogens

XX Example 9; Page 51; 102pp; English.

PS Isolated regulatory sequences of plants that are operable in

XX dividing cells, in particular the meristem cells of plants are useful

CC in the genetic engineering of plants. The regulatory sequences can

CC be used to control the expression of foreign genes placed under their

CC control. Such methods are useful for producing transgenic plants with

CC altered shape and/or size. The sequences are also useful for

CC producing transgenic plants capable of rapid regeneration following

CC harvest or plants having improved resistance to pathogens. This

CC sequence has been shown to regulate nitrate metabolism in the

CC fungus Neurospora crassa. It occurs multiple times in the meristem

CC regulatory sequence of Tobacco described in GENESQ record AA293567.

XX Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
|
DB 4 G 4

RESULT 42

AA289330/C

ID AA289330 standard; DNA: 5 BP.

AC AA289330;

DT 13-JUN-2000 (first entry)

DE Human UCP3 promoter fragment #10.

XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;

XX fat metabolism; ss.

OS Homo sapiens.

XX DE19838837-A1.

PN 02-MAR-2000.


```
XX 27-AUG-1998; 98DE-1038837.
PF
XX
PR 27-AUG-1998; 98DE-1038837.
XX
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX (NOVO ) NOVO-NORDISK AS.
PI Esterbauer H, Oberkofler H, Patsch W;
XX WPI: 2000-272214/24.
DR
XX
PT Recombinant fat and muscle tissue specific uncoupling protein 3
XX promoters useful for identifying UCP3 modulators
XX
PS Claim 25; Page 12; 38pp; German.
XX
CC This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases
CC with inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.
XX
SO Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 C 2

RESULT 43
AAZ89331
ID AAZ89331 standard; DNA: 5 BP.
XX
AC AAZ89331;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human UCP3 promoter fragment #11.
XX
UE UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
KM fat metabolism; ss.
XX
OS Homo sapiens.
XX
PN DE19838837-A1.
XX
PD 02-MAR-2000.
XX
PF 27-AUG-1998; 98DE-1038837.
XX
PR 27-AUG-1998; 98DE-1038837.
XX
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX (NOVO ) NOVO-NORDISK AS.
PI Esterbauer H, Oberkofler H, Patsch W;
XX WPI: 2000-272214/24.
DR
XX
PT Recombinant fat and muscle tissue specific uncoupling protein 3
XX promoters useful for identifying UCP3 modulators
XX
```

```
PS Claim 26; Page 12; 38pp; German.
XX
CC This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases
CC with inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.
XX
SO Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 4 g 4

RESULT 44
AAZ89332
ID AAZ89332 standard; DNA: 5 BP.
XX
AC AAZ89332;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human UCP3 promoter fragment #12.
XX
UE UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
KM fat metabolism; ss.
XX
OS Homo sapiens.
XX
PN DE19838837-A1.
XX
PD 02-MAR-2000.
XX
PF 27-AUG-1998; 98DE-1038837.
XX
PR 27-AUG-1998; 98DE-1038837.
XX
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX (NOVO ) NOVO-NORDISK AS.
PI Esterbauer H, Oberkofler H, Patsch W;
XX WPI: 2000-272214/24.
DR
XX
PT Recombinant fat and muscle tissue specific uncoupling protein 3
XX promoters useful for identifying UCP3 modulators
XX
PS Claim 31; Page 12; 38pp; German.
XX
CC This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases
CC with inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.
XX
SO Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other:
```

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 9 1
 1 1
 Db 4 g 4

Db 1 9 1

Search completed: July 15, 2002, 23:10:11
 Job time: 16429 sec

RESULT 4:

AA248433

ID AA248433 standard; DNA: 5 BP.

XX AA248433:

AC 27-MAR-2000 (first entry)

UT 27-MAR-2000 (first entry)

XX First DNA arm segment.

DE First DNA arm segment.

XX First DNA arm segment.

KM Microorganism: virus; polymerase chain reaction: food; cosmetic;

XX clinical diagnostic; molecular beacon; PCR primer; ss.

OS Synthetic.

XX WO9963112-A2.

PN 09-DEC-1999.

XX 09-DEC-1999.

PD 09-DEC-1999.

XX 09-DEC-1999.

PF 18-MAY-1999; 99WO-US10940.

XX 18-MAY-1999; 98US-0086025.

PR 17-MAY-1999; 99US-0086025.

XX 17-MAY-1999; 99US-0086025.

PA (HUNT-) HUNT WESSON INC.

XX (HUNT-) HUNT WESSON INC.

PI Romick TL, Fraser MS;

XX Romick TL, Fraser MS;

PI WPI: 2000-086985/07.

XX WPI: 2000-086985/07.

DR Detection of microorganisms and viruses, for use in the food and

PT cosmetic industries and for clinical diagnostics

PS Claim 51: Page 40: 63pp: English.

XX Claim 51: Page 40: 63pp: English.

CC The invention provides a novel in vitro method for the detection of

CC microorganisms and viruses. The method comprises: (1) forming a

CC polymerase chain reaction (PCR) mixture by combining a predetermined

CC volume of a sample to be tested for the presence of a nucleic acid

CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer

CC comprising 5'-GCTAAGCTCTCTAAGC-3', and a second primer comprising

CC 5'-AGAACGCTCTCTAAGC-3', and PCR reagents; (2) forming a PCR product by

CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,

CC to replicate and attain 0.25-10000mg nucleotide product/mul mixture; (3)

CC adding a probe containing DNA comprising 5'-GCTGCTCTCTAAGC-3' to

CC the PCR mixture or to the PCR product to cause the DNA to hybridize with

CC the nucleic acid sequence, if present, and change the conformation of the

CC probe; and (4) determining whether or not bacteria are present in the

CC sample by detecting the conformational change of the probe, a

CC conformational change indicating the presence of bacteria in the sample.

CC The methods can be used for the detection of viruses and microorganisms,

CC including bacteria, yeast, molds and protista. They can be used in the

CC food and cosmetic industry and in clinical diagnostics. Using the method

CC it is not necessary to remove non-hybridized probe from the system.

XX Sequence 5 BP: 1 A; 1 C; 2 G; 1 T; 0 other:

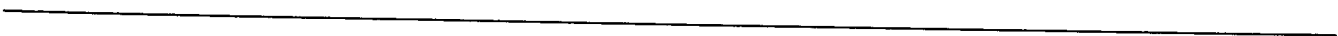
SO Sequence 5 BP: 1 A; 1 C; 2 G; 1 T; 0 other:

XX Query Match 100.0%; Score 1; DB 21; Length 5;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 9 1



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:38 : Search time 223.79 Seconds
(without alignments)

1.098 Million cell updates/sec

Title: US-09-375-248-1_COPY_3164_3164

Perfect score: 191

Scoring table: OLIGO_NUC
Gapop 60.0, Capext 60.0

Searched: 38353 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued Patents NA:*

- 1: /cgn2_6/plodata/2/ina/5A.COMB.seq:*
- 2: /cgn2_6/plodata/2/ina/5B.COMB.seq:*
- 3: /cgn2_6/plodata/2/ina/6A.COMB.seq:*
- 4: /cgn2_6/plodata/2/ina/6B.COMB.seq:*
- 5: /cgn2_6/plodata/2/ina/pCTUS.COMB.seq:*
- 6: /cgn2_6/plodata/2/ina/backli1est.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	1	2	US-08-268-679B-8	Sequence 8, Appl1
2	100.0	1	2	US-08-484-192-16	Sequence 16, Appl1
3	100.0	1	2	US-08-361-024-3	Sequence 3, Appl1
4	100.0	1	2	US-08-361-024-3	Sequence 3, Appl1
5	100.0	1	2	US-08-361-024-3	Sequence 3, Appl1
6	100.0	1	3	US-07-791-213D-46	Sequence 46, Appl1
7	100.0	1	3	US-07-791-213D-46	Sequence 46, Appl1
8	100.0	1	3	US-07-791-213D-46	Sequence 46, Appl1
9	100.0	1	3	US-07-791-213D-62	Sequence 62, Appl1
10	100.0	1	3	US-08-268-679B-7	Sequence 62, Appl1
11	100.0	1	3	US-08-602-036A-2	Sequence 2, Appl1
12	100.0	1	3	US-08-602-036A-2	Sequence 2, Appl1
13	100.0	1	3	US-08-293-150A-46	Sequence 46, Appl1
14	100.0	1	3	US-08-293-150A-46	Sequence 46, Appl1
15	100.0	1	3	US-08-293-150A-62	Sequence 62, Appl1
16	100.0	1	3	US-08-502-374A-2	Sequence 2, Appl1
17	100.0	1	3	US-08-502-374A-2	Sequence 2, Appl1
18	100.0	1	3	US-08-642-407A-2	Sequence 2, Appl1
19	100.0	1	3	US-08-642-407A-2	Sequence 2, Appl1
20	100.0	1	3	US-08-873-709-9	Sequence 9, Appl1
21	100.0	1	3	US-09-032-365A-36	Sequence 36, Appl1
22	100.0	1	3	US-08-793-634B-12	Sequence 12, Appl1
23	100.0	1	3	US-08-973-568-55	Sequence 55, Appl1
24	100.0	1	4	US-07-755-462-2	Sequence 2, Appl1
25	100.0	1	4	US-07-755-462-2	Sequence 2, Appl1
26	100.0	1	4	US-08-169-950-6	Sequence 6, Appl1
27	100.0	1	4	US-08-169-950-6	Sequence 6, Appl1

28	1	100.0	4	1	US-07-630-288A-7	Sequence 7, Appl1
29	1	100.0	4	1	US-07-630-288A-11	Sequence 11, Appl1
30	1	100.0	4	1	US-07-630-288A-11	Sequence 11, Appl1
31	1	100.0	4	1	US-07-630-288A-13	Sequence 13, Appl1
32	1	100.0	4	1	US-07-630-288A-14	Sequence 14, Appl1
33	1	100.0	4	1	US-07-630-288A-14	Sequence 14, Appl1
34	1	100.0	4	1	US-07-630-288A-34	Sequence 34, Appl1
35	1	100.0	4	1	US-07-630-288A-34	Sequence 34, Appl1
36	1	100.0	4	1	US-08-126-594-25	Sequence 25, Appl1
37	1	100.0	4	1	US-08-126-594-25	Sequence 25, Appl1
38	1	100.0	4	1	US-08-188-943-1	Sequence 1, Appl1
39	1	100.0	4	1	US-08-188-943-1	Sequence 1, Appl1
40	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
41	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
42	1	100.0	4	1	US-08-465-811A-25	Sequence 25, Appl1
43	1	100.0	4	1	US-08-465-811A-25	Sequence 25, Appl1
44	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1
45	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-268-679B-8
Sequence 8, Application US/08268679B
Patent No. 5674729
GENERAL INFORMATION:
APPLICANT: WIMMER, ECKARD; MOLLA,
APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.
TITLE OF INVENTION: DE NOVO CELL-FREE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,679B
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07\846,914
FILING DATE: 06-MAR-1992
CLASSIFICATION: 435
APPLICATION NUMBER: 07\719,761
FILING DATE: 24-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C.H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 0887-4095 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE: N.A.

POSITION IN GENOME: N.A.
US-08-268-679B-8

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
1
DB 1 G 1

RESULT 2
US-08-484-192-16

Sequence 16, Application US/08484192
Patent No. 5756291
GENERAL INFORMATION:
APPLICANT: GRIFFIN, LINDA C.
APPLICANT: ALBRECHT, GLENN
APPLICANT: LATHAM, JOHN
APPLICANT: LEUNG, LAWRENCE
APPLICANT: VERMAAS, ERIC
APPLICANT: TOOLE, JOHN J.
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
METHODS OF MAKING
NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,192
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,387
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 246102002221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc.difference
LOCATION: replace(1,"")
OTHER INFORMATION: /note="This is a biotin-17
US-08-484-192-16
OTHER INFORMATION: nucleotide stretch of abasic residues."

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 9 1

DB 2 G 2

RESULT 3
US-08-361-024-3
Sequence 3, Application US/08361024
Patent No. 6207368
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
TITLE OF INVENTION: Method, Reagent and Kit
for Detection and
Amplification of
TITLE OF INVENTION: Nucleic Acid Sequence
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
COUNTRY: USA
ZIP: 92634

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 MB
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,024
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/925,059
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Burgoon, Richard P.
REGISTRATION NUMBER: 34,787
REFERENCE/DOCKET NUMBER: 1280-126
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: yes
ANTI-SENSE: no
US-08-361-024-3

Query Match. 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
1
DB 1 G 1

RESULT 4

US-08-361-024-3/C
Sequence 3, Application US/08361024
Patent No. 6207368
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
TITLE OF INVENTION: Method, Reagent and Kit
for Detection and
Amplification of
TITLE OF INVENTION: Nucleic Acid Sequence

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
COUNTRY: USA
ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 MB
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,024
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/925,059
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Burgoon, Richard P.
REGISTRATION NUMBER: 34,787
REFERENCE/DOCKET NUMBER: 128D-126
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: yes
ANTI-SENSE: no
US-08-361-024-3

Query Match
Best Local Similarity 100.0%; Score 1; DB 4; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
1
Db 2 g 2

RESULT 5
US-07-791-213D-46
Sequence 46, Application US/0791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
1
Db 2 g 2

RESULT 6
US-07-791-213D-46/c
Sequence 46, Application US/0791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
db 3 G 3

RESULT 7
US-07-791-213D-62
Sequence 62, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

db 2 G 2

RESULT 8
US-07-791-213D-62/c
Sequence 62, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
db 3 G 3

RESULT 9
US-08-268-679B-7
Sequence 7, Application US/08268679B
Patent No. 5674729
GENERAL INFORMATION:
APPLICANT: WIMMER, Eckard; MOLLA,
AKHTERUZZAMAN; PAUL, ANIKO V.
TITLE OF INVENTION: DE NOVO CELL-FREE
SYNTHESIS PICORNAVIRUS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,679B
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07\846,914
FILING DATE: 06-MAR-1992
CLASSIFICATION: 435
APPLICATION NUMBER: 07\719,761
FILING DATE: 24-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C.H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 0887-4095 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE: N.A.
POSITION IN GENOME: N.A.
US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 2 G 2

RESULT 10
US-08-602-036A-2
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oegystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-5000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-6000
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 1 G 1

RESULT 11
US-08-602-036A-2/c
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oegystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 3 G 3

RESULT 12
US-08-293-150A-46
Sequence 46, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-46

Query Match 100.0%; Score 1; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 G 2

RESULT 13
US-08-293-150A-46/C
Sequence 46, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 3 G 3

RESULT 14
US-08-293-150A-62
Sequence 62, Application US/08293150A
Patent No. 5792629

GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 9 1
DB 2 G 2
RESULT 15
US-08-293-150A-62/c
Sequence 62, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 9 1
DB 3 G 3
RESULT 16
US-08-502-374A-2
Sequence 2, Application US/08502374A
Patent No. 5872007
GENERAL INFORMATION:
APPLICANT: Fodstad, Oeystein
APPLICANT: Hovig, Elvind
APPLICANT: Engestraten, Olav
APPLICANT: Maelandsmo, Gunhild H.
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,374A
FILING DATE: 14-Jul-1995

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 9 1
1
Db 1 G 1

RESULT 17
US-08-502-374A-2/c
Sequence 2, Application US/08502374A
Patent No. 5872007
GENERAL INFORMATION:
APPLICANT: Fodstad, Oeystein
APPLICANT: Hovig, Eivind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,374A
FILING DATE: 14-Jul-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO

ANTI-SENSE: YES
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 9 1
1
Db 3 G 3

RESULT 18
US-08-642-407A-2
Sequence 2, Application US/08642407A
Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Eivind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1
1
Db 1 G 1

RESULT 19
US-08-642-407A-2/c
Sequence 2, Application US/08642407A

Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oestlein, Rodstad
APPLICANT: Hovig, Eivind
APPLICANT: Engebraaten, Olav
APPLICANT: MacLandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kettner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
1
DB 3 G 3

RESULT 20
US-08-873-709-9
Sequence 9, Application US/08873709
Patent No. 6037126
GENERAL INFORMATION:
APPLICANT: Grossman, Abraham
TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND
TITLE OF INVENTION: APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abraham Grossman
STREET: 666 Washington Avenue
CITY: Pleasantville
STATE: NY
COUNTRY: USA
ZIP: 10570
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,709
FILING DATE: 12-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Janluk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: 0001/002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-747-9108
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-873-709-9

Query Match 100.0%; Score 1; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
1
DB 1 G 1

RESULT 21
US-09-032-365A-36
Sequence 36, Application US/09032365A
Patent No. 6114502
GENERAL INFORMATION:
APPLICANT: No. 6114502th, Michael
APPLICANT: Nishina, Patsy
APPLICANT: Nagart, Jaryen
APPLICANT: No. 6114502en-Trauth, Konrad
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-2CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:

LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-032-365A-36

Query Match 100.0%: Score 1; DB 3; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 g 1

RESULT 22
US-08-793-634B-12
Sequence 12, Application US/08793634B
Patent No. 6211431
GENERAL INFORMATION:
APPLICANT: Boevink, Petra C.
APPLICANT: Surin, Brian P.
APPLICANT: Keesee, Paul K.
APPLICANT: Chu, Paul W.G.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Khan, Rafiqul I.
APPLICANT: Larkin, Philip J.
APPLICANT: Taylor, William C.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,634B
FILING DATE: June 9, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digillo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10530
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-793-634B-12

Query Match 100.0%: Score 1; DB 4; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 g 2

RESULT 23
US-08-973-568-55
Sequence 55, Application US/08973568B
Patent No. 6277634
GENERAL INFORMATION:
APPLICANT: McCall, Maxine J.
APPLICANT: Hendry, Philip
APPLICANT: Lockelt, Trevor
TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF
FILE REFERENCE: 47203ppctus
CURRENT APPLICATION NUMBER: US/08/973,568B
CURRENT FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 3
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
FEATURE: Synthetic Ribozyme or portion thereof
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
US-08-973-568-55

Query Match 100.0%: Score 1; DB 4; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 g 1

RESULT 24
US-07-755-462-2
Sequence 2, Application US/07755462
Patent No. 5273881
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calhoun, Cornelia J.
APPLICANT: Zarling, David A.
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,462
FILING DATE: 19910904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4255-0001.30
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 9 1
Db 1 G 1

RESULT 25
US-07-755-462-2/C
Sequence 2, Application US/07755462
Patent No. 5273881
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calhoun, Cornelia J.
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
NUMBER OF INVENTION: Formation
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,462
FILING DATE: 19910904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4255-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 9 1
Db 4 G 4

RESULT 26
US-08-169-950-6
Sequence 6, Application US/08169950
Patent No. 5366882
GENERAL INFORMATION:
APPLICANT: LUNNEN, KEITH D.
APPLICANT: WILSON, GEOFFREY G.
TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI
RESTRICTION ENDONUCLEASE AND METHYLASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,950
FILING DATE: 17-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 9 1
Db 1 G 1

RESULT 27
US-08-169-950-6/C
Sequence 6, Application US/08169950
Patent No. 5366882
GENERAL INFORMATION:
APPLICANT: LUNNEN, KEITH D.
APPLICANT: WILSON, GEOFFREY G.
TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI
RESTRICTION ENDONUCLEASE AND METHYLASE

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,950
FILING DATE: 17-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 4 G 4

RESULT 28
US-07-630-288A-7
Sequence 7, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-7

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 G 1

RESULT 29
US-07-630-288A-11
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1 g 1
Db 1 g 1

RESULT 30
US-07-630-288A-11/c
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1 g 1
Db 1 g 1

Db 4 G 4

RESULT 31
US-07-630-288A-13
Sequence 13, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-13

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1 g 1
Db 1 g 1

RESULT 32
US-07-630-288A-14
Sequence 14, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
DB 1 G 1

RESULT 33
US-07-630-288A-14/C
Sequence 14, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
DB 4 G 4

RESULT 34
US-07-630-288A-34
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0% Score 1: DB 1: Length 4:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1
Db 2 G 2

RESULT 35
US-07-630-288A-34/C
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630.288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0% Score 1: DB 1: Length 4:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1
Db 4 G 4

RESULT 36
US-08-126-594-25
Sequence 25, Application US/08126594
Patent No. 5482845
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstratiadis, Algis
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPM/ARC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-25

Query Match 100.0% Score 1: DB 1: Length 4:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1
Db 3 G 3

RESULT 37
US-08-126-594-25/C
Sequence 25, Application US/08126594
Patent No. 5482845
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstratiadis, Algis
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1
DB 4 G 4

RESULT 38
US-08-188-943-1
Sequence 1, Application US/08188943
Patent No. 565347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtiss, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1
DB 3 G 3

RESULT 39
US-08-188-943-1/C
Sequence 1, Application US/08188943
Patent No. 565347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtiss, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 g 1
1
Db 4 C 4

RESULT 40

US-08-188-943-2
Sequence 2, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudlbande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 g 1
1
Db 1 C 1

RESULT 41

US-08-188-943-2/C
Sequence 2, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudlbande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 g 1
1
Db 2 G 2

RESULT 42

US-08-465-811A-25
Sequence 25, Application US/08465811A
Patent No. 5637685
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstratiadis, Argiris
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
NORMALIZED CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,811A
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JIW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 3 G 3

RESULT 43
US-08-465-811A-25/C
Sequence 25, Application US/08465811A
Patent No. 5637685
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstratiadis, Argiris
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,811A
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 4 G 4

RESULT 44
US-08-199-317-2
Sequence 2, Application US/08199317
Patent No. 5670316
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calloun, Cornelia J.
APPLICANT: Zarling, David A.
TITLE OF INVENTION: Diagnostic Applications of Double D-loop
FORMATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,317
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,791
FILING DATE: 09-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,462
FILING DATE: 04-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stralford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 9150-0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for Dpn I
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 1 G 1

RESULT 45
US-08-199-317-2/c
: Sequence 2, Application US/08199317
: Patent No. 5670316
: GENERAL INFORMATION:
: APPLICANT: Sena, Elissa P.
: APPLICANT: Calhoun, Cornelia J.
: APPLICANT: Zarling, David A.
: TITLE OF INVENTION: Diagnostic Applications of Double D-loop
: TITLE OF INVENTION: Formation
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Ave., Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/199,317
: FILING DATE: 25-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/910,791
: FILING DATE: 09-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/755,462
: FILING DATE: 04-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/520,321
: FILING DATE: 07-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Stratford, Carol A.
: REGISTRATION NUMBER: 34,444
: REFERENCE/DOCKET NUMBER: 9150-0004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-324-0880
: TELEFAX: 415-324-0960
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Cleavage site for Dpn I
: US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

oy 1 g 1
db 4 G 4

Search completed: July 15, 2002, 23:07:39
Job time: 22992 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:26 ; Search time 12941.8 Seconds

(without alignments)
1.672 Million cell updates/sec

Title: US-09-375-248-1_COPY_3164_3164

Perfect score: 1 g 1

Sequence: 1 g 1

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Gapop 60.0 , Capext 60.0

Searched: 21979536 seqs, 1081744937 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	100.0	100.0	2	US-07-934-385-14	Sequence 14, Appl
2	100.0	100.0	2	US-08-107-721-46	Sequence 46, Appl
3	100.0	100.0	2	US-08-107-721B-46	Sequence 46, Appl
4	100.0	100.0	2	US-09-172-828-15	Sequence 15, Appl
5	100.0	100.0	2	US-09-284-725-201	Sequence 201, Appl
6	100.0	100.0	2	US-09-306-333A-32	Sequence 32, Appl
7	100.0	100.0	2	US-09-387-777-7	Sequence 7, Appl
8	100.0	100.0	2	US-09-387-777-5	Sequence 5, Appl
9	100.0	100.0	2	US-09-387-777-10	Sequence 10, Appl
10	100.0	100.0	2	US-09-387-777-11	Sequence 11, Appl
11	100.0	100.0	2	US-09-387-777-12	Sequence 12, Appl
12	100.0	100.0	2	US-09-387-777-14	Sequence 14, Appl
13	100.0	100.0	2	US-09-472-035A-19	Sequence 19, Appl
14	100.0	100.0	2	US-09-472-035A-20	Sequence 20, Appl
15	100.0	100.0	2	US-09-634-306B-51869	Sequence 51869, A
16	100.0	100.0	2	US-09-634-306B-52280	Sequence 52280, A
17	100.0	100.0	2	US-09-634-306B-52357	Sequence 52357, A
18	100.0	100.0	2	US-09-634-306B-53003	Sequence 53003, A
19	100.0	100.0	2	US-09-634-306B-58305	Sequence 58305, A
20	100.0	100.0	2	US-09-634-306B-175312	Sequence 175312, A
21	100.0	100.0	2	US-09-634-306B-175337	Sequence 175337, A
22	100.0	100.0	2	US-09-634-306B-175354	Sequence 175354, A

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33 1 100.0 2 24 US-09-634-306B-175403 Sequence 175403,
34 1 100.0 2 24 US-09-634-306B-175415 Sequence 175415,
35 1 100.0 2 24 US-09-634-306B-175419 Sequence 175419,
36 1 100.0 2 24 US-09-634-306B-175426 Sequence 175426,
37 1 100.0 2 24 US-09-634-306B-175433 Sequence 175433,
38 1 100.0 2 24 US-09-634-306B-175449 Sequence 175449,
39 1 100.0 2 24 US-09-634-306B-176848 Sequence 176848,
40 1 100.0 2 24 US-09-634-306B-176849 Sequence 176849,
41 1 100.0 2 24 US-09-634-306B-176880 Sequence 176880,
42 1 100.0 2 24 US-09-634-306B-178420 Sequence 178420,
43 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440,
44 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440,
45 1 100.0 2 24 US-09-634-306B-178617 Sequence 178617,

ALIGNMENTS

RESULT 1
US-07-934-385-14
Sequence 14, Application US/07934385
GENERAL INFORMATION:
APPLICANT: LATHAM, JOHN
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,385
FILING DATE: 19920821
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 24610-20022.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(1,"")
OTHER INFORMATION: /note="This position is a
OTHER INFORMATION: biotin-17 nucleotide stretch of random sequences."
US-07-934-385-14

Query Match 100.0%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
1
Db 2 G 2

RESULT 2
US-08-107-721-46
Sequence 46, Application US/08107721
GENERAL INFORMATION:
APPLICANT: TOOLE, JOHN J.
APPLICANT: GRIFFIN, LINDA C.
APPLICANT: BOCK, LOUIS C.
APPLICANT: LATHAM, JOHN A.
APPLICANT: MUENCHAU, DARYL D.
APPLICANT: KRANCZYK, STEVEN
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
METHODS OF MAKING
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSEE: GILEAD SCIENCES, INC.
STREET: 344 LAKEVIEW DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,721
FILING DATE: 20-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28216
REFERENCE/DOCKET NUMBER: 24610-20022.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)574-3000
TELEFAX: (415)578-9264
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1
OTHER INFORMATION: /note="This is a biotin-17
OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-107-721-46

Query Match 100.0%; Score 1; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
1
Db 2 G 2

RESULT 3
US-08-107-721B-46
Sequence 46, Application US/08107721B
GENERAL INFORMATION:
APPLICANT: TOOLE, JOHN J.
APPLICANT: GRIFFIN, LINDA C.
APPLICANT: BOCK, LOUIS C.
APPLICANT: LATHAM, JOHN A.
APPLICANT: MUENCHAU, DARYL D.
APPLICANT: KRANCZYK, STEVEN
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
METHODS OF MAKING

NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: GILEAD SCIENCES, INC.
STREET: 344 LAKE SIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,721B
FILING DATE: 20-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28216
REFERENCE/DOCKET NUMBER: 24610-20022.20
TELEPHONE: (415)574-3000
TELEFAX: (415)578-9264
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note="This is a biotin-17
OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-107-721B-46

Query Match 100.0%; Score 1; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
DB 2 G 2

RESULT 4
US-09-172-828-15
Sequence 15, Application US/09172828
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
APPLICANT: Klagsbrun, Michael
APPLICANT: Elenius, Klaus
TITLE OF INVENTION: Novel Human EGF Receptors and Use
FILE REFERENCE: 47758-PCT
CURRENT APPLICATION NUMBER: US/09/172,828
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 2
TYPE: DNA
ORGANISM: mouse
US-09-172-828-15

Query Match 100.0%; Score 1; DB 15; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
DB 1 g 1

RESULT 5
US-09-284-725-201/C
Sequence 201, Application US/09284725
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
APPLICANT: Van Doorn, Leendert
TITLE OF INVENTION: Probes, methods and kits for detection and
TITLE OF INVENTION: Typing of Helicobacter pylori nucleic acids in biological
NUMBER OF SEQUENCES: 280
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/284,725
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP96/870131.8
FILING DATE: 16-OCT-1996
APPLICATION NUMBER: PCT/EP97/05614
FILING DATE: 10-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: INNOG2.001APC
TELEPHONE: (949) 760-0404
TELEFAX: (949) 760-9395
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-284-725-201

Query Match 100.0%; Score 1; DB 16; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
DB 2 G 2

RESULT 6
US-09-306-333A-32
Sequence 32, Application US/09306333A
GENERAL INFORMATION:
APPLICANT: Academy of Applied Science
TITLE OF INVENTION: BRCAL and hMLH1 Gene Primer Sequences and Method for
FILE REFERENCE: BRCAL
CURRENT APPLICATION NUMBER: US/09/306,333A
CURRENT FILING DATE: 1999-05-06

09-375-248-1-copy-3164-2200

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/387,777
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION NUMBER:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Friedmann, Mark M. 883
 REGISTRATION NUMBER: 33/40
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 972-3-5625553
 TELEFAX: 972-3-5625554
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

[illegible]

RESULT 9
US-09-387-777-3
Sequence 3, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kiess
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
POLYMERIZATION USING OLIGONUCLEOTIDE
TRIPHOSPHATES BUILDING BLOCKS
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
TITLE OF INVENTION: 88
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 2.0 converted
SOFTWARE: word for ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-3

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 2 G 2

RESULT 10
US-09-387-777-5/c
Sequence 5, Application US/09387777
GENERAL INFORMATION:

APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-5

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 G 1

RESULT 11

US-09-387-777-6/c
Sequence 6, Application US/09387777
GENERAL INFORMATION:

APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-6

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 2 G 2

RESULT 12
US-09-387-777-7

Sequence 7, Application US/09387777
GENERAL INFORMATION:

APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

```

: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2.1
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-7
:
: Query Match          100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 g 1
: Db 2 g 2
:
: RESULT 13
: US-09-387-777-7/C
: Sequence 7, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Klees
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2.1
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-8
```

```

: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-7
```

```

: Query Match          100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 g 1
: Db 1 g 1
```

```

: RESULT 14
: US-09-387-777-8/C
: Sequence 8, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Klees
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2.1
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-8
```

```

: Query Match          100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 g 1
```

Db 1 g 1

RESULT 15

US-09-387-777-9

Sequence 9, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-9

Query Match 100.0%; Score 1; DB 17; Length 2;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 1 g 1

RESULT 16

US-09-387-777-10

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-10

Query Match 100.0%; Score 1; DB 17; Length 2;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 1 g 1

RESULT 17

US-09-387-777-10/c

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-10

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
DB 2 G 2

RESULT 18
US-09-387-777-11
Sequence 11, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-11

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
DB 1 G 1

RESULT 19
US-09-387-777-12
Sequence 12, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-12

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
DB 1 G 1

RESULT 20
US-09-387-777-14/C
Sequence 14, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-14
Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
DB 2 g 2
RESULT 21
US-09-387-777-15
Sequence 15, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-15
Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 g 1
DB 2 g 2
RESULT 22
US-09-472-035A-19
Sequence 19, Application US/09472035A
GENERAL INFORMATION:
APPLICANT: Yechezkel Kashi et al.
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
SOFTWARE: an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472,035A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 74/77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-472-035A-19

Query Match 100.0%: Score 1; DB 18; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 1 G 1

RESULT 23
US-09-472-035A-20/c
Sequence 20, Application US/09472035A
GENERAL INFORMATION:
APPLICANT: Yechezkel Kashi et al.
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimole-890rx
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472,035A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 74/77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-472-035A-20

Query Match 100.0%: Score 1; DB 18; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 G 2

RESULT 24

US-09-634-306B-51869/c
Sequence 51869, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51869
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-51869

Query Match 100.0%: Score 1; DB 24; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
1
Db 2 G 2

RESULT 25
US-09-634-306B-52280/c
Sequence 52280, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52280
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-52280

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1
Db 2 g 2

RESULT 26
US-09-634-306B-52357/c
; Sequence 52357, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52357
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52357

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1
Db 2 g 2

RESULT 27
US-09-634-306B-53003/c
; Sequence 53003, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53003
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-53003

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1
Db 2 g 2

RESULT 28
US-09-634-306B-58305/c
; Sequence 58305, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58305
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58305

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1
Db 2 g 2

RESULT 29
US-09-634-306B-175312
; Sequence 175312, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21

```

: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 175312
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175312
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 30
US-09-634-306B-175337
: Sequence 175337, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 175337
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175337
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 31
US-09-634-306B-175354
: Sequence 175354, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 175354
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175354
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 32
US-09-634-306B-175401
: Sequence 175401, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 175401
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
```

US-09-634-306B-175401

```
Query Match      100.0%; Score 1; DB 24; Length 2
Host Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Index
```

Qy	1	9	1
Db	1	9	1

RESULT 33
US-09-634-306B-175403

```

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotid
TITLE OF INVENTION: Polymorphisms in the human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 175403
LENGTH: 2
TYPE: DNA
ORGANISM: Human
OS-09-634-306B-175403

```

Query Match	100.0%;	Score 1;	DB 24;	Length 2;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches	1;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0

Qy	1	g	1
Db	1	g	1

RESULT 34

US-09-634-306B-175415
Sequence 175415, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotides
TITLE OF INVENTION: Polymorphisms In the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634, 306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218, 006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198, 676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193, 483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185, 218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167, 363

```

:
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEO ID NOS: 325720
: SOFTWARE: FASTISO for Windows Version 4.0
: SEO ID NO: 175415
:

```

Query Match	100.0%	Score 1:	DB 24:	Length 2:
Best Local Similarity	100.0%	Pred. No. 0:		
Matches	1:	Conservative	0:	Mismatches
				0:
				Gaps
				0:

QY	1	9	1
Db	1	9	1

```

RESULT 35
US-09-634-306B-175419
; Sequence 175419
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotided
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: fastSeq for Windows Version 4.0
SEQ ID NO 175419
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-175419

```

```

Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY	1	g	1
Db	1	g	1

```

RESULT 36
US-09-634-306B-175426
: Sequence 175426, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms In the Human Genome
: FILE REFERENCE: 108827.129

```

```

: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175426
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175426
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```
RESULT 37
US-09-634-306B-175433
: Sequence 175433, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175433
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175433
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
```

```
Db       1 g 1
```

```

RESULT 38
US-09-634-306B-175849
: Sequence 175849, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175849
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```
RESULT 39
US-09-634-306B-176848
: Sequence 176848, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176848
: LENGTH: 2
```

TYPE: DNA
ORGANISM: Human
US-09-634-306B-176848

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 1 g 1

RESULT 40
US-09-634-306B-176849
; Sequence 176849, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-176849

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 1 g 1

RESULT 41
US-09-634-306B-176880
; Sequence 176880, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176880
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-176880

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 1 g 1

RESULT 42
US-09-634-306B-178420
; Sequence 178420, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178420
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178420

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 1 g 1

RESULT 43
US-09-634-306B-178440
; Sequence 178440, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178440
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-178440
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
Db      1 g 1
```

```

RESULT 44
US-09-634-306B-178440/C
: Sequence 178440, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178440
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-178440
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
Db      2 g 2
```

```

RESULT 45
US-09-634-306B-178617
: Sequence 178617, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178617
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-178617
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
Db      2 g 2
```

Search completed: July 16, 2002, 02:50:26
Job time: 31279 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:57:00 ; Search time 808.35 seconds
(without alignments)
2.105 Million cell updates/sec

Title: US-09-375-248-1_COPY_3164_3164

Perfect score: 1 g 1

Sequence: 1 g 1

Scoring table: OLIGO-NUC

Searched: 1163369 seqs, 850982142 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Pending_Patents_MA_New:*
1: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1	100.0	2	6	US-10-027-632-51869 Sequence 51869, A
C 2	1	100.0	2	6	US-10-027-632-52280 Sequence 52280, A
C 3	1	100.0	2	6	US-10-027-632-52357 Sequence 52357, A
C 4	1	100.0	2	6	US-10-027-632-53003 Sequence 53003, A
C 5	1	100.0	2	6	US-10-027-632-58305 Sequence 58305, A
C 6	1	100.0	2	6	US-10-027-632-175312 Sequence 175312, A
C 7	1	100.0	2	6	US-10-027-632-175337 Sequence 175337, A
C 8	1	100.0	2	6	US-10-027-632-175401 Sequence 175401, A
C 9	1	100.0	2	6	US-10-027-632-175403 Sequence 175403, A
C 10	1	100.0	2	6	US-10-027-632-175415 Sequence 175415, A
C 11	1	100.0	2	6	US-10-027-632-175419 Sequence 175419, A
C 12	1	100.0	2	6	US-10-027-632-175426 Sequence 175426, A
C 13	1	100.0	2	6	US-10-027-632-175433 Sequence 175433, A
C 14	1	100.0	2	6	US-10-027-632-175849 Sequence 175849, A
C 15	1	100.0	2	6	US-10-027-632-176848 Sequence 176848, A
C 16	1	100.0	2	6	US-10-027-632-176880 Sequence 176880, A
C 17	1	100.0	2	6	US-10-027-632-178420 Sequence 178420, A
C 18	1	100.0	2	6	US-10-027-632-178440 Sequence 178440, A
C 19	1	100.0	2	6	US-10-027-632-178617 Sequence 178617, A
C 20	1	100.0	2	6	US-10-027-632-178640 Sequence 178640, A
C 21	1	100.0	2	6	US-10-027-632-52136 Sequence 52136, A
C 22	1	100.0	2	6	US-10-027-632-52402 Sequence 52402, A
C 23	1	100.0	2	6	US-10-027-632-52403 Sequence 52403, A
C 24	1	100.0	2	6	US-10-027-632-52410 Sequence 52410, A
C 25	1	100.0	2	6	US-10-027-632-52417 Sequence 52417, A
C 26	1	100.0	2	6	US-10-027-632-52418 Sequence 52418, A

C 27	1	100.0	3	6	US-10-027-632-52403 Sequence 52403, A
C 28	1	100.0	3	6	US-10-027-632-52404 Sequence 52404, A
C 29	1	100.0	3	6	US-10-027-632-52410 Sequence 52410, A
C 30	1	100.0	3	6	US-10-027-632-52417 Sequence 52417, A
C 31	1	100.0	3	6	US-10-027-632-52418 Sequence 52418, A
C 32	1	100.0	3	6	US-10-027-632-52419 Sequence 52419, A
C 33	1	100.0	3	6	US-10-027-632-52425 Sequence 52425, A
C 34	1	100.0	3	6	US-10-027-632-52491 Sequence 52491, A
C 35	1	100.0	3	6	US-10-027-632-52495 Sequence 52495, A
C 36	1	100.0	3	6	US-10-027-632-52496 Sequence 52496, A
C 37	1	100.0	3	6	US-10-027-632-52508 Sequence 52508, A
C 38	1	100.0	3	6	US-10-027-632-52512 Sequence 52512, A
C 39	1	100.0	3	6	US-10-027-632-52513 Sequence 52513, A
C 40	1	100.0	3	6	US-10-027-632-52515 Sequence 52515, A
C 41	1	100.0	3	6	US-10-027-632-52533 Sequence 52533, A
C 42	1	100.0	3	6	US-10-027-632-52561 Sequence 52561, A
C 43	1	100.0	3	6	US-10-027-632-52751 Sequence 52751, A
C 44	1	100.0	3	6	US-10-027-632-52758 Sequence 52758, A
C 45	1	100.0	3	6	US-10-027-632-52761 Sequence 52761, A

ALIGNMENTS

RESULT 1
US-10-027-632-51869/C
; Sequence 51869, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/146, 002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51869

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 2
US-10-027-632-52280/C
; Sequence 52280, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/146, 002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51869


```
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 52280
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52280
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 g 1
Db 2 G 2

```
RESULT 3
US-10-027-632-52357/c
SEQUENCE 52357, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 52357
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52357
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 g 1

Db 2 G 2

```
RESULT 4
US-10-027-632-53003/c
SEQUENCE 53003, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 53003
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-53003
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 g 1
Db 2 G 2

```
RESULT 5
US-10-027-632-58305/c
SEQUENCE 58305, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 58305
```

```
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58305
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
Db       1 g 1
```

```
RESULT 6
US-10-027-632-175312
; Sequence 175312, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175312
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
Db       1 g 1
```

```
RESULT 7
US-10-027-632-175337
; Sequence 175337, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175337
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
Db       1 g 1
```

```
RESULT 8
US-10-027-632-175354
; Sequence 175354, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175354
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
Db       1 g 1
```

```
RESULT 9
US-10-027-632-175401
; Sequence 175401, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401

```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 g 1
        |
Db      1 g 1

```

```

RESULT 10
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403

```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
        |
Db      1 g 1

```

```

RESULT 11
US-10-027-632-175415
; Sequence 175415, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175415

```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 g 1
        |
Db      1 g 1

```

```

RESULT 12
US-10-027-632-175419
; Sequence 175419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

```

```
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175419
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-175419
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 1 g 1
```

```
RESULT 13
US-10-027-632-175426
; Sequence 175426, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 1 g 1
```

```
RESULT 14
US-10-027-632-175433
; Sequence 175433, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
```

```
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175433
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-175433
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 1 g 1
```

```
RESULT 15
US-10-027-632-175849
; Sequence 175849, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175849
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 1 g 1
```

```
RESULT 16
US-10-027-632-175848
; Sequence 175848, Application US/10027632
```

```

: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176848
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176848
```

```

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```

RESULT 17
US-10-027-632-176849
: Sequence 176849, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176849
```

```
Query Match          100.0%: Score 1; DB 6; Length 2;
```

```

Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```

RESULT 18
US-10-027-632-176880
: Sequence 176880, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176880
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176880
```

```

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```

RESULT 19
US-10-027-632-178420
: Sequence 178420, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
```

;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 178420
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-178420

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 20
US-10-027-632-178440
;; Sequence 178440, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 178440
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-178440

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 21
US-10-027-632-178440/C
;; Sequence 178440, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12

;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 178440
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-178440

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 g 2

RESULT 22
US-10-027-632-178617
;; Sequence 178617, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 178617
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-178617

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 g 2

RESULT 23

```
US-10-027-632-178640
: Sequence 178640, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-10
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178640
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-178640
```

```
Query Match      100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1 g 1
|
Db 2 g 2

```
RESULT 24
PCT-US02-00351-20/C
: Sequence 20, Application PC/TUS0200351
: GENERAL INFORMATION:
: APPLICANT: Chel, Ilan
: APPLICANT: Vileto, Ada
: TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING
: FILE REFERENCE: 02/23682
: CURRENT APPLICATION NUMBER: PCT/US02/00351
: CURRENT FILING DATE: 2002-05-05
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 20
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: motif found in the URSS of both ech42 and prt1 genes
PCT-US02-00351-20
```

```
Query Match      100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1 g 1
|
Db 3 g 3

RESULT 25

```
US-10-027-632-52136
: Sequence 52136, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52136
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52136
```

```
Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1 g 1
|
Db 3 g 3

```
RESULT 26
US-10-027-632-52402/C
: Sequence 52402, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52402
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52402
```

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

```
RESULT 27
US-10-027-632-52403/C
; Sequence 52403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52403
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52403
```

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

```
RESULT 28
US-10-027-632-52404/C
; Sequence 52404, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52404
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52404
```

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

```
RESULT 29
US-10-027-632-52410/C
; Sequence 52410, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52410
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52410
```

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 3 g 3

```
RESULT 30
US-10-027-632-52417/C
; Sequence 52417, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
```



```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52417
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52417
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 q 1
Db 2 g 2
```

```
RESULT 31
US-10-027-632-52418/c
; Sequence 52418, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52418
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52418
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 q 1
Db 2 g 2
```

```
RESULT 32
US-10-027-632-52419/c
; Sequence 52419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52419
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52419
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 q 1
Db 2 g 2
```

```
RESULT 33
US-10-027-632-52425/c
; Sequence 52425, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52425
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
```

US-10-027-632-52425

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1
Db 3 g 3

RESULT 34

US-10-027-632-52491
; Sequence 52491, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52491
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52491

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1
Db 2 g 2

RESULT 35

US-10-027-632-52495/c
; Sequence 52495, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52495
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52495

US-10-027-632-52495

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1
Db 3 g 3

RESULT 36

US-10-027-632-52496
; Sequence 52496, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52496
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52496

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1
Db 2 g 2

RESULT 37

US-10-027-632-52508
; Sequence 52508, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

```

: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52508
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52508
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
Db 2 g 2
```

```

RESULT 38
US-10-027-632-52512/c
: Sequence 52512, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52512
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52512
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
```

```

Db 3 G 3
RESULT 39
US-10-027-632-52513
: Sequence 52513, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52513
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52513
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
Db 2 g 2
```

```

RESULT 40
US-10-027-632-52615
: Sequence 52615, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52615
: LENGTH: 3
```

TYPE: DNA
ORGANISM: Human
US-10-027-632-52615

Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 2 g 2

RESULT 41
US-10-027-632-52633
Sequence 52633, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52633
LENGTH: 3
TYPE: DNA
ORGANISM: Human
US-10-027-632-52633

Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 2 g 2

RESULT 42
US-10-027-632-52651
Sequence 52651, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52651
LENGTH: 3
TYPE: DNA
ORGANISM: Human
US-10-027-632-52651

Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 2 g 2

RESULT 43
US-10-027-632-52753
Sequence 52753, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52753
LENGTH: 3
TYPE: DNA
ORGANISM: Human
US-10-027-632-52753

Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
|
Db 2 g 2

RESULT 44
US-10-027-632-52758/C
Sequence 52758, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52758
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52758
```

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
db       1 G 1
```

```

RESULT 45
US-10-027-632-52761
; Sequence 52761, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52761
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52761
```

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
db       1 G 1
```

Search completed: July 16, 2002, 02:57:00
Job time: 24558 sec

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	1	100.0	2	2	HSN003817	A103941 Homo sapi
c 2	1	100.0	2	2	HSN007187	A104237 Homo sapi
c 3	1	100.0	2	2	HSN008709	A104385 Homo sapi
c 4	1	100.0	2	2	HSN011919	A1047069 Homo sapi
c 5	1	100.0	2	10	B1817789	B1817789 G3-G32 A
c 6	1	100.0	2	10	C55081	C55081 C55081 Tyu
c 7	1	100.0	2	10	BE351920	BE351920 894053D0
c 8	1	100.0	2	12	AZ463604	AZ463604 1M0272J00
c 9	1	100.0	3	9	AM672605	AM672605 2XA Expla
c 10	1	100.0	3	12	AZ438202	AZ438202 1M0228I0
c 11	1	100.0	3	12	CG2650KC	A1077515 Drosophi
c 12	1	100.0	4	2	BG328576	Bg928576 HNC56-1 A
c 13	1	100.0	4	2	BG326576	Bg926576 HNC56-1 A
c 14	1	100.0	4	2	HSN003901	A1039425 Homo sapi
c 15	1	100.0	4	2	HSN010467	A1045617 Homo sapi
c 16	1	100.0	4	2	HSN010467	A1045617 Homo sapi
c 17	1	100.0	4	9	AM672622	AM672622 73C Expla

C	18	1	100.0	4	12	CNS004RB	AL054121	Drosophila
C	19	1	100.0	5	2	HSM007310	A1042460	Homo sapi
C	20	1	100.0	5	2	HSM007835	A1042985	Homo sapi
C	21	1	100.0	5	2	HSM011053	A1046203	Homo sapi
C	22	1	100.0	6	2	BG927410	Bg927410	HNC1-1-G7
C	23	1	100.0	6	2	HSM003844	A1039368	Homo sapi
C	24	1	100.0	6	2	HSM004423	A1039947	Homo sapi
C	25	1	100.0	6	2	HSM007334	A1042484	Homo sapi
C	26	1	100.0	6	2	HSM007683	A1042833	Homo sapi
C	27	1	100.0	6	2	HSM008014	A1043164	Homo sapi
C	28	1	100.0	6	2	HSM010918	A1046068	Homo sapi
C	29	1	100.0	6	2	HSM010918	A1046068	Homo sapi
C	30	1	100.0	6	10	BE726686	BE726686	894095D11
C	31	1	100.0	6	10	BE726686	BE726686	894095D11
C	32	1	100.0	7	2	BG897546	BG897546	HOA14-1-H
C	33	1	100.0	7	2	BG897546	Bg997346	HOA14-1-H
C	34	1	100.0	7	2	HSM007412	A1042562	Homo sapi
C	35	1	100.0	7	2	HSM007412	A1042562	Homo sapi
C	36	1	100.0	7	2	HSM007502	A1042652	Homo sapi
C	37	1	100.0	7	2	HSM007502	A1042652	Homo sapi
C	38	1	100.0	7	10	C58888	C58888	C58888
C	39	1	100.0	8	2	HSM001420	A1037095	Homo sapi
C	40	1	100.0	8	2	HSM011743	A1037413	Homo sapi
C	41	1	100.0	8	2	HSM004451	A1039975	Homo sapi
C	42	1	100.0	8	2	HSM004451	A1039975	Homo sapi
C	43	1	100.0	8	2	HSM007277	A1042427	Homo sapi
C	44	1	100.0	8	2	HSM007277	A1042427	Homo sapi
C	45	1	100.0	8	2	HSM007323	A1042473	Homo sapi

ALIGNMENTS

RESULT	1
HSMM003817/c	
ID	HSMM003817
XX	standard; RNA; EST; 2 BP

AL039341.1

12-MAR-1999 (REL. 59, Last updated, Version 1)

... (from clone DKFZp434F2010)

EST1: expressed sequence tag.

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia
Eutheria; Primates; Catarrhini; Hominoidea; Homo.

11-12

MEWES W., Gassenhuber J., Wiemann S.

MLPS, Am Klopfersplitz 18a D-82152 Martinsried, GERMANY

sequencing consortium of the German Genome Project.

NO SI sequence available

Please contact the RZPD: Ressourcenzentrum. H

berlin-charlottenburg, GERMANY; Email: clone@rzpd.de

Location/Qualifiers

Source

```

FT source 1. .2
FT /db.xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434F2010"
FT /clone_1b="434 (synonym: htes3). Vector nSport. host"

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FT DH10B: sites NOTI + SalI"
 FT /dev-stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 2 BP: 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 DB 2 G 2

RESULT 2
 HSM007187/c
 ID HSM007187 standard; RNA: EST; 2 BP.
 AC AL042337;
 XX AL042337.1
 SV AL042337.1
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA: EST DKFZp43400820_r1 (from clone DKFZp43400820)
 DE EST: expressed sequence tag.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 XX
 XX [1]
 RN 1-2
 RP 1-2
 RA Ottenwelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopsterspitz 18a D-82152 Martinsried, GERMANY
 RL
 XX
 CC Clone from S. Wiemann, sequenced by MedGenomix within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No si sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 CC
 XX
 FH Key Location/Qualifiers
 FH
 FT source
 FT 1..2
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp43400820"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B: sites NOTI + SalI"
 FT /dev-stage="adult"
 FT /tissue_type="testis"
 FT
 XX
 SQ Sequence 2 BP: 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 DB 2 G 2

RESULT 3

HSM008709/c
 ID HSM008709 standard; RNA: EST; 2 BP.
 XX
 AC AL043859;
 XX AL043859.1
 SV AL043859.1
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA: EST DKFZp434B2128_r1 (from clone DKFZp434B2128)
 DE EST: expressed sequence tag.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 XX
 XX [1]
 RN 1-2
 RP 1-2
 RA Bloeker H., Boecker M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopsterspitz 18a D-82152 Martinsried, GERMANY
 RL
 XX
 CC Clone from S. Wiemann, sequenced by GBF within the cDNA
 CC sequencing consortium of the German Genome Project
 CC si sequence also available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 CC
 XX
 FH Key Location/Qualifiers
 FH
 FT source
 FT 1..2
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434B2128"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B: sites NOTI + SalI"
 FT /dev-stage="adult"
 FT /tissue_type="testis"
 FT
 XX
 SQ Sequence 2 BP: 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 DB 2 G 2

RESULT 4
 HSM011919/c
 ID HSM011919 standard; RNA: EST; 2 BP.
 AC AL047069;
 XX AL047069.1
 SV AL047069.1
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA: EST DKFZp586P0517_r1 (from clone DKFZp586P0517)
 DE EST: expressed sequence tag.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.


```

XX  [1]
KN  Kocher K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RP  1-2
RA  Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RT  M185, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
RL  :
XX  :
CC  Clone from S. Wiemann, sequenced by BMFZ within the CDNA
CC  sequencing consortium of the German Genome Project
CC  No sl sequence available
CC  This clone is available at the RZPD in Berlin
CC  Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC  Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de
XX
FH  Key
FH  Location/Qualifiers
FT  source
FT  1..2
FT  /db_xref="taxon:9606"
FT  /organism="Homo sapiens"
FT  /clone_lib="DKFZP586P0517"
FT  /clone_lib="586 (synonym: hntel). Vector pSport1: host
FT  DH10B; sites NciI + SalI/MluI"
FT  /dev_stage="adult"
FT  /tissue_type="uterus"
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SO  Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1 g 1
    1
Db  2 G 2

RESULT  5
B1817789/c      2 bp  mRNA  linear  EST 04-OCT-2001
LOCUS          B1817789
DEFINITION     G3-c22 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
                to Putative ribosomal protein S2, mRNA sequence.
ACCESSION      B1817789.1 GI:15951401
VERSION        EST.
KEYWORDS       axolotl.
SOURCE         Ambystoma mexicanum
ORGANISM       Ambystoma mexicanum
                Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomidae;
                Ambystoma.
REFERENCE      1 (bases 1 to 2)
AUTHORS        Voss,S.R., King,D., Maness,N., Smith,J.J., Kondel,M., Bryant,S.V.,
                Gardiner,D.M. and Parichy,D.M.
TITLE          Unpublished sequence tags from an axolotl limb regeneration library
JOURNAL        unpublished (2001)
COMMENT        Contact: Voss SR
                Department of Biology
                Colorado State University
                Fort Collins, CO 80523, USA
                Tel: 970 491 4869
                Fax: 970 491 0649
                Email: svoss@lamar.colostate.edu
                Single pass sequence from 5' end. Low quality sequence was trimmed
                from the ends (FHRD error rate ~ 5%). Trace file available:
                svoss@lamar.colostate.edu.
                Location/Qualifiers
                1..2
                /organism="Ambystoma mexicanum"
                /db_xref="taxon:8296"
                /clone_lib="Axolotl Lambda Zap Library"
                /tissue_type="Regenerating forelimb"
                /dev_stage="Medium-bud blastema"

FEATURES
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BASE COUNT      0 a      1 c      0 g      1 t
ORIGIN
Query Match      100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1 g 1
    1
Db  2 G 2

RESULT  7
BE351920
LOCUS          BE351920
DEFINITION     894053D07.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
ACCESSION      BE351920
VERSION        BE351920.1 GI:9263773
KEYWORDS       EST.
SOURCE         Chlamydomonas reinhardtii.
ORGANISM       Chlamydomonas reinhardtii
                Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                Chlamydomonadaceae; Chlamydomonas.
REFERENCE      1 (bases 1 to 2)

```

AUTHORS

Crossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J.P., Sillfow, C., Stern, D. and Surzycki, R.

TITLE

Analysis of the Chlamydomonas reinhardtii genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants: project phase 2

JOURNAL

Unpublished (2000)

COMMENT

Contact: Elizabeth H. Harris
DCMB Box 91000

Duke University
Durham, NC 27708-1000, USA

Fax: 919 613 8164

Tel: 919 613 8177

Email: chlamy@duke.edu

FEATURES

source
1..2
Location/Qualifiers

/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db.xref="taxon:3055"
/clone.lib="C. reinhardtii CC-1690, normalized, lambda zap
11"

/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO₂ and HS medium bubbled with 5% CO₂.
Polya mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
zap clones by superinfection with Exsistist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldi et al (1996) Genome Research 6: 791-806."

BASE COUNT
ORIGIN
0 a 0 c 2 g 0 t

Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 1 g 1

RESULT 8

AZ463604

LOCUS

DEFINITION

AZ463604 2 bp DNA linear GSS 04-OCT-2000
1M0272J05R Mouse 10kb plasmid UGCCIM library Mus musculus genomic
clone UGCCIM0272J05 R. DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical

Research Bldg., 20 S. 2030 E., SLC, UT

Tel: 801 585 5606

Fax: 801 585 7177

FEATURES

source

1..2
Location/Qualifiers

/organism="Mus musculus"

/strain="C57Bl/6J"

/db.xref="taxon:10090"

/clone.lib="UCCIM0272J05"

/clone.lib="Mouse 10kb plasmid UGCCIM library"

/sex="Male"

/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57Bl/6J (male) was obtained from the Jackson

laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (911473211419b1AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT
ORIGIN
0 a 0 c 1 g 1 t

Query Match 100.0%; Score 1; DB 12; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 1 g 1

RESULT 9

AM672605

LOCUS

DEFINITION

AM672605 3 bp mRNA linear EST 26-SEP-2001
2XA Explanted metanephric mesenchyme induced to differentiate into
epithelial structures of the nephron ex vivo. Rattus norvegicus
cDNA similar to: gb|AF022811.1|AF022811 Mus musculus
cornichon mRNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 3)

Pilsov, S.Y., Ivanov, S.V., Yoshino, K., Dove, L.F., Pilsova, T.M.,

Higginbotham, K.G., Karavanova, I., Lerman, M. and Perantoni, A.O.

Mesenchymal-epithelial transition in the developing metanephric

kidney: gene expression study by differential display

Genesis 27 (1), 22-31 (2000)

20321327

Contact: Pilsov S.Y.

Laboratory of Comparative Carcinogenesis

National Cancer Institute

FCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA

Tel: 301 846 1242
 Fax: 301 846 4956
 Email: plisov@mail.ncicrf.gov
 PCR Primers
 FORWARD: ctccgagctccctc
 BACKWARD: ttaagcttcttcttc
 Insert Length: 350 Std Error: 0.00
 Seq primer: SP6
 High quality sequence stop: 261.
 Location/Qualifiers
 1..3
 /organism="Mus musculus"
 /db_xref="taxon:10116"
 /clone_lib="Explanted melanephric mesenchyme induced to
 differentiate into epithelial structures of the nephron ex
 vivo."
 /tissue_type="Melanephric mesenchyme"
 /cell_type="Mesenchymal/Epithelial"
 /dev_stage="13 dpc-16dpc"
 /lab_host="JMI09"
 /note="Organ: Kidney; Vector: pGEM-Teasy (Promega);
 Restriction Enzymes: 1: AclI, AclI, SphI, NcoI, BstZ1,
 NotI, SacII, and EcoRI; SpeI, EcoRI, NotI, BstZ1,
 SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment
 PCR-amplified in mRNA differential display analysis;
 cloned in pGEM-Teasy (Promega); its expression is
 developmentally regulated during mesenchymal-epithelial
 conversion in the melanephric kidney."

BASE COUNT
 ORIGIN
 1 a
 0 c
 2 g
 0 t

Query Match
 Best Local Similarity 100.0%; Score 1; DB 9; Length 3;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 1 g 1
 Db 1 g 1

RESULT 10
 A2438202/c
 LOCUS
 DEFINITION A2438202 3 bp DNA linear GSS 03-OCT-2000
 clone UGCCIM0228108 F. DNA sequence.
 ACCESSION A2438202
 VERSION A2438202.1 GI:10562215
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 3)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0228 row: 1 Column: 08
 Seq primer: CGTCTAAACGACGCCACT
 Class: plasmid ends

FEATURES
 source
 High quality sequence stop: 302.
 Location/Qualifiers
 1..3
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="UGCCIM0228108"
 /clone_lib="Mouse 10kb plasmid UGCCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (G1473211419b1A129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance.

BASE COUNT
 ORIGIN
 1 a
 1 c
 0 g
 1 t

Query Match
 Best Local Similarity 100.0%; Score 1; DB 12; Length 3;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 1 g 1
 Db 1 g 1

RESULT 11
 CNS00KCV
 LOCUS
 DEFINITION CNS00KCV 3 bp DNA linear GSS 03-JUN-1999
 Drosophila melanogaster genome survey sequence TET3 end of BAC:
 BACR17D19 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL077515
 VERSION AL077515.1 GI:4956992
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 3)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osogawa and
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw^{sp}, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1..3
/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone_lib="RPC1-98"

/clone="BACR17D19"

/note="end : TET3"

BASE COUNT 0 a 0 c 3 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 G 1

RESULT 12

BC926576 standard; RNA; EST; 4 BP.

AC BC926576;

SV BC926576.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

DE EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RP 1-4

RP MEDLINE: 21482651.

RX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J., Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries";

RL Osteoarthritic Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay_kumar-1@gsk.com

CC Seq primer: T7.

XX Key

PH Location/Qualifiers

FT 1..4
FT /db_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

FT /organism="Homo sapiens"

FT /clone_lib="HNC (Human Normal Cartilage)"

FT /tissue_type="Cartilage"

FT /lab_host="E.coli DH10 B"

XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

SO

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 4 G 4

RESULT 13

BC926576/c standard; RNA; EST; 4 BP.

AC BC926576;

SV BC926576.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

DE EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RP 1-4

RP MEDLINE: 21482651.

RX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J., Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries";

RL Osteoarthritic Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay_kumar-1@gsk.com

CC Seq primer: T7.

XX Key

PH Location/Qualifiers

FT 1..4
FT /db_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

FT /organism="Homo sapiens"

FT /clone_lib="HNC (Human Normal Cartilage)"

FT /tissue_type="Cartilage"

FT /lab_host="E.coli DH10 B"

FT Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

OY 1 g 1


```

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, Germany; Email: clone@rzpd.de
XX Key Location/Qualifiers
PH source
FT 1..4
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434O245"
FT /clone_11b="434 (synonym: htesj). Vector psport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 4 BP: 0 A; 2 C; 1 G; 1 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 2 g 2

RESULT 17
LOCUS AM672622
DEFINITION 4 bp mRNA linear EST 26-SEP-2001
73c Explanted metanephric mesenchyme induced to differentiate into
epithelial structures of the nephron ex vivo. Rattus norvegicus
CDNA similar to: embjAL049970.1|HSM800317 Homo sapiens
mRNA: cDNA DKFZp564B102 (from clone DKFZp564B102);, mRNA sequence.
AM672622
AM672622.1 GI:7541102
EST.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 4)
Pilsav,S.Y., Ivanov,S.V., Yoshino,K., Dove,L.F., Pilsava,T.M.,
Higginbotham,K.G., Karavanova,I., Lerman,M. and Perantoni,A.O.,
Mesenchymal-epithelial transition in the developing metanephric
kidney: gene expression study by differential display
Genesis 27 (1), 22-31 (2000)
20321327
COMMENT Contact: Pilsav S.Y.
Laboratory of Comparative Carcinogenesis
National Cancer Institute
FCRDC, Bldg 538, Room 205, Frederick, MD 21702, USA
Tel: 301 846 1242
Fax: 301 846 4956
Email: pilsav@mail.ncifcrf.gov
PCR Primers
FORWARD: ctgagctccgcgc
BACKWARD: ttaagcttttttttg
Insert length: 262 Std Error: 0.00
Seq primer: SP6
High quality sequence stop: 262
POLY-A=yes.

FEATURES
source
1..4
Location/Qualifiers
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone_11b="Explanted metanephric mesenchyme induced to
differentiate into epithelial structures of the nephron ex
vivo."
/tissue_type="Metanephric mesenchyme"
/cell_type="Mesenchymal/Epithelial"
/dev_stage="13 dpc-16dpc"
/lab_host="JMI09"

```

```

/note="Organ: kidney; Vector: pGEM-Teasy (Promega).;
Restriction Enzymes: I, ApaI, AatII, SphI, NcoI, BstXI,
NotI, SacII, and EcoRI SpeI, EcoRI, NcoI, BstXI, PstI,
SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment
PCR-amplified in mRNA differential display analysis;
cloned in pGEM-Teasy (Promega); Its expression is
developmentally regulated during mesenchymal-epithelial
conversion in the metanephric kidney."

BASP COUNT
ORIGIN 1 a 0 c 3 g 0 t

```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 9; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 g 1
Db 1 g 1

```

```

RESULT 18
LOCUS CNS004RB/c
DEFINITION 4 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL054121
AL054121.1 GI:4931932
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 4)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL

```

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COMMENT

```

```

FEATURES
source
1..4
Location/Qualifiers
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_11b="RPCI-98"
/clone="BACR10A06"
/note="end : TET3"

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```

BASP COUNT
ORIGIN 1 a 1 c 0 g 2 t

```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 12; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 g 1

```

Db 4 C 4

RESULT 19
HSM007310

ID HSM007310 standard; RNA; EST: 5 BP.

XX AC AL042460:

XX SV AL042460.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434E1821_r1 (from clone DKFZp434E1821)

XX EST: expressed sequence tag.

XX OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX BL Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

XX MI Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPs, Am Klopferplatz 18a D-82152 Martinsried, GERMANY

XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA

XX sequencing consortium of the German Genome Project

XX No st sequence available

XX This clone is available at the RZPD in Berlin

XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX FT Key Location/Qualifiers

XX FT source 1.5

XX FT /db_xref="taxon:9606"

XX FT /organism="Homo sapiens"

XX FT /clone_id="DKFZp434E1821"

XX FT /clone_lib="434 (synonym: hies3). Vector pSport1; host

XX FT DH10B; sites NotI + SalI"

XX FT /dev_stage="adult"

XX FT /rsize_type="testis"

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

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XX

Sequence 5 BP; 2 A; 1 C; 0 G; 0 T; 2 other;

Query Match 100.0%; Score 1; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1

DB 5 G 5

RESULT 21
HSM011053

ID HSM011053 standard; RNA; EST: 5 BP.

XX AC AL046203:

XX SV AL046203.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434D137_r1 (from clone DKFZp434D137)

XX EST: expressed sequence tag.

XX OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX

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XX

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX
 FH Key Location/Qualifiers
 FT source 1..5
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434D137"
 FT /clone_lib="434 (synonym: hies3). Vector pSPORT1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 Db 1 G 1

RESULT 22
 BG927410/C
 ID HG927410 standard; RNA; EST: 6 BP.
 XX
 AC HG927410;
 XX
 SV HG927410.1
 XX
 DT 09-JUN-2001 (Rel. 68, Created)
 DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)
 XX
 IX HNC1-1-G7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
 XX
 KW EST.
 XX
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Heteria; Primates; Catarrhini; Homindae; Homo.
 XX
 [1]
 RP 1-6
 RX MEDLINE; 21482651.
 RX PUBMED; 11597177.
 RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
 RA Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
 RT "Identification and initial characterization of 5000 expressed sequenced
 RT tags (ESTs) each from adult human normal and osteoarthritis cartilage cDNA
 RT libraries";
 RT Osteoarthritis Cartilage 9(7):641-653(2001).
 XL
 XX
 CC Contact: Sanjay Kumar
 CC UW2109
 CC GlaxoSmithKline
 CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 CC Tel: 610-270-7245
 CC Fax: 610-270-5598
 CC Email: sanjay_kumar-1@sk.com
 CC Seq primer: T7.
 CC
 XX Key Location/Qualifiers
 FH
 FH source 1..6
 FT /db_xref="taxon:9606"
 FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 FT Directional"
 FT /organism="Homo sapiens"
 FT /clone_lib="HNC (Human Normal Cartilage)"
 FT /tissue_type="cartilage"

FT /lab_host="E.coli DH10 B"
 XX
 SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 Db 6 G 6

RESULT 23
 HSM003844
 ID HSM003844 standard; RNA; EST: 6 BP.
 XX
 AC AL039368;
 XX
 SV AL039368.1

DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
 XX
 KW EST; expressed sequence tag.

XX
 XX Homo sapiens (human)
 OS
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homindae; Homo.

XX
 RN [1]
 RP 1-6
 RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Kiofeperspit 18a D-82152 Martinsried, GERMANY
 XX

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No sl sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 CC
 XX

FH Key Location/Qualifiers

FH source 1..6
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434I0110"
 FT /clone_lib="434 (synonym: hies3). Vector pSPORT1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 FT
 XX

SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 Db 1 G 1

RESULT 24
 HSM004423
 ID HSM004423 standard; RNA; EST: 6 BP.


```

RP 1-6 Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MFS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No S1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434Gf0321"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;
+
Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
+
QY 1 G 1
+
Db 1 G 1
+
RESULT 26
HSM007683/G standard; RNA; EST; 6 BP.
ID HSM007683
XX
AC AL042833;
XX
SV AL042833.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX
DE EST: expressed sequence tag.
XX
KM Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
XX 1-6
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MFS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No S1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source
FT 1..6
FT /db_xref="taxon:9606"

```

```

FT      /organism="Homo sapiens"
FT      /clone_id="DKFZp434G1622"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites Ncli + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SU      Sequence 6 BP: 2 A; 2 C; 0 G; 2 T; 0 other;

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```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
DB      6 G 6

```

```

RESULT 27
HSM008014/C
ID      HSM008014 standard; RNA; EST; 6 BP.
XX
AC      AL043164;
XX
SV      AL043164.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434F1123_s1 (from clone DKFZp434F1123)
XX
KM      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN      [1]
RP      1-6
KA      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
KT      Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
KL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      r1 sequence also available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key      Location/Qualifiers
FH      source      1..6
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434F1123"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites Ncli + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 6 BP: 1 A; 2 C; 0 G; 3 T; 0 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
DB      5 G 5

```

```

RESULT 28
HSM010918
ID      HSM010918 standard; RNA; EST; 6 BP.
XX
AC      AL046068;
XX
SV      AL046068.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434F1672_r1 (from clone DKFZp434F1672)
XX
KM      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN      [1]
RP      1-6
RA      Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by DKFZ within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key      Location/Qualifiers
FH      source      1..6
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434F1672"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites Ncli + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 6 BP: 0 A; 2 C; 2 G; 0 T; 2 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
DB      1 G 1

```

```

RESULT 29
HSM010918/C
ID      HSM010918 standard; RNA; EST; 6 BP.
XX
AC      AL046068;
XX
SV      AL046068.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434F1672_r1 (from clone DKFZp434F1672)
XX
KM      EST; expressed sequence tag.
XX

```

File	Location/Qualifiers
FT	source
FT	1..6
FT	/db_xref="taxon:9606"
FT	/organism="Homo sapiens"
FT	/clone="DKFZp434F172"
FT	/clone_11b="434 (synonym: hhes3). Vector pSport1; host
FT	DH10B; sites NotI + SalI"
FT	/dev_stage="adult"
FT	/tissue_type="testis"
FT	
XX	
SO	Sequence 6 BP; 0 A; 2 C; 2 G; 0 T; 2 other;

Query Match	100.0%	Score 1:	DB 2:	Length 6:	
Best local	100.0%	Pred. No. 0:			
Matches	1:	Conservative	0:	Mismatches	0:
QY	1 q 1				
Db	5 G 5				
RESULT 30					
BE726686					
LOCUS	BE726686	6 bp	mRNA	linear	EST 14-SEP-2000
DEFINITION	894095D11.y1 C. reinhardtii CC-1690, normalized, Lambda zap II				
ACCESSION	Chlamydomonas reinhardtii cDNA, mRNA sequence.				
VERSION	BE726686				
KEYWORDS	BE726686.1 GI:10128110				
SOURCE	EST.				
ORGANISM	Chlamydomonas reinhardtii.				
REFERENCE	Chlamydomonas reinhardtii				
AUTHORS	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;				
	Chlamydomonadaceae; Chlamydomonas.				
	1 (bases 1 to 6)				
TITLE	Grossman, A., Daviles, J., Federspiel, N., Harris, E., Lefebvre, P.,				
	McGermolt, J.P., Silflow, C., Stern, D. and Surzycki, R.				
JOURNAL	Analyses of the Chlamydomonas reinhardtii Genome: A Model,				
COMMENT	Unicellular System for Analyzing Gene Function and Regulation in				
	Vascular Plants: Project phase 2				
	Unpublished (2000)				
	Contact: Charles Hauser				

```
FEATURES
SOURCE
    Location/Qualifiers
    1..6
    /organism="Chlamydomonas reinhardtii"
    /strain="CC-1690 wild type mt+ 21gr"
    /db_xref="taxon:3055"
    /clone_11b="C. reinhardtii CC-1690, normalized, lambda Zap
```

Query Match	100.0%	Score 1	DB 10	Length 6
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1 g 1			
Db	1 G 1			
RESULT 31				
BE726686/c				
LOCUS	BE726686	6 bp	mRNA	linear
DEFINITION	894095D11.y1 C. reinhardtii CC-1690, normalized, Lambda zap II		EST 14-SEP-2000	
ACCESSION	Chlamydomonas reinhardtii cDNA, mRNA sequence.			
	BE726686			

SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE Eukaryota: Viridiplantae; Chlorophyta: Chlorophyceae; Volvocales;
AUTHORS Chlamydomonadaceae; Chlamydomonas.
TITLE 1 (bases 1 to 6)
JOURNAL Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
COMMENT McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.
DCMB Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES Location/Qualifiers
1..6

/db.xref="taxon:30555"
/clone.lib="C. reinhardtii CC-1690, normalized, Lambda zap
II."
/note="Vector: pBluescript II SK⁺, Site 1: EcoRI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO₂ and HS medium bubbled with 5% CO₂.
pOLYA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK⁺ plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT 0 a 1 c 5 g 0 t
 ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 1
 Db 2 G 2

RESULT 32

BC897546

ID BC897546 standard; RNA; EST; 7 BP.

XX BC897546;

XX BC897546.1

SV BC897546.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens CDNA, mRNA

DE sequence.

XX EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RP 1-7

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,

RT Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced

XX tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA

XX libraries";

XX Osteoarthritic Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

XX UW2109

XX GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay_kumar-1@gsk.com

CC Seq primer: T7.

XX Key

XX Location/Qualifiers

XX source

XX 1..7

XX /db_xref="taxon:9606"

XX /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

XX Directional"

XX /organism="Homo sapiens"

XX /clone_lib="HOA (Human Osteoarthritic Cartilage)"

XX /tissue_type="cartilage"

XX /lab_host="E.coli DH10 B"

XX SO Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

OY 1 g 1

1

Query Match 100.0%; Score 1; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

1

Db 6 G 6

RESULT 33

BC897546/C

ID BC897546 standard; RNA; EST; 7 BP.

XX BC897546;

XX BC897546.1

SV BC897546.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens CDNA, mRNA

DE sequence.

XX EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RP 1-7

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,

RT Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced

XX tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA

XX libraries";

XX Osteoarthritic Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

XX UW2109

XX GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay_kumar-1@gsk.com

CC Seq primer: T7.

XX Key

XX Location/Qualifiers

XX source

XX 1..7

XX /db_xref="taxon:9606"

XX /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

XX Directional"

XX /organism="Homo sapiens"

XX /clone_lib="HOA (Human Osteoarthritic Cartilage)"

XX /tissue_type="cartilage"

XX /lab_host="E.coli DH10 B"

XX SO Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

OY 1 g 1

1

Query Match 100.0%; Score 1; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

1

RESULT 34

HS0007412

ID HSM007412 standard; RNA; EST; 7 BP.

XX AL042562;

XX AL042562.1

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XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
DE Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
XX EST: expressed sequence tag.
KM Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
RN Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RP 1-7
KA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RT MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No. 51 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH
FH source
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:
SQ

```

```

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No. 51 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH
FH source
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:
SQ

```

```

Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 9 1
Db 2 G 2

```

```

RESULT 35
HSM007412/c
ID HSM007412 standard; RNA; EST: 7 BP.
XX
XX AL042562;
XX
XX AL042562.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
DE Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
XX
XX EST: expressed sequence tag.
KM Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
RN Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RP 1-7
KA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RT MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No. 51 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH
FH source
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:
SQ

```

FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 Db 2 G 2

RESULT 37
 HSM007502/c
 ID HSM007502 standard; RNA; EST; 7 BP.
 AC AL042652;
 XX AL042652.1
 SV
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA: EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
 XX
 KW EST; expressed sequence tag.
 XX
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
 XX
 RN [1]
 RP 1-7
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by LMU within the CDNA
 CC sequencing consortium of the German Genome Project
 CC No st sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX
 FH Key Location/Qualifiers
 FT source 1..7
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone_lib="DKFZp434N1921"
 FT DH10B; sites NOTI + SalI
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 Db 1 G 1

RESULT 38
 C58888

LOCUS C58888 7 bp mRNA linear EST 22-SEP-1997
 DEFINITION C58888 Yujii Kohara unpublished cDNA Caenorhabditis elegans cDNA
 clone yk383a7 3', mRNA sequence.
 ACCESSION C58888
 VERSION C58888.1 GI:2417593
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae
 ; Rhabditidae; Peleoderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 7)
 Kohara,Y., Mochizuki,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
 ,M., Miyata,A. and Nishigaki,A.
 Expression map of the C.elegans genome
 Unpublished (1996)
 COMMENT Contact: Yujii Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.
 FEATURES
 source Location/Qualifiers
 1..7
 /organism="Caenorhabditis elegans"
 /strain="CBI489 him-8(e1489)"
 /db_xref="taxon:6239"
 /clone="yk383a7"
 /clone_lib="Yujii Kohara unpublished cDNA"
 /sex="hermaphrodite, male"
 /tissue_type="whole animal"
 /dev_stage="varied"

BASE COUNT 2 a 1 g 3 t 1 others
 ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 Db 7 G 7

RESULT 39
 HSM001420/c
 ID HSM001420 standard; RNA; EST; 8 BP.
 AC AL037095;
 XX AL037095.1
 SV
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA: EST DKFZp564L2064_r1 (from clone DKFZp564L2064)
 XX
 KW EST; expressed sequence tag.
 XX
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
 XX
 RN [1]
 RP 1-8
 RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA
 CC sequencing consortium of the German Genome Project

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CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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FH Key Location/Qualifiers
FH
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FT 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp564L2064"
FT /clone_lib="564 (synonym: hibr2). Vector pAMP1: host
FT x1-2blue: sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 9 1
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Db 7 G 7

RESULT 40
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ID HSM001741 standard; RNA; EST; 8 BP.
XX
AC AL037413;
XX
SV AL037413.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp564L0771_s1 (from clone DKFZp564L0771)
XX
KW EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX
RN 11
RN 1-8
RP Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by GBF within the CDNA
CC sequencing consortium of the German Genome Project
CC No r1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
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FT source
FT 1..8
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FT x1-2blue: sites NotI + SalI"
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SQ Sequence 8 BP; 1 A; 7 C; 0 G; 0 T; 0 other;
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Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 9 1
   |
Db 7 G 7

RESULT 41
HSM004451
ID HSM004451 standard; RNA; EST; 8 BP.
XX
AC AL039975;
XX
SV AL039975.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
XX
KW EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX
RN 11
RN 1-8
RP Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 9 1
   |
Db 1 G 1

RESULT 42
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XX
AC AL039975;
XX
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SV      AL039975.1
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DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
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XX
XX      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      1-8
XX      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by Olagen within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No s1 sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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XX      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      1 g 1
DB      8 C 8

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RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No s1 sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
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XX                  /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX                  DH10B; sites NotI + SalI"
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XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      1 g 1
DB      1 C 1

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RESULT 44
HSM007277/c standard; RNA: EST; 8 BP.
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AC      AL042427;
XX
SV      AL042427.1
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XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
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DE      Homo sapiens mRNA: EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX
XX      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No s1 sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
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XX
OY      1 g 1
DB      1 C 1

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 Job time: 14494 sec

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SO Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1
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 DB 8 G 8

RESULT 45

HSM007323
 ID HSM007323 standard; RNA; EST; 8 BP.

AC AL042473;
 XX

SV AL042473.1
 XX

DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434F0121_r1 (from clone DKFZp434F0121)
 XX

EST; expressed sequence tag.

OS Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 XX

RN [1]
 RP 1-8

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
 RT ;

RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the CDNA
 CC sequencing consortium of the German Genome Project

CC No 81 sequence available at the RZPD in Berlin
 CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

Key Location/Qualifiers

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 FT DH10B; sites NotI + SalI"

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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1
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DB 1 G 1

Tue Jul 16 09:39:30 2002

us-09-375-248-1_copy_3164_3164.oli.rst

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
DB 2 c 2

RESULT 2
AX092442 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092442/c
DEFINITION Sequence 3 from Patent WO0116366.
ACCESSION AX092442
VERSION AX092442.1 GI:13444537
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 1 g 0 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
DB 2 c 2

RESULT 3
AX092444 2 bp DNA linear PAT 23-MAR-2001
LOCUS AX092444
DEFINITION Sequence 5 from Patent WO0116366.
ACCESSION AX092444
VERSION AX092444.1 GI:13444539
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
DB 1 c 1

RESULT 4
AX092445 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092445
DEFINITION Sequence 6 from Patent WO0116366.
ACCESSION AX092445
VERSION AX092445.1 GI:13444540
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source Location/Qualifiers
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/note="synthetic oligonucleotide;"

BASE COUNT 0 a 2 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
DB 1 c 1

RESULT 5
AX092446 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092446
DEFINITION Sequence 7 from Patent WO0116366.
ACCESSION AX092446
VERSION AX092446.1 GI:13444541
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 1 c 1

RESULT 6
AX092446/c 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092446
DEFINITION Sequence 7 from Patent WO0116366.
ACCESSION AX092446
VERSION AX092446.1 GI:13444541
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 7 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)
FEATURES
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/note="synthetic oligonucleotide;"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
1
Db 2 c 2

RESULT 7
AX092447 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092447
DEFINITION Sequence 8 from Patent WO0116366.
ACCESSION AX092447
VERSION AX092447.1 GI:13444542
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 8 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 1 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
1

Db 1 c 1

RESULT 8
AX092448/c 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092448
DEFINITION Sequence 9 from Patent WO0116366.
ACCESSION AX092448
VERSION AX092448.1 GI:13444543
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 9 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
1
Db 1 c 1

RESULT 9
AX092449 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092449
DEFINITION Sequence 10 from Patent WO0116366.
ACCESSION AX092449
VERSION AX092449.1 GI:13444544
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 10 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)
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Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
1
Db 2 c 2

RESULT 10
AX092449/c
LOCUS AX092449 2 bp DNA PAT 21-MAR-2001
DEFINITION Sequence 10 from Patent WO0116366.
ACCESSION AX092449
VERSION AX092449.1 GI:13444544
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 10 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 1 c 1

RESULT 11
AX092450/c
LOCUS AX092450 2 bp DNA PAT 21-MAR-2001
DEFINITION Sequence 11 from Patent WO0116366.
ACCESSION AX092450
VERSION AX092450.1 GI:13444545
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 11 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 2 c 2

RESULT 12
AX092451/c
LOCUS AX092451 2 bp DNA PAT 21-MAR-2001

DEFINITION Sequence 12 from Patent WO0116366.
ACCESSION AX092451
VERSION AX092451.1 GI:13444546
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 12 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
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/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 0 c 1 g 1 t
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Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 1 c 1

RESULT 13
AX092453
LOCUS AX092453 2 bp DNA PAT 21-MAR-2001
DEFINITION Sequence 14 from Patent WO0116366.
ACCESSION AX092453
VERSION AX092453.1 GI:13444548
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
unclassified.
1 (bases 1 to 2)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 14 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
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/db_xref="taxon:32644"
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BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 2 c 2

RESULT 14
AX092454/c
LOCUS AX092454 2 bp DNA PAT 21-MAR-2001
DEFINITION Sequence 15 from Patent WO0116366.
ACCESSION AX092454
VERSION AX092454.1 GI:13444549

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 15 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN 0 a 0 c 1 g 1 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 2 c 2

RESULT 15
AX092528
LOCUS AX092528 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 89 from Patent WO0116366.
ACCESSION AX092528
VERSION AX092528.1 GI:13444623
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 89 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN 1 a 1 c 0 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 1 c 1

RESULT 16
AX092529
LOCUS AX092529 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 90 from Patent WO0116366.
ACCESSION AX092529
VERSION AX092529.1 GI:13444624
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE unclassified.
AUTHORS 1 (bases 1 to 2)
TITLE Kless, H.
JOURNAL Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 90 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN 0 a 2 c 0 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 2 c 2

RESULT 17
AX092530/c
LOCUS AX092530 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 91 from Patent WO0116366.
ACCESSION AX092530
VERSION AX092530.1 GI:13444625
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 91 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN 1 a 0 c 1 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 2 c 2

RESULT 18
AX092538/c
LOCUS AX092538 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 99 from Patent WO0116366.
ACCESSION AX092538
VERSION AX092538.1 GI:13444633
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 016366-A 99-08-MAR-2001;
VPDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..2 /organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN /note="synthetic oligonucleotide:"

Query Match 100.0%; Score 1; DB 6; Length 2;
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1
Db 1 c 1

RESULT 19
LOCUS AX175286 2 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 50 from Patent WO0144465.
ACCESSION AX175286
VERSION AX175286.1 GI:14598654
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2)
AUTHORS Phillips,N.C. and Fillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 50 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
source Location/Qualifiers
1..2 /organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1
Db 1 c 1

RESULT 20
LOCUS AX175287 2 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 51 from Patent WO0144465.
ACCESSION AX175287
VERSION AX175287.1 GI:14598655
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 2)
AUTHORS Phillips,N.C. and Fillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 51 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
source Location/Qualifiers
1..2 /organism="synthetic construct"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN /db_xref="taxon:32630"

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1
Db 2 c 2

RESULT 21
LOCUS BD009609 2 bp DNA linear PAT 31-JAN-2002
DEFINITION Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples.
ACCESSION BD009609
VERSION BD009609.1 GI:18637982
KEYWORDS JP 2001502536-A/201.
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 2)
AUTHORS Quint,W. and Doorn,L.J.V.
TITLE Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples
JOURNAL Patent: JP 2001502536-A 201 27-FEB-2001;
INNOGENETICS NV,DDL BV
OS Unidentified
PN JP 2001502536-A/201
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN
PC C12Q1/68,C07K14/205,C12N15/11
CC
FH Key
FT source Location/Qualifiers

FEATURES
source Location/Qualifiers
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/db_xref="taxon:32644"

BASE COUNT 0 a 0 c 1 g 0 t 1 others
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Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1
Db 2 c 2

RESULT 22
LOCUS CNS01C99/c 2 bp mRNA linear PLN 02-SEP-1999
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ACCESSION AL15237
VERSION AL15237.1 GI:5829856
KEYWORDS cDNA library; nitrogen deprivation.
SOURCE Botryotinia fuckelliana.
ORGANISM Botryotinia fuckelliana.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

REFERENCE 1 (bases 1 to 2)
AUTHORS Bliton,F., Levis,C., Fortini,D., Pradler,J.M. and Brygoo,Y.


```

TITLE      Direct Submission
JOURNAL    Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
REFERENCE  78026 Versailles, France
AUTHORS    2 (bases 1 to 2)
JOURNAL    Genoscope.
TITLE      Direct Submission
JOURNAL    Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
REFERENCE  Cp 5706 91057 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
AUTHORS    - Web : www.genoscope.cns.fr)
JOURNAL    The cDNA library to be analyzed within the framework of this
COMMENT     project was created using a Botrytis cinerea strain which was grown
            under conditions of nitrogen deprivation, which is the normal
            situation for B. cinerea during its development on its host plant.
            The library was produced in an oriented direction, in the pBSII
            vector.

FEATURES
SOURCE      location/Qualifiers
            1..2
            /organism="Botryocinia fuckelliana"
            /strain="T4"
            /db_xref="taxon:40559"
            /note="Genoscope sequence ID : M04F091"

BASE COUNT  0 a 0 c 1 g 1 t

ORIGIN
Query Match      100.0%; Score 1; DB 8; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 1 c 1

RESULT 23
AC079635/c 3 bp DNA linear HTG 14-AUG-2001
LOCUS      AC079635
DEFINITION Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC079635
VERSION    AC079635.3 GI:14647267
KEYWORDS   HTG: HTGS_PHASE0.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 3)
REFERENCE  1 McCombie, W.R., Baker, J.P., Bahret, A., Yang, C., Balija, V.,
            Dedbia, N.N., de la Bastide, M., Kuit, K., King, L., Kirchoff, K.A.,
            Miller, B., Mascimendo, L.U., O'Shaughnessy, A.L., Preston, R.R.,
            Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Palmer, L.,
            Vil, M.D. and Zutavern, T.
            Mouse Genomic Sequence
            Unpublished
            2 (bases 1 to 3)
REFERENCE  2 McCombie, W.R.
            Direct Submission
            Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing
            Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
            Harbor, NY 11724, USA
            On Jul 10, 2001 this sequence version replaced gi:14595773.
            * NOTE: This record contains 1 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            1
            3: contig of 3 bp in length.
            This entry has been temporarily removed. An update for RP23-152L20

FEATURES
SOURCE      will be submitted as soon as it becomes available.
            Location/Qualifiers
            1..3
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /clone="RP23-152L20"

BASE COUNT  1 a 0 c 1 g 1 t

ORIGIN
Query Match      100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 1 c 1

RESULT 24
CHKNCAMC5/c 3 bp DNA linear VRT 17-JUL-2000
LOCUS      CHKNCAMC5
DEFINITION Chicken cardiac neural cell adhesion (NCAM) gene, exon 12D.
ACCESSION  M23994 J04140
VERSION    M23994.1 GI:212442
KEYWORDS   SEGMENT
            5 of 6
            SOURCE
            chicken.
            Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 3)
REFERENCE  1 Prediger, E.A., Hoffman, S., Edelman, G.M. and Cunningham, B.A.
            Four exons encode a 93-base-pair insert in three neural cell
            adhesion molecule mRNAs specific for chicken heart and skeletal
            muscle
            Proc. Natl. Acad. Sci. U.S.A. 85 (24), 9616-9620 (1988)
            3200847
            MEDLINE
            JOURNAL
            COMMENT
            FEATURES
            SOURCE
            Exon 12D represents a very small exon.
            Location/Qualifiers
            1..3
            /organism="Gallus gallus"
            /db_xref="taxon:9031"
            /clone="pcc101b"
            /tissue_type="cardiac muscle"
            /dev_stage="day 10 embryo"
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            /gene="NACM"
            /number=12

BASE COUNT  2 a 0 c 1 g 0 t

ORIGIN
Query Match      100.0%; Score 1; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 3 c 3

RESULT 25
A97991 3 bp DNA linear PAT 26-JAN-2000
LOCUS      A97991
DEFINITION Sequence 21 from Patent M09914366.
ACCESSION  A97991
VERSION    A97991.1 GI:6781229
KEYWORDS   SOURCE
            unidentified.
            ORGANISM
            unidentified

```

unclassified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Pongers-Willieme, M.J. and Van, D.J.
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)
FEATURES
source 1..3
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/db_xref="taxon:32644"
BASE COUNT 0 a 1 c 2 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
Db 1 c 1

RESULT 26
LOCUS A97991 3 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 21 from Patent WO9914366.
ACCESSION A97991
VERSION A97991.1 GI:6781229
KEYWORDS
SOURCE
ORGANISM
unclassified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Pongers-Willieme, M.J. and Van, D.J.
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)
FEATURES
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 1 c 2 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
Db 1 c 1

RESULT 27
LOCUS AX092457 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 18 from Patent W00116366.
ACCESSION AX092457
VERSION AX092457.1 GI:13444552
KEYWORDS
SOURCE
ORGANISM
unclassified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 18 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)
FEATURES
source Location/Qualifiers

source 1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
Db 3 c 3

RESULT 28
LOCUS AX092458/c 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 19 from Patent W00116366.
ACCESSION AX092458
VERSION AX092458.1 GI:13444553
KEYWORDS
SOURCE
ORGANISM
unclassified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 19 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 2 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
Db 3 c 3

RESULT 29
LOCUS AX092460 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 21 from Patent W00116366.
ACCESSION AX092460
VERSION AX092460.1 GI:13444555
KEYWORDS
SOURCE
ORGANISM
unclassified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 21 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)
FEATURES
source 1..3
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 2 C 2

RESULT 30
AX092461
LOCUS AX092462/c 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 22 from Patent W00116366.
ACCESSION AX092461
VERSION AX092461.1 GI:13444556
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

unidentified.
unclassified.
1 (bases 1 to 3)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 22 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers

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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 2 C 2

RESULT 31
AX092462
LOCUS AX092462 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 23 from Patent W00116366.
ACCESSION AX092462
VERSION AX092462.1 GI:13444557
KEYWORDS
SOURCE
ORGANISM

unidentified.
unclassified.
1 (bases 1 to 3)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 23 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers

1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 2 C 2

RESULT 32
AX092462
LOCUS AX092462/c 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 23 from Patent W00116366.
ACCESSION AX092462
VERSION AX092462.1 GI:13444557
KEYWORDS
SOURCE
ORGANISM

unidentified.
unclassified.
1 (bases 1 to 3)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 23 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers

1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
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Db 3 C 3

RESULT 33
AX092463
LOCUS AX092463 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 24 from Patent W00116366.
ACCESSION AX092463
VERSION AX092463.1 GI:13444558
KEYWORDS
SOURCE
ORGANISM

unidentified.
unclassified.
1 (bases 1 to 3)
Kless, H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 24 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers

1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 2 C 2

RESULT 34
AX092464/C
LOCUS AX092464 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 25 from Patent WO0116366.
ACCESSION AX092464
VERSION AX092464.1 GI:13444559
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 3)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 25 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
ORIGIN
2 a 0 c 1 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 2 C 2

RESULT 35
AX092465
LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 3)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 26 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
ORIGIN
1 a 1 c 1 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 3 C 3

RESULT 36
AX092465/C
LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 3)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 26 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
ORIGIN
1 a 1 c 1 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 2 C 2

RESULT 37
AX092466
LOCUS AX092466 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 27 from Patent WO0116366.
ACCESSION AX092466
VERSION AX092466.1 GI:13444561
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 3)
Kless, H.
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 27 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
ORIGIN
1 a 0 c 2 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 3 C 3

RESULT 38
AX092467/c
LOCUS AX092467 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 28 from Patent WO0116366.
ACCESSION AX092467
VERSION AX092467.1 GI:13444562
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 39
AX092469
LOCUS AX092469 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 30 from Patent WO0116366.
ACCESSION AX092469
VERSION AX092469.1 GI:13444564
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 40

AX092470/c
LOCUS AX092470 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 31 from Patent WO0116366.
ACCESSION AX092470
VERSION AX092470.1 GI:13444565
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 41
AX092472
LOCUS AX092472 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 33 from Patent WO0116366.
ACCESSION AX092472
VERSION AX092472.1 GI:13444567
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 42
AX092473
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 34 from Patent WO0116366.

ACCESSION AX092473
VERSION AX092473.1 GI:13444568
KEYWORDS

SOURCE

unidentified.

ORGANISM

unclassified.
1 (bases 1 to 3)

REFERENCE

Kless, H.

AUTHORS

Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks

TITLE

Patent: WO 0116366-A 34 08-MAR-2001;

JOURNAL

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES

Location/Qualifiers

1..3

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT 1 a 2 c 0 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 1 c 1

RESULT 43

LOCUS

AX092474 3 bp DNA

DEFINITION

Sequence 35 from Patent WO0116366. linear PAT 21-MAR-2001

ACCESSION

AX092474

VERSION

AX092474.1 GI:13444569

KEYWORDS

unidentified.

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 3)

AUTHORS

Kless, H.

TITLE

Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks

JOURNAL

Patent: WO 0116366-A 35 03-MAR-2001;

FEATURES

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

SOURCE

Location/Qualifiers

1..3

/organism="unidentified"

/db_xref="taxon:32644"

/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 1 c 1

RESULT 44
AX092474/c
LOCUS AX092474
DEFINITION Sequence 35 from Patent WO0116366. 3 bp DNA linear PAT 21-MAR-2001
ACCESSION AX092474
VERSION AX092474.1 GI:13444569
KEYWORDS

SOURCE unidentified.

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 3)

AUTHORS

Kless, H.

TITLE

Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks

JOURNAL

Patent: WO 0116366-A 35 08-MAR-2001;

FEATURES

Location/Qualifiers

1..3

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT 1 a 1 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 3 c 3

RESULT 45

LOCUS

AX092475 3 bp DNA

DEFINITION

Sequence 36 from Patent WO0116366. linear PAT 21-MAR-2001

ACCESSION

AX092475

VERSION

AX092475.1 GI:13444570

KEYWORDS

unidentified.

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 3)

AUTHORS

Kless, H.

TITLE

Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks

JOURNAL

Patent: WO 0116366-A 36 08-MAR-2001;

FEATURES

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

SOURCE

Location/Qualifiers

1..3

/organism="unidentified"

/db_xref="taxon:32644"

/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 1 c 1

Search completed: July 15, 2002, 23:28:08
Job time: 24541 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:10:10 ; Search time 932.4 Seconds

(without alignments)
1.841 Million cell updates/sec

Title: US-09-375-248-1_COPY_3360_3360

Perfect score: 1 c 1

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	3	17	AAT33326	CAPL trinucleotide
2	100.0	3	17	AAT33326	CAPL trinucleotide
3	100.0	3	17	AAAG4655	Human TUB gene pro
4	100.0	3	22	AA120244	Human breast cance
5	100.0	4	16	AAO81664	bGCF binding oligo
6	100.0	4	16	AAO81664	bGCF binding oligo
7	100.0	4	16	AAO81665	bGCF binding oligo
8	100.0	4	16	AAO81665	bGCF binding oligo
9	100.0	4	18	AAT86385	Probe for target n

C	10	1	100.0	4	18	AAT86385	Probe for target n
C	11	1	100.0	4	18	AAT77252	Immunostimulatory
C	12	1	100.0	4	18	AAT77252	Immunostimulatory
C	13	1	100.0	4	22	AA117191	Human breast cance
C	14	1	100.0	4	22	AA117191	Human breast cance
C	15	1	100.0	4	22	AA124357	Human breast cance
C	16	1	100.0	4	22	AA61450	Cyclin binding ham
C	17	1	100.0	5	10	AAO93676	Synthetic probe to
C	18	1	100.0	5	15	AAO68752	CHA255 heavy chain
C	19	1	100.0	5	16	AAO81667	bGCF binding oligo
C	20	1	100.0	5	17	AA12043	Cleavable replicab
C	21	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
C	22	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
C	23	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
C	24	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
C	25	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	26	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	27	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	28	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	29	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	30	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	31	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	32	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	33	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	34	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	35	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	36	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	37	1	100.0	5	20	AAV61663	Fusarium sp. 18S r
C	38	1	100.0	5	21	AAV61663	Fusarium sp. 18S r
C	39	1	100.0	5	21	AAV61663	Fusarium sp. 18S r
C	40	1	100.0	5	21	AAV61663	Fusarium sp. 18S r
C	41	1	100.0	5	21	AAV61663	Fusarium sp. 18S r
C	42	1	100.0	5	21	AAV61663	Fusarium sp. 18S r
C	43	1	100.0	5	21	AAV61663	Fusarium sp. 18S r
C	44	1	100.0	5	21	AAV61663	Fusarium sp. 18S r
C	45	1	100.0	5	21	AAV61663	Fusarium sp. 18S r

ALIGNMENTS

```
RESULT 1
ID AAT33326 standard; RNA; 3 BP.
XX AAT33326;
XX
XX 12-NOV-1996 (first entry)
XX
XX CAPL trinucleotide.
DE
XX
XX CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
XX osteosarcoma; therapy; ss.
XX
XX Synthetic.
XX
XX MO9625499-A1.
XX
XX 22-AUG-1996.
XX
XX 16-FEB-1996; 96WO-US02108.
XX
XX 17-FEB-1995; 95US-0391375.
XX
XX (HYBR-) HYBRIDON INC.
XX (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
XX Von Hofe E;
XX WPI: 1996-393400/39.
XX
XX Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
PT
```


PT useful to inhibit metastatic cancer, partic. osteosarcoma
 XX
 PS Claim 2: Page 56; 70pp; English.
 XX
 CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5',
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.
 XX
 SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 OY 1 c 1
 DB 1 c 1

RESULT 2
 AAT33326/c
 ID AAT33326 standard; RNA; 3 BP.
 XX
 AC AAT33326:
 XX
 DT 12-NOV-1996 (first entry)
 XX
 DE CAPL trinucleotide.
 XX
 KW CAPL: antisense oligonucleotide; ribozyme; cancer; metastasis;
 KM osteosarcoma; therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO9625499-A1.
 XX
 PD 22-AUG-1996.
 XX
 PF 16-FEB-1996; 96WO-US02108.
 XX
 PR 17-FEB-1995; 95US-0391375.
 XX
 PA (HYBR-) HYBRIDON INC.
 XX
 PA (NORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.
 XX
 PI Agrawal S, Engebraten O, Fodstad O, Hovig E, Maeldandsmo GJ;
 PI Von Hofe E;
 XX
 DR WPI: 1996-393400/39.
 XX
 PT Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
 PT useful to inhibit metastatic cancer, partic. osteosarcoma
 XX
 PS Claim 2: Page 56; 70pp; English.
 XX
 CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5',
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.
 XX
 SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 OY 1 c 1
 DB 3 C 3

RESULT 3
 AAA94655/c
 ID AAA94655 standard; DNA; 3 BP.
 XX
 AC AAA94655:
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Human TUB gene probe #2.
 XX
 KM Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;
 KM TUB; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6114502-A.
 XX
 PD 05-SEP-2000.
 XX
 PF 27-FEB-1998; 98US-0032365.
 XX
 PR 22-AUG-1996; 96US-0701380.
 PR 04-SEP-1996; 96US-0706282.
 PR 10-APR-1996; 96US-0630592.
 PR 17-SEP-1996; 96US-0714991.
 PR 30-APR-1997; 97US-0850218.
 PR 01-AUG-1997; 97US-0904699.
 PR 17-SEP-1997; 97US-0932306.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI North M, Nishina P, Noben-Trauth K, Naggett J;
 XX
 DR WPI: 2000-586483/55.
 XX
 PT Mammalian proteins expressed in retina and brain, useful for producing
 PT antibodies and for diagnosing neurosensory defects including cochlear
 PT degeneration, peripheral retinal degeneration and cone-rod retinal
 PT dystrophy -
 XX
 PS Disclosure; Columns 81-82; 61pp; English.
 XX
 CC The present invention relates to human and murine cDNAs from a
 CC neurosensory defect associated gene family. The novel cDNAs are mouse
 CC tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB
 CC form 6 (see AAA94632), human TUB form I (see AAA94630), human TUB
 CC AAA94633), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
 CC immunogens to raise antibodies that specifically identify TUB/TULP
 CC expressing cells and in drug screening assays directed at neurosensory
 CC defects. The novel proteins encoded by the present sequence can be used
 CC for the treatment of neurosensory degenerative conditions e.g. retinal
 CC dystrophies. The present sequence is a probe used to isolate the novel
 CC genes of the present invention.
 XX
 SO Sequence 3 BP: 0 A; 0 C; 3 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 c 1
 DB 3 C 3

RESULT 4
AAL20244
ID AAL20244 standard; cDNA: 3 BP.
XX
AC AAL20244:
XX
XX 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 12701.
XX
XX Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001: 2001WO-US00798.
XX
PR 14-JAN-2000: 2000US-0176077.
PR 14-MAR-2000: 2000US-0189167.
PR 24-MAR-2000: 2000US-0192099.
PR 29-MAR-2000: 2000US-0193480.
PR 15-MAY-2000: 2000US-0205230.
PR 09-JUN-2000: 2000US-0211315.
PR 25-JUL-2000: 2000US-0220534.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI: 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS Claim 1: Page 2245; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising, treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
DB 2 c 2

XX inhibition; enhance; neovascularisation; solid tumour; cancer;
KM metastasis; diagnosis; gene therapy; ss.
XX
XX Synthetic.
XX
XX WO9500528-A.
XX
XX 05-JAN-1995.
XX
XX 17-JUN-1994: 94WO-US06884.
XX
XX 18-JUN-1993: 93US-0079677.
PR 07-JAN-1994: 94US-0179491.
XX
XX (PHAR-) PHARMAGENICS INC.
XX
XX Beutel BA, Joesten ME;
XX
PI WPI: 1995-051992/07.
XX
DR New oligo-nucleotide(s) that bind to basic fibroblast growth
XX factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.
XX
XX Claim 3: Page 25; 44pp; English.
XX
XX The sequences given in AAO81642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AAO81664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.
XX
SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
DB 4 c 4

RESULT 6
AAO81664/c
ID AAO81664 standard; RNA: 4 BP.
XX
AC AAO81664:
XX
XX 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
XX Basic; fibroblast growth factor; bFGF; stem-loop structure;
KM bubble structure; pseudoknot; receptor; heparin; competition;
KM inhibition; enhance; neovascularisation; solid tumour; cancer;
XX metastasis; diagnosis; gene therapy; ss.
XX
XX Synthetic.
XX
XX WO9500528-A.

PD 05-JAN-1995.
 XX
 PF 17-JUN-1994: 94WO-US06884.
 XX
 PR 18-JUN-1993: 93US-0079677.
 PR 07-JAN-1994: 94US-0179491.
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DK WPI: 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 factor - modulating, esp. inhibiting, its activity, useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp; English.
 XX
 CC The sequences given in AA081642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SQ Sequence 4 BP: 0 A: 1 C: 2 G: 1 U: 0 other;

Query Match
 Best Local Similarity 100.0%; Score 1; DB 16; Length 4;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
 |
 Db 3 c 3

RESULT 7
 ID AA081665 standard; RNA: 4 BP.
 AC AA081665;
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #2.
 XX
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;
 KW metastasis; diagnosis; gene therapy; ss.
 OS Synthetic.
 XX
 PN WO9500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994: 94WO-US06884.
 XX
 PR 18-JUN-1993: 93US-0079677.
 PR 07-JAN-1994: 94US-0179491.
 XX

PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI: 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 factor - modulating, esp. inhibiting, its activity, useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp; English.
 XX
 CC The sequences given in AA081642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SQ Sequence 4 BP: 0 A: 2 C: 1 G: 1 U: 0 other;

Query Match
 Best Local Similarity 100.0%; Score 1; DB 16; Length 4;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
 |
 Db 1 c 1

RESULT 8
 ID AA081665/C
 AA081665 standard; RNA: 4 BP.
 AC AA081665;
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #2.
 XX
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;
 KW metastasis; diagnosis; gene therapy; ss.
 OS Synthetic.
 XX
 PN WO9500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994: 94WO-US06884.
 XX
 PR 18-JUN-1993: 93US-0079677.
 PR 07-JAN-1994: 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI: 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth

f factor - modulating, esp. inhibiting, its activity, useful in
f treating cancer, preventing metastasis, and diagnosis.

S Claim 3; Page 25; 44pp: English.

CC The sequences given in AA081642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AA081664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. Particularly, they inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.

CC Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 3 C 3

RESULT 9

AA0816385
ID AA0816385 standard; DNA; 4 BP.

AC AA0816385;

DT 23-APR-1998 (first entry)

DE Probe for target nucleic acid sequence P0.

XX Point mutation detection; nucleic acid sequence analysis; probe;
KW viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /note= "C-5' phosphate"

PN WO9738131-A1.

PD 16-OCT-1997.

PF 11-APR-1996; 96MO-RU00087.

PR 11-APR-1996; 96MO-RU00087.

XX (DYMSHITS G M.
PA (IVANOV) IVANOVA E M.
PA (KRIV) KRIVENKO A A.
PA (KULI) KULIKOVA V F.
PA (LOKH) LOKHOV S G.
PA (PYSH) PYSHNY D V.

XX Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
PI Lohkov SG, Pyshny DV;
XX WPI: 1997-512737/47.

XX WPI: 1997-512737/47.

PT Detection of target nucleic acid sequence - based on ligation of
PT hybridised short probe to flanking target-complementary sequences
XX Example; Page 4; 15pp: Russian.

CC This sequence represents a probe for the target sequence P0 (shown in
CC AA0816376). This sequence was used to test the method of the invention.
CC The method of the invention is for detecting a nucleic acid sequence to
CC be analysed, and comprises hybridisation of an oligonucleotide probe
CC complementary to the sequence to be analysed and bearing a reporter
CC group, the novelty is that detection of a sequence is based on the
CC ligation of a short oligonucleotide (with a length of 4-6 units) with
CC flanking oligonucleotide sequences (or their derivatives bearing
CC polycyclic aromatic groups). The method is especially useful for
CC detecting point mutations. Diagnosis of viral, genetic and other
CC diseases is also mentioned.

CC Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 10

AA0816385/C
ID AA0816385 standard; DNA; 4 BP.

AC AA0816385;

DT 23-APR-1998 (first entry)

DE Probe for target nucleic acid sequence P0.

XX Point mutation detection; nucleic acid sequence analysis; probe;
KW viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /note= "C-5' phosphate"

PN WO9738131-A1.

PD 16-OCT-1997.

PF 11-APR-1996; 96MO-RU00087.

PR 11-APR-1996; 96MO-RU00087.

XX (DYMSHITS G M.
PA (IVANOV) IVANOVA E M.
PA (KRIV) KRIVENKO A A.
PA (KULI) KULIKOVA V F.
PA (LOKH) LOKHOV S G.
PA (PYSH) PYSHNY D V.

XX Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
PI Lohkov SG, Pyshny DV;
XX WPI: 1997-512737/47.

XX WPI: 1997-512737/47.
PT Detection of target nucleic acid sequence - based on ligation of
PT hybridised short probe to flanking target-complementary sequences
XX Example; Page 4; 15pp: Russian.

XX This sequence represents a probe for the target sequence P0 (shown in
 CC AAT86376). This sequence was used to test the method of the invention.
 CC The method of the invention is for detecting a nucleic acid sequence to
 CC be analysed, and comprises hybridisation of an oligonucleotide probe to
 CC complementary to the sequence to be analysed and bearing a reporter
 CC group, the novelty is that detection of a sequence is based on the
 CC ligation of a short oligonucleotide (with a length of 4-6 units) with
 CC flanking oligonucleotide sequences (or their derivatives bearing
 CC polycyclic aromatic groups). The method is especially useful for
 CC detecting point mutations. Diagnosis of viral, genetic and other
 CC diseases is also mentioned.

SO Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 C 1
 Db 3 C 3

RESULT 11

AAT77252
 ID AAT77252 standard; DNA; 4 BP.

AC AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

KW Immunostimulatory polynucleotide; ISP: palindrome; vaccine;
 KW immune response; antigen; naked gene expression vector; IGE;
 KW antibody; immunotherapy; ss.

OS Synthetic.

PN MO9728259-A1.

PD 07-AUG-1997.

PF 28-JAN-1997; 97WO-US01277.

PR 30-JAN-1996; 96US-0593554.

PA (REGC) UNIV CALIFORNIA.

PI Carson DA, Raz E;

WIPI: 1997-402613/37.

Recombinant vector containing immunostimulatory palindromic
 PT polynucleotide - useful for selectively enhancing the TH1 immune
 PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide
 CC (ISP) comprised of at least one strand of a palindrome, which includes
 CC at least one dinucleotide consisting of adjacent, unmodified cytosine
 CC and guanine residues. ISP's could be used in vaccination methods
 CC for enhancing the immune response of a host to an antigen. Administration
 CC of naked gene expression vectors which encode antigens or their
 CC immunostimulatory fragments suppresses IGE antibody production
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.
 CC Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 C 1
 Db 2 C 2

RESULT 12

AAT77252/C
 ID AAT77252 standard; DNA; 4 BP.

AC AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

KW Immunostimulatory polynucleotide; ISP: palindrome; vaccine;
 KW immune response; antigen; naked gene expression vector; IGE;
 KW antibody; immunotherapy; ss.

OS Synthetic.

PN MO9728259-A1.

PD 07-AUG-1997.

PF 28-JAN-1997; 97WO-US01277.

PR 30-JAN-1996; 96US-0593554.

PA (REGC) UNIV CALIFORNIA.

PI Carson DA, Raz E;

WIPI: 1997-402613/37.

Recombinant vector containing immunostimulatory palindromic
 PT polynucleotide - useful for selectively enhancing the TH1 immune
 PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide
 CC (ISP) comprised of at least one strand of a palindrome, which includes
 CC at least one dinucleotide consisting of adjacent, unmodified cytosine
 CC and guanine residues. ISP's could be used in vaccination methods
 CC for enhancing the immune response of a host to an antigen. Administration
 CC of naked gene expression vectors which encode antigens or their
 CC immunostimulatory fragments suppresses IGE antibody production
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.
 CC Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1
 Db 3 C 3

RESULT 13

AAL17191
 ID AAL17191 standard; cDNA; 4 BP.

AC AAL17191;

DT 07-DEC-2001 (first entry)

```
XX DE Human breast cancer expressed polynucleotide 9648.
XX KW Human: breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX FD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX DR WPI: 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer -
XX PS Claim 1: Page 1720; 3695pp; English.
XX SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
CC SQ
SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;
Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 C 1
Db 3 C 3
RESULT 14
AAL17191/c
ID AAL17191 standard; cDNA: 4 BP.
XX AAL17191:
XX AC
XX AC AAL17191:
XX DT 07-DEC-2001 (first entry)
XX DE Human breast cancer expressed polynucleotide 9648.
XX KW Human: breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR
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```
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX DR WPI: 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer -
XX PS Claim 1: Page 1720; 3695pp; English.
XX SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
CC SQ
SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;
Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 C 1
Db 1 C 1
RESULT 15
AAL24357
ID AAL24357 standard; cDNA: 4 BP.
XX AAL24357:
XX AC
XX AC AAL24357:
XX DT 07-DEC-2001 (first entry)
XX DE Human breast cancer expressed polynucleotide 16814.
XX KW Human: breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX DR WPI: 2001-451856/48.
```

XX New peptide useful as a marker for the diagnosis of breast cancer -
 PT
 XX
 PS Claim 1: Page 3087: 3695pp; English.
 CC
 CC The invention relates to human breast cancer expressed polynucleotides
 CC (AA107544-AA126789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterizing treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity.
 CC
 SO Sequence 4 BP: 0 A: 1 C: 0 G: 3 T: 0 other:

Query Match 100.0%; Score 1: DB 22: Length 4:
 Best Local Similarity 100.0%; Pred. No. 0:
 Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 C 1
 |
 Db 3 C 3

RESULT 16
 ID AAF61450/c
 ID AAF61450 standard; RNA: 4 BP.
 AC AAF61450:
 XX
 XX
 DT 18-JUN-2001 (first entry)
 XX

XX Cyclin binding hammerhead ribozyme 3' catalytic fragment SEQ ID 19.
 XX
 KW Hammerhead ribozyme; cyclin E; restenosis; catalytic; angioplasty;
 XX cyclin E2F1; vasotropic; gene therapy; cell cycle arrest; ss.
 XX
 OS Synthetic.
 XX
 PN WO200121789-A1.
 XX

XX 29-MAR-2001.
 PD
 PF 22-SEP-1999: 99WO-EP07049.
 XX
 XX 22-SEP-1999: 99WO-EP07049.
 PK
 XX

PA (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.
 XX
 XX Graessl G, Kuhn AC, Kandolf R;
 PI
 XX
 DR WPI: 2001-257985/26.
 XX

XX New catalytically acting RNA molecule comprising hammerhead ribozyme
 PT directed against mRNA molecules encoding cyclin E or E2F1, useful for
 PT inhibiting vascular smooth muscle cell proliferation and restenosis -
 XX
 PS Claim 12: Page 28: 40pp; German.
 XX

CC This invention describes a novel catalytic RNA molecule which is directed
 CC against mRNA molecules (II) which encode the cell-relevant protein cyclin
 CC E or E2F1. The products of the invention have vasotropic activity and can
 CC be used for gene therapy. The use of (I), or a DNA molecule or a plasmid
 CC of the invention is claimed for obtaining a vector for gene therapy and
 CC for inhibiting restenosis of blood vessel after angioplasty; therapeutic
 CC compositions containing these components are also claimed. (I)
 CC efficiently induces cell cycle arrest by combined inactivation of cyclin
 CC E and E2F1.
 CC
 SO Sequence 4 BP: 2 A: 0 C: 1 G: 0 U: 1 other:

Query Match 100.0%; Score 1: DB 22: Length 4:
 Best Local Similarity 100.0%; Pred. No. 0:
 Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 C 1
 |
 Db 2 C 2

RESULT 17
 ID AAN93676
 ID AAN93676 standard; DNA: 5 BP.
 AC AAN93676:
 XX

XX 24-JUN-1990 (first entry)
 DT
 XX
 DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber
 DE variant (HSV-c) and HSV grape variant (HSV-g).
 XX

XX Hop growth retarding viroid; cucumber variant; grape variant; probe: ss.
 XX
 OS Hop growth retarding viroid.
 XX
 PN JP01040000-A.
 XX

PD 10-FEB-1989.
 XX

PF 05-AUG-1987: 87JP-0194377.
 XX

PR 05-AUG-1987: 87JP-0195377.
 XX

PA (YUKI) YUKI GOSEI YAKUHIN.
 XX

DR WPI: 1989-089715/12.
 XX

PT Fractionating and detecting hop growth retarding viroids -
 PT using synthetic DNA probe concy. specific base sequence
 XX

PS Disclosure; page 3: 5pp; Japanese.
 XX

CC The synthetic probes is complementary to the RNA of HSV-g bases 53-59.
 CC HSV, HSV-c and HSV-g are fractionated and detected using the synthetic
 CC probe. The probe is 15-25mer. The probe can be used to diagnose HSV
 CC infections in plants.
 XX

SO Sequence 5 BP: 1 A: 3 C: 0 G: 1 T: 0 other:

Query Match 100.0%; Score 1: DB 10: Length 5:
 Best Local Similarity 100.0%; Pred. No. 0:
 Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 C 1
 |
 Db 2 C 2

RESULT 18
 ID AAO68752/c
 ID AAO68752 standard; DNA: 5 BP.
 AC AAO68752:
 XX

XX 22-FEB-1995 (first entry)
 DT
 XX

DE CHA255 heavy chain CDR1 clone 3.3.3. coding sequence.
 XX

KW Polymerase chain reaction; primer: PCR; amplify; heavy; light;
 KW chain; complementarity determining region; CDR; variable; constant;
 KW region; monoclonal antibody; MAb; binding affinity; EDPA; DOTA;

KW tumour; cancer; colorectal; breast; metal chelate; hapten; ss.
XX Synthetic.
OS
PN AU9350602-A.
XX
PD 26-MAY-1994.
XX
PF 10-NOV-1993; 93AU-0050602.
XX
PR 12-NOV-1992; 92US-0975230.
XX
PA (HYBR-) HYBRITTECH INC.
XX
PI Ahweller PM, Moore MD;
XX
DR WPI: 1994-209063/26.
UK P-PSDB: AAR54150.
XX
PT Polypeptide used in imaging and treatment of carcinomas and
PT tumours - comprising subunit antibody CDR having binding affinity
PT for metal chelate of EDTA or DETA or analogues
XX
PS Claim 25: Fig 3A; 61pp: English.
XX
XX The sequences given in AA068747-57 encode the wild type and mutagenised
CC versions of the complementarity determining region 1 (CDR1) of the
CC antibody designated CHA255. CHA255 is a murine monoclonal antibody
CC (Mab) which is capable of binding complexes. Mutagenesis of these
CC CDRs causes the production of polypeptides with a particularly
CC high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3
CC of the heavy chain, and CDR2 and -3 of the light chain were targeted
CC for mutagenesis. Five residues of both CDR1 and -3 of the CHA255
CC heavy chain, five of seven residues of light chain CDR and six of
CC nine light chain CDR3 residues were specifically targeted for
CC codon-based mutagenesis. The mutagenised Mab's can be used in
CC compositions for in vivo imaging of malignant tissues or tumours. They
CC are also useful for the treatment of malignant tissues or tumours eg.
CC colorectal or breast cancer. Both methods involve the use of
CC radionuclides which bind to metal chelates or haptens which are
CC specifically delivered to the target site by a targeting molecule.
CC derived peptides may be used to construct bi-functional antibodies.
CC having dual specificities, or as donor or recipients of CDR sequences.
XX
SQ Sequence 5 BP: 0 A; 0 G; 1 G; 1 T; 3 other;

Query Match 100.0%; Score 1; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
DB 1 c 1

RESULT 19
AA081667
ID AA081667 standard; RNA: 5 BP.
XX
AC AA081667;
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #4.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX

PN WO9500528-A.
XX
PD 05-JAN-1995.
XX
PF 17-JUN-1994; 94WO-US06884.
XX
PR 18-JUN-1993; 93US-0079677.
XX
PR 07-JAN-1994; 94US-0179491.
XX
PA (PHAR-) PHARMAGENICS INC.
XX
PI Beutzel BA, Joesten ME;
XX
DR WPI: 1995-051992/07.
XX
PT New oligo-nucleotide(s) that bind to basic fibroblast growth
PT factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.
XX
PS Claim 3; Page 25; 44pp: English.
XX
XX The sequences given in AA081642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AA081664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC pseudoknot or a closed, circular structure, a bubble structure, a
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.
XX
SQ Sequence 5 BP: 2 A; 2 C; 0 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
DB 4 c 4

RESULT 20
AAT12043
ID AAT12043 standard; RNA: 5 BP.
XX
AC AAT12043;
XX
DT 17-JUL-1996 (first entry)
XX
DE Cleavable replicable-inhibiting sequence.
XX
KW Ribozyme; hairpin; hammerhead; probe; MDV-1; midvariant-1;
KW replication; cleavage; ss.
XX
OS Synthetic.
XX
PN US5472840-A.
XX
PD 05-DEC-1995.
XX
PF 30-SEP-1988; 88US-0252243.
XX
PR 17-DEC-1990; 90US-0630288.
PR 30-SEP-1988; 88US-0252243.
PR 22-JUN-1989; 89US-0370218.


```

AC  AAT96299;
XX
DT  08-APR-1998 (first entry)
XX
DE  Fungal telomeric nucleic acid sequence.
XX
KW  Detection: eukaryotic pathogen; telomeric nucleic acid sequence;
KM  telomerase activity; diagnosis; fungal infection; fungus; fungi;
XX  malarial infection; malaria; ss.
OS  Saccharomyces cerevisiae.
XX
PN  US5695932-A.
XX
PD  09-DEC-1997.
XX
PF  13-MAY-1993; 93US-0060952.
XX
PR  13-MAY-1993; 93US-0060952.
XX  13-MAY-1992; 92US-0882438.
XX  24-MAR-1993; 93US-0038766.
XX
PA  (REGC ) UNIV CALIFORNIA.
XX  (TEXA ) UNIV TEXAS SYSTEM.
XX
PI  Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;
XX  WPI: 1998-041292/04.
XX
DR  Detection of eukaryotic pathogens, especially fungal or Plasmidium
XX  spp. - by detecting telomerase activity
XX
PT  Claim 5: Columns 81-82; 82pp; English.
XX
PS  The present sequence can be used in a novel method for detecting a
XX  eukaryotic pathogen in a patient. The method comprises obtaining a
XX  sample of somatic tissue or cells from the patient, determining if
XX  telomerase activity is present and correlating this with the
XX  presence of the pathogen. The method is useful for diagnosis of
XX  fungal infections, especially a fungus of the genus Candida,
XX  Kluyveromyces, Saccharomyces, Sporobolus, Coccidioides,
XX  Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,
XX  Aspergillus, Mucor or Rhizopus, or malarial infections, especially
XX  Plasmidium vivax, P. ovale, P. malariae or P. falciparum.
XX
SQ  Sequence 5 BP: 0 A; 0 C; 3 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 C 1
    |
DB  5 C 5

RESULT 24
AAZ10695/C
ID  AAZ10695 standard; DNA: 5 BP.
XX
AC  AAZ10695;
XX
DT  23-NOV-1999 (first entry)
XX
DE  Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW  p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KM  UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX  atopic dermatitis; allergic rhinitis; conjunctivitis; photoging;
XX  skin cancer; ss.
OS  Synthetic.

```

```

XX
PN  GB2336157-A.
XX
PD  13-OCT-1999.
XX
PF  24-MAR-1999; 99GB-0006758.
XX
PR  26-MAR-1998; 98US-0048927.
XX
PA  (UYBO-) UNIV BOSTON.
XX
PI  Gilchrist BA, Yaar M, Eller M;
XX  WPI: 1999-543520/46.
XX
DR  DNA fragments useful for increasing p53 activity in a cell and reducing
XX  susceptibility to UV-induced hyperproliferative diseases -
XX
PT  Claim 11: Page 30; 44pp; English.
XX
PS  AAZ10692-97 represent DNA fragments that are used for increasing p53
XX  activity in a cell. The oligonucleotides are UV mimetics and
XX  protect cells against subsequent exposure to UV-irradiation or
XX  chemicals. The oligonucleotides are useful for increasing p53 activity
XX  in a cell, reducing the susceptibility to UV-induced hyperproliferative
XX  diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
XX  rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoging
XX  and reducing susceptibility to skin cancer.
XX
SQ  Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 C 1
    |
DB  5 C 5

RESULT 25
AAZ10696
ID  AAZ10696 standard; DNA: 5 BP.
XX
AC  AAZ10696;
XX
DT  23-NOV-1999 (first entry)
XX
DE  Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW  p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KM  UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX  atopic dermatitis; allergic rhinitis; conjunctivitis; photoging;
XX  skin cancer; ss.
OS  Synthetic.
XX
PN  GB2336157-A.
XX
PD  13-OCT-1999.
XX
PF  24-MAR-1999; 99GB-0006758.
XX
PR  26-MAR-1998; 98US-0048927.
XX
PA  (UYBO-) UNIV BOSTON.
XX
PI  Gilchrist BA, Yaar M, Eller M;
XX  WPI: 1999-543520/46.
XX
DR  DNA fragments useful for increasing p53 activity in a cell and reducing
XX

```

PT susceptibility to UV-induced hyperproliferative diseases -
XX
PS Claim 11: Page 30; 44pp; English.
XX
CC AA10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 1 c 1

RESULT 26
AAZ11611/c
ID AAZ11611 standard; DNA: 5 BP.
XX
AC AAZ11611;

XX 16-NOV-1999 (first entry)
XX
DE DNA enhancer sequence present in an upstream element.

KM Plant promoter: TATA motif; transcription start site: upstream element;
KM gene expression; oxalate oxidase; plant resistance; pathogen; maize;
KW ubi-1 promoter; Syn II core promoter; ss.
XX
OS Synthetic.

XX WO943838-A1.
XX
PD 02-SEP-1999.

XX 23-FEB-1999; 99WO-US03863.
XX
PR 24-FEB-1998; 98US-0028819.

XX (PION-) PIONEER HI-BRED INT INC.
XX
PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;

XX WPI: 1999-540601/45.
XX
DR

PT New synthetic promoter functional in plants to provide non-tissue
PT specific, constitutive expression, particularly of oxalate oxidase for
PT increased resistance to pathogens -
XX
PS Claim 39; Page 47; 61pp; English.

CC The invention provides a new synthetic plant promoter that comprises a
CC TATA motif; a transcription start site (TSS) and a region between TATA
CC and TSS containing at least 64 percent GC content. The synthetic core
CC promoter, optionally containing additional upstream elements are used to
CC increase expression, provides non-tissue specific, constitutive
CC transcription of heterologous genes in any sort of plant, especially the
CC gene for oxalate oxidase for increasing plant resistance to pathogens.
CC The upstream activating elements can be used to increase transcription
CC from any promoter. A combination of the synthetic core promoter with
CC synthetic upstream elements can induce expression 10 times greater than
CC that provided by the maize ubi-1 promoter. The present sequence
CC represents a DNA enhancer OSC-like motif present in an upstream element

CC sequence.

XX
SQ Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 5 c 5

RESULT 27
AAZ11611/c
ID AAZ11611 standard; DNA: 5 BP.
XX
AC AAZ11611;

XX 16-NOV-1999 (first entry)
XX
DE DNA enhancer sequence present in an upstream element.

KM Plant promoter: TATA motif; transcription start site: upstream element;
KM gene expression; oxalate oxidase; plant resistance; pathogen; maize;
KW ubi-1 promoter; Syn II core promoter; ss.
XX
OS Synthetic.

XX WO943838-A1.
XX
PD 02-SEP-1999.

XX 23-FEB-1999; 99WO-US03863.
XX
PR 24-FEB-1998; 98US-0028819.

XX (PION-) PIONEER HI-BRED INT INC.
XX
PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;

XX WPI: 1999-540601/45.
XX
DR

PT New synthetic promoter functional in plants to provide non-tissue
PT specific, constitutive expression, particularly of oxalate oxidase for
PT increased resistance to pathogens -
XX
PS Claim 39; Page 47; 61pp; English.

CC The invention provides a new synthetic plant promoter that comprises a
CC TATA motif; a transcription start site (TSS) and a region between TATA
CC and TSS containing at least 64 percent GC content. The synthetic core
CC promoter, optionally containing additional upstream elements are used to
CC increase expression, provides non-tissue specific, constitutive
CC transcription of heterologous genes in any sort of plant, especially the
CC gene for oxalate oxidase for increasing plant resistance to pathogens.
CC The upstream activating elements can be used to increase transcription
CC from any promoter. A combination of the synthetic core promoter with
CC synthetic upstream elements can induce expression 10 times greater than
CC that provided by the maize ubi-1 promoter. The present sequence
CC represents a DNA enhancer OSC-like motif present in an upstream element
CC sequence.

SQ Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|

DB 4 C 4

RESULT 28

AAV72347
ID AAV72347 standard; DNA: 5 BP.

AC AAV72347;

DT 28-JUL-1999 (first entry)

DE US5908745 primer #4.

XX DNA sequencing: disease-associated allele; polyacrylamide matrix;
 KW continuous/contiguous stacking hybridization technique; detection;
 KM mutation; diagnosis; primer; ss.

OS Synthetic.

PN US5908745-A.

PD 01-JUN-1999.

PF 16-JAN-1996; 96US-0587332.

PR 16-JAN-1996; 96US-0587332.

PA (UYCH-) UNIV CHICAGO.

PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

PI Parinov SV, Yershov GM;

DR WPI: 1999-347002/29.

PT Detecting disease-associated alleles using continuous/contiguous
 PT stacking hybridization as a diagnostic tool

PS Example 1: Column 9; 16pp; English.

XX This invention describes novel methods for sequencing and analysing DNA
 CC samples to detect disease-associated alleles, by continuous/contiguous
 CC stacking hybridization techniques (utilizing universal bases) with
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
 CC be used to detect multiple DNA base mutations which are specific for
 CC certain diseases. The methods of the invention provide accurate and
 CC efficient and sensitive methods for diagnosing disease by detecting
 CC multiple mutation sequences in patient DNA. The method require the
 CC minimum number of oligonucleotides and few stacking hybridization steps
 CC than prior art methods. The methods are also efficient enough to
 CC discriminate between perfect and imperfect duplexes. The methods also
 CC obviate the need for the fabrication and array placement of large numbers
 CC of immobilized oligomers.

SQ Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

DB 1 C 1

RESULT 29

AAV72348
ID AAV72348 standard; DNA: 5 BP.

AC AAV72348;

DT 28-JUL-1999 (first entry)

XX

DE US5908745 primer #5.

XX DNA sequencing: disease-associated allele; polyacrylamide matrix;
 KW continuous/contiguous stacking hybridization technique; detection;
 KM mutation; diagnosis; primer; ss.

OS Synthetic.

PN US5908745-A.

PD 01-JUN-1999.

PF 16-JAN-1996; 96US-0587332.

PR 16-JAN-1996; 96US-0587332.

PA (UYCH-) UNIV CHICAGO.

PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

PI Parinov SV, Yershov GM;

DR WPI: 1999-347002/29.

PT Detecting disease-associated alleles using continuous/contiguous
 PT stacking hybridization as a diagnostic tool

PS Example 1: Column 9; 16pp; English.

XX This invention describes novel methods for sequencing and analysing DNA
 CC samples to detect disease-associated alleles, by continuous/contiguous
 CC stacking hybridization techniques (utilizing universal bases) with
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
 CC be used to detect multiple DNA base mutations which are specific for
 CC certain diseases. The methods of the invention provide accurate and
 CC efficient and sensitive methods for diagnosing disease by detecting
 CC multiple mutation sequences in patient DNA. The method require the
 CC minimum number of oligonucleotides and few stacking hybridization steps
 CC than prior art methods. The methods are also efficient enough to
 CC discriminate between perfect and imperfect duplexes. The methods also
 CC obviate the need for the fabrication and array placement of large numbers
 CC of immobilized oligomers.

SQ Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

DB 1 C 1

RESULT 30

AAV72348/c
ID AAV72348 standard; DNA: 5 BP.

AC AAV72348;

DT 28-JUL-1999 (first entry)

DE US5908745 primer #5.

XX DNA sequencing: disease-associated allele; polyacrylamide matrix;
 KW continuous/contiguous stacking hybridization technique; detection;
 KM mutation; diagnosis; primer; ss.

OS Synthetic.

PN US5908745-A.

PD 01-JUN-1999.

```

XX 16-JAN-1996: 96US-0587332.
XX 16-JAN-1996: 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
XX
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD:
XX Parinov SV, Vershov GM:
XX WPI: 1999-347002/29.
XX
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9; 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
XX
XX Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other:
XX

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```

Query Match
Best Local Similarity 100.0%; Score 1; DB 20; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 c 1
Db 2 c 2

```

```

RESULT 31
AAV72349
ID AAV72349 standard; DNA: 5 BP.
XX
XX AAV72349:
XX
XX 28-JUL-1999 (first entry)
XX
XX US5908745 primer #6.
XX
XX DNA sequencing; disease-associated allele: polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer; ss.
XX
XX Synthetic.
XX
XX US5908745-A.
XX
XX 01-JUN-1999.
XX
XX 16-JAN-1996: 96US-0587332.
XX
XX 16-JAN-1996: 96US-0587332.
XX
XX 16-JAN-1996: 96US-0587332.
XX
XX (UYCH-) UNIV CHICAGO.
XX
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD:
XX Parinov SV, Vershov GM:
XX WPI: 1999-347002/29.
XX

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```

XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9; 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
XX
XX Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other:
XX

```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 20; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 c 1
Db 1 c 1

```

```

RESULT 32
AAV72350
ID AAV72350 standard; DNA: 5 BP.
XX
XX AAV72350:
XX
XX 28-JUL-1999 (first entry)
XX
XX US5908745 primer #7.
XX
XX US5908745-A.
XX
XX 01-JUN-1999.
XX
XX 16-JAN-1996: 96US-0587332.
XX
XX 16-JAN-1996: 96US-0587332.
XX
XX 16-JAN-1996: 96US-0587332.
XX
XX (UYCH-) UNIV CHICAGO.
XX
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD:
XX Parinov SV, Vershov GM:
XX WPI: 1999-347002/29.
XX
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9; 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods
XX be used to detect multiple DNA base mutations which are specific for
XX

```

CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method requires the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.

XX
SQ Sequence 5 BP; 3 A; 2 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1
Db 4 c 4

RESULT 33

AA556964
ID AAX56964 standard; DNA; 5 BP.

XX
AC AAX56964;

XX
UT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

XX
KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
cell growth inhibitor; treatment; cancer; ras protein; ss.

XX
OS Synthetic.

XX
PN MO9922772-A1.

XX
PD 14-MAY-1999.

XX
PF 28-OCT-1998; 98WO-US22821.

XX
PR 31-OCT-1997; 97US-0961469.

XX
PA (ISIS-) ISIS PHARM INC.

XX
PI Geary RS, Hardee GE, Howard R, Levin A, Mehra RC;

XX
PI Templin MV;

XX
DR WPI: 1999-313181/26.

XX
PT Liposome-encapsulated oligonucleotides useful for treating or
preventing cancers associated with ras gene activation

XX
PS Example 1; Page 107; 120pp; English.

XX
CC This invention describes novel compositions comprising oligonucleotides
(AAX56957-X57017), entrapped within liposomes, that hybridize
specifically to a target DNA or mRNA which encodes a mutant or wild-type
ras protein. The products of the invention have anticancer activity and
specifically bring about the antisense inhibition of ras genes or mRNA.
The products of the invention are used to modulate expression of a ras
gene in cells, tissue, organs or organisms, particularly to inhibit cell
growth and especially to treat or prevent cancers associated with
activation of a ras gene. Encapsulating the oligonucleotide reduces the
rate at which it is cleared from the blood when compared with
non-encapsulated material, and the oligonucleotides become distributed to
practically all parts of the body.

XX
SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1
Db 1 c 1

RESULT 34

AA556964/C
ID AAX56964 standard; DNA; 5 BP.

XX
AC AAX56964;

XX
DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

XX
KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
cell growth inhibitor; treatment; cancer; ras protein; ss.

XX
OS Synthetic.

XX
PN MO9922772-A1.

XX
PD 14-MAY-1999.

XX
PF 28-OCT-1998; 98WO-US22821.

XX
PR 31-OCT-1997; 97US-0961469.

XX
PA (ISIS-) ISIS PHARM INC.

XX
PI Geary RS, Hardee GE, Howard R, Levin A, Mehra RC;

XX
PI Templin MV;

XX
DR WPI: 1999-313181/26.

XX
PT Liposome-encapsulated oligonucleotides useful for treating or
preventing cancers associated with ras gene activation

XX
PS Example 1; Page 107; 120pp; English.

XX
CC This invention describes novel compositions comprising oligonucleotides
(AAX56957-X57017), entrapped within liposomes, that hybridize
specifically to a target DNA or mRNA which encodes a mutant or wild-type
ras protein. The products of the invention have anticancer activity and
specifically bring about the antisense inhibition of ras genes or mRNA.
The products of the invention are used to modulate expression of a ras
gene in cells, tissue, organs or organisms, particularly to inhibit cell
growth and especially to treat or prevent cancers associated with
activation of a ras gene. Encapsulating the oligonucleotide reduces the
rate at which it is cleared from the blood when compared with
non-encapsulated material, and the oligonucleotides become distributed to
practically all parts of the body.

XX
SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1
Db 5 c 5

RESULT 35

AA556964/C

ID AAX21608 standard; DNA; 5 BP.

XX
AC AAX21608;

```
XX 14-MAY-1999 (first entry)
DT Mutant H-ras specific antisense oligo ISIS #2563.
DE Human: N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
KM diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.
XX Synthetic.
OS WO9902732-A1.
PN 21-JAN-1999.
XX 06-JUL-1998; 98WO-US13966.
PF 08-JUL-1997; 97US-0889296.
PR (ISIS-) ISIS PHARM INC.
PA Cowser LM, Manoharan M, Monia BP;
PI WPI: 1999-120932/10.
XX New oligonucleotide targeting human N-ras nucleic acid - is
XX capable of inhibiting human N-ras expression, useful for preventing
XX or treating conditions arising from the activation of a human N-ras
XX oncogene
XX Disclosure: Page 22; 97pp; English.
XX The invention relates to oligonucleotides, which target a nucleic acid
XX encoding human N-ras, and are capable of inhibiting human N-ras
XX expression. The antisense oligonucleotides form a pharmaceutical
XX composition, which is useful for modulating the expression of human
XX N-ras, inhibiting the proliferation of cancer cells, and preventing or
XX treating conditions arising from the activation of a human N-ras
XX oncogene. The oligonucleotides are also useful in diagnostics,
XX therapeutics, and as research reagents and kits. The oligonucleotides
XX enable the specific modulation of activated human N-ras expression,
XX which is associated with tumour formation. Sequences AAX21601-619
XX represent antisense oligonucleotides targeted to mutant H-ras.
XX Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;
SQ
Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
DB 1 c 1
RESULT 36
AAX21608/c
ID AAX21608 standard; DNA; 5 BP.
XX
AC AAX21608;
XX
DT 14-MAY-1999 (first entry)
XX
DE Mutant H-ras specific antisense oligo ISIS #2563.
XX
KM Human: N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
XX diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.
OS Synthetic.
XX WO9902732-A1.
XX
PN 21-JAN-1999.
XX
```

```
XX 06-JUL-1998; 98WO-US13966.
PF 08-JUL-1997; 97US-0889296.
PR (ISIS-) ISIS PHARM INC.
XX
XX Cowser LM, Manoharan M, Monia BP;
PI WPI: 1999-120932/10.
XX
XX New oligonucleotide targeting human N-ras nucleic acid - is
XX capable of inhibiting human N-ras expression, useful for preventing
XX or treating conditions arising from the activation of a human N-ras
XX oncogene
XX Disclosure: Page 22; 97pp; English.
XX The invention relates to oligonucleotides, which target a nucleic acid
XX encoding human N-ras, and are capable of inhibiting human N-ras
XX expression. The antisense oligonucleotides form a pharmaceutical
XX composition, which is useful for modulating the expression of human
XX N-ras, inhibiting the proliferation of cancer cells, and preventing or
XX treating conditions arising from the activation of a human N-ras
XX oncogene. The oligonucleotides are also useful in diagnostics,
XX therapeutics, and as research reagents and kits. The oligonucleotides
XX enable the specific modulation of activated human N-ras expression,
XX which is associated with tumour formation. Sequences AAX21601-619
XX represent antisense oligonucleotides targeted to mutant H-ras.
XX Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;
SQ
Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
DB 5 C 5
RESULT 37
AAA56981
ID AAA56981 standard; cDNA; 5 BP.
XX
AC AAA56981;
XX
DT 14-NOV-2000 (first entry)
XX
DE Human colon cancer cell cDNA sequence #109.
XX
XX Human: arbitrary primer; cDNA synthesis; contig sequence construction;
XX open reading frame; ORF; low stringency; cDNA sequencing; ss.
OS Homo sapiens.
XX
XX WO200031299-A2.
XX
XX 02-JUN-2000.
XX
XX 19-NOV-1999; 99WO-US27430.
XX
XX 20-NOV-1998; 98US-0196716.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Simpson AJG, Dias Neto E, Brentani RR;
PI WPI: 2000-400100/34.
XX
XX Method for determining open reading frames of the genome of an organism
XX using primers at low stringency conditions, useful in the construction
XX
```

PT of contigs or constructs of sequenced nucleic acid molecules -
 XX
 PS Example 6; Page 47: 113pp; English.
 XX

CC The present sequence is a cDNA sequence obtained using a method for
 CC determining open reading frames (ORFs) of the genome of an
 CC organism. An aliquot of mRNA from human colon cancer cells was mixed
 CC with a single, arbitrary primer. Moloney murine leukaemia virus reverse
 CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
 CC incubated under low stringency conditions to yield single stranded
 CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
 CC than providing nucleotide sequence information from the non-coding
 CC terminal of nucleic acid molecules, the method provides information on
 CC the more interesting and relevant internal portions, such as ORFs. The
 CC method also permits the construction of contigs of sequenced nucleic
 CC acid molecules.

SO Sequence 5 BP: 0 A; 3 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 c 1
 Db 1 c 1

RESULT 38
 ID AAA56981/C
 AC AAA56981 standard; cDNA: 5 BP.

AA56981:
 DT 14-NOV-2000 (first entry)
 DE Human colon cancer cell cDNA sequence #109.

Human: arbitrary primer; cDNA synthesis; contig sequence construction;
 open reading frame; ORF; low stringency; cDNA sequencing; ss.

XX Homo sapiens.
 OS
 PN WO200031299-A2.

PD 02-JUN-2000.

PF 19-NOV-1999: 99MO-US27430.

PR 20-NOV-1998: 98US-0196716.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Simpson AJC, Dias Neto E, Brentani RR;

DR WPI: 2000-400100/34.

PT Method for determining open reading frames of the genome of an organism
 PT using primers at low stringency conditions, useful in the construction
 PT of contigs or constructs of sequenced nucleic acid molecules -
 XX
 PS Example 6; Page 47: 113pp; English.

CC The present sequence is a cDNA sequence obtained using a method for
 CC determining open reading frames (ORFs) of the genome of an
 CC organism. An aliquot of mRNA from human colon cancer cells was mixed
 CC with a single, arbitrary primer. Moloney murine leukaemia virus reverse
 CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
 CC incubated under low stringency conditions to yield single stranded
 CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
 CC than providing nucleotide sequence information from the non-coding
 CC terminal of nucleic acid molecules, the method provides information on

CC the more interesting and relevant internal portions, such as ORFs. The
 CC method also permits the construction of contigs of sequenced nucleic
 CC acid molecules.
 CC
 XX

SO Sequence 5 BP: 0 A; 3 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 c 1
 Db 3 C 3

RESULT 39
 ID AA293601
 AC AA293601 standard; DNA: 5 BP.

AA293601:
 DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

XX Regulatory sequence; meristem; genetic engineering;
 KW gene expression; crop protection; transgenic plant; resistance;
 KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

OS Synthetic.
 OS Nicotiana glauca.

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999: 99MO-AU00692.

PR 26-AUG-1998: 98AU-0005498.

PA (UYOU) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing
 PT transgenic plants with improved characteristics such as resistance to
 PT pathogens
 XX
 PS Example 9; Page 51: 102pp; English.

CC Isolated regulatory sequences of plants that are operable in
 CC dividing cells, in particular the meristem cells of plants are useful
 CC in the genetic engineering of plants. The regulatory sequences can
 CC be used to control the expression of foreign genes placed under their
 CC control. Such methods are useful for producing transgenic plants with
 CC altered shape and/or size. The sequences are also useful for
 CC producing transgenic plants capable of rapid regeneration following
 CC harvest or plants having improved resistance to pathogens. This
 CC sequence has been shown to bind a factor involved in the activation
 CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three
 CC times in the meristem regulatory sequence of Tobacco described in
 CC GENESEQ record AA293567.

SO Sequence 5 BP: 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
Db 1 c 1

RESULT 40

AA293601/c
ID AA293601 standard; DNA: 5 BP.

AC AA293601;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KW gene expression; crop protection; transgenic plant; resistance;

XX tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

OS Synthetic.

OS Nicotiana acuminata.

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing
transgenic plants with improved characteristics such as resistance to
pathogens

PS Example 9: Page 51; 102pp; English.

CC Isolated regulatory sequences of plants that are operable in
dividing cells, in particular the meristem cells of plants are useful

CC in the genetic engineering of plants. The regulatory sequences can
be used to control the expression of foreign genes placed under their

CC control. Such methods are useful for producing transgenic plants with
altered shape and/or size. The sequences are also useful for

CC producing transgenic plants capable of rapid regeneration following
harvest or plants having improved resistance to pathogens. This

CC sequence has been shown to bind a factor involved in the activation
of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three

CC times in the meristem regulatory sequence of Tobacco described in
GENESCO record AA293567.

CC Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match

Best Local Similarity 100.0%; Score 1; DB 21; Length 5;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
Db 5 c 5

RESULT 41

AA293602

ID AA293602 standard; DNA: 5 BP.

AC AA293602;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KW gene expression; crop protection; transgenic plant; resistance;

XX tobacco; transcription factor; NIT2; nitrate; ss.

OS Synthetic.

OS Nicotiana acuminata.

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing
transgenic plants with improved characteristics such as resistance to
pathogens

PS Example 9: Page 51; 102pp; English.

CC Isolated regulatory sequences of plants that are operable in
dividing cells, in particular the meristem cells of plants are useful

CC in the genetic engineering of plants. The regulatory sequences can
be used to control the expression of foreign genes placed under their

CC control. Such methods are useful for producing transgenic plants with
altered shape and/or size. The sequences are also useful for

CC producing transgenic plants capable of rapid regeneration following
harvest or plants having improved resistance to pathogens. This

CC sequence has been shown to regulate nitrate metabolism in the
fungus Neurospora crassa. It occurs multiple times in the meristem

CC regulatory sequence of Tobacco described in GENESCO record AA293567.

CC Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

OY 1 c 1
Db 4 c 4

RESULT 42

AA289330

ID AA289330 standard; DNA: 5 BP.

AC AA289330;

DT 13-JUN-2000 (first entry)

DE Human UCP3 promoter fragment #10.

KW UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;

XX fat metabolism; ss.

OS Homo sapiens.

PN DE19838837-A1.

PD 02-MAR-2000.

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 c 2
Search completed: July 15, 2002, 23:10:11
Job time: 18429 sec

OY 1 c 1
Db 5 c 5

RESULT: 45

AA248433
ID AA248433 standard; DNA: 5 BP.

XX
AC AA248433;

XX
DT 27-MAR-2000 (first entry)

XX
DE First DNA arm segment.

XX
KW Microorganism; virus; polymerase chain reaction; food; cosmetic;
XX clinical diagnostic; molecular beacon; PCR primer; ss.

OS Synthetic.

XX
PN WO9963112-A2.

XX
PD 09-DEC-1999.

XX
PF 18-MAY-1999; 99WO-US10940.

XX
PR 18-MAY-1998; 98US-0086025.

XX
PR 17-MAY-1999; 99US-0086025.

XX
PA (HUNT-) HUNT WESSON INC.

XX
PI Romick TL, Fraser MS;

XX
DR WPI: 2000-086985/07.

XX
PT Detection of microorganisms and viruses, for use in the food and
XX cosmetic industries and for clinical diagnostics

XX
PS Claim 51: Page 40; 63pp; English.

XX
CC The invention provides a novel in vitro method for the detection of
CC microorganisms and viruses. The method comprises: (1) forming a
CC polymerase chain reaction (PCR) mixture by combining a predetermined
CC volume of a sample to be tested for the presence of a nucleic acid
CC sequence comprising 5'-TAGAACC-3', known amounts of a first primer
CC comprising 5'-GCTAAGTCCCAAGT-3', and a second primer comprising
CC 5'-AGAACCTCTCCACC-3', and PCR reagents; (2) forming a PCR product by
CC cycling the PCR mixture to amplify the nucleic acid sequence; (3)
CC to replicate and attain 0.25-1000nmg nucleotide product/ml mixture; (3)
CC adding a probe containing DNA comprising 5'-GGTGGCTCTTACCCACC-3' to
CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
CC the nucleic acid sequence, if present, and change the conformation of the
CC sample by detecting the conformational change of the probe; and
CC conformational change indicating the presence of bacteria in the sample.
CC The methods can be used for the detection of viruses and microorganisms,
CC including bacteria, yeast, molds and protozoa. They can be used in the
CC food and cosmetic industry and in clinical diagnostics. Using the method
CC it is not necessary to remove non-hybridized probe from the system.
XX
SO Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:38 ; Search time 223.79 Seconds
(without alignments)
1.098 Million cell updates/sec

Title: US-09-375-248-1_COPY_3360_3360

Perfect score: 1 c 1

Sequence: 1 c 1

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents_NA: *
1: /cgn2_6/prodata/2/1na/5A.COMB.seq: *
2: /cgn2_6/prodata/2/1na/5B.COMB.seq: *
3: /cgn2_6/prodata/2/1na/6A.COMB.seq: *
4: /cgn2_6/prodata/2/1na/6B.COMB.seq: *
5: /cgn2_6/prodata/2/1na/PCRTUS.COMB.seq: *
6: /cgn2_6/prodata/2/1na/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	1	100.0	2	1 US-08-268-679B-8	Sequence 8, Appl
C 2	1	100.0	2	1 US-08-484-192-16	Sequence 16, Appl
C 3	1	100.0	2	4 US-08-361-024-3	Sequence 3, Appl
C 4	1	100.0	2	4 US-08-361-024-3	Sequence 3, Appl
C 5	1	100.0	3	1 US-07-791-213D-46	Sequence 46, Appl
C 6	1	100.0	3	1 US-07-791-213D-46	Sequence 46, Appl
C 7	1	100.0	3	1 US-07-791-213D-62	Sequence 62, Appl
C 8	1	100.0	3	1 US-07-791-213D-62	Sequence 62, Appl
C 9	1	100.0	3	1 US-08-268-679B-7	Sequence 7, Appl
C 10	1	100.0	3	1 US-08-602-036A-2	Sequence 2, Appl
C 11	1	100.0	3	1 US-08-602-036A-2	Sequence 2, Appl
C 12	1	100.0	3	1 US-08-293-150A-46	Sequence 46, Appl
C 13	1	100.0	3	1 US-08-293-150A-46	Sequence 46, Appl
C 14	1	100.0	3	1 US-08-293-150A-62	Sequence 62, Appl
C 15	1	100.0	3	1 US-08-293-150A-62	Sequence 62, Appl
C 16	1	100.0	3	2 US-08-502-374A-2	Sequence 2, Appl
C 17	1	100.0	3	2 US-08-502-374A-2	Sequence 2, Appl
C 18	1	100.0	3	2 US-08-642-407A-2	Sequence 2, Appl
C 19	1	100.0	3	2 US-08-642-407A-2	Sequence 2, Appl
C 20	1	100.0	3	3 US-08-873-709-9	Sequence 9, Appl
C 21	1	100.0	3	3 US-09-032-365A-36	Sequence 36, Appl
C 22	1	100.0	3	4 US-08-793-634B-12	Sequence 12, Appl
C 23	1	100.0	3	4 US-08-793-634B-12	Sequence 12, Appl
C 24	1	100.0	4	1 US-07-755-462-2	Sequence 55, Appl
C 25	1	100.0	4	1 US-07-755-462-2	Sequence 55, Appl
C 26	1	100.0	4	1 US-08-169-950-6	Sequence 6, Appl
C 27	1	100.0	4	1 US-08-169-950-6	Sequence 6, Appl

C 28	1	100.0	4	1 US-07-630-288A-7	Sequence 7, Appl
C 29	1	100.0	4	1 US-07-630-288A-11	Sequence 11, Appl
C 30	1	100.0	4	1 US-07-630-288A-11	Sequence 11, Appl
C 31	1	100.0	4	1 US-07-630-288A-13	Sequence 13, Appl
C 32	1	100.0	4	1 US-07-630-288A-13	Sequence 13, Appl
C 33	1	100.0	4	1 US-07-630-288A-14	Sequence 14, Appl
C 34	1	100.0	4	1 US-07-630-288A-14	Sequence 14, Appl
C 35	1	100.0	4	1 US-07-630-288A-34	Sequence 34, Appl
C 36	1	100.0	4	1 US-07-630-288A-34	Sequence 34, Appl
C 37	1	100.0	4	1 US-08-126-594-25	Sequence 25, Appl
C 38	1	100.0	4	1 US-08-126-594-25	Sequence 25, Appl
C 39	1	100.0	4	1 US-08-188-943-1	Sequence 1, Appl
C 40	1	100.0	4	1 US-08-188-943-1	Sequence 1, Appl
C 41	1	100.0	4	1 US-08-188-943-2	Sequence 2, Appl
C 42	1	100.0	4	1 US-08-188-943-2	Sequence 2, Appl
C 43	1	100.0	4	1 US-08-465-811A-25	Sequence 25, Appl
C 44	1	100.0	4	1 US-08-465-811A-25	Sequence 25, Appl
C 45	1	100.0	4	1 US-08-199-317-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-268-679B-8/C
Sequence 8, Application US/08268679B
Patent No. 5674729
GENERAL INFORMATION:
APPLICANT: WIMMER, ECKARD; MOLLA,
AKHTERUZZAMAN; PAUL, ANIKO V.
TITLE OF INVENTION: DE NOVO CELL-FREE
SYNTHESIS OF SEQUENCES: 8
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,679B
FILING DATE: 30-JUN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/846,914
FILING DATE: 06-MAR-1992
CLASSIFICATION: 435
APPLICATION NUMBER: 07/19,761
FILING DATE: 24-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C. H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 0887-4095 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6649
TELEX: 421792
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE: N.A.

POSITION IN GENOME: N.A.
US-08-268-6798-8

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
Db 2 c 2

RESULT 2

US-08-484-192-16/c
Sequence 16, Application US/08484192
Patent No. 5756291
GENERAL INFORMATION:
APPLICANT: GRIFFIN, LINDA C.
APPLICANT: ALBRECHT, GLENN
APPLICANT: LATHAM, JOHN
APPLICANT: LEUNG, LAWRENCE
APPLICANT: VERMAAS, ERIC
APPLICANT: TOOLE, JOHN J.
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
TITLE OF INVENTION: METHODS OF MAKING
NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,192
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/934,387
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 246102002221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc-difference
LOCATION: replace(1, "")
OTHER INFORMATION: /note="This is a biotin-17
US-08-484-192-16
OTHER INFORMATION: nucleotide stretch of abasic residues."

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1

Db 2 c 2

RESULT 3
US-08-361-024-3
Sequence 3, Application US/08361024
Patent No. 6207368
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
TITLE OF INVENTION: Method, Reagent and Kit
TITLE OF INVENTION: for Detection and
TITLE OF INVENTION: Amplification of
TITLE OF INVENTION: Nucleic Acid Sequence
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
COUNTRY: USA
ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch,
MEDIUM TYPE: 1.44 Mb
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,024
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/925,059
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Burgoon, Richard P.
REGISTRATION NUMBER: 34,787
REFERENCE/DOCKET NUMBER: 128D-126
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: yes
ANTI-SENSE: no
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
Db 2 c 2

RESULT 4
US-08-361-024-3/c
Sequence 3, Application US/08361024
Patent No. 6207368
GENERAL INFORMATION:
APPLICANT: Adams, Craig W.
TITLE OF INVENTION: Method, Reagent and Kit
TITLE OF INVENTION: for Detection and
TITLE OF INVENTION: Amplification of
TITLE OF INVENTION: Nucleic Acid Sequence

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
COUNTRY: USA
ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,024
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/925,059
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Burgoon, Richard P.
REGISTRATION NUMBER: 34,787
REFERENCE/DOCKET NUMBER: 128D-126
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: yes
ANTI-SENSE: no
US-08-361-024-3

Query Match
Best Local Similarity 100.0%; Score 1; DB 4; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 5
US-07-791-213D-46
Sequence 46, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 3 C 3

RESULT 6
US-07-791-213D-46/C
Sequence 46, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

;; INFORMATION FOR SEQ ID NO: 46:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 7
US-07-791-213D-62
; Sequence 62, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 C 1
Db 2 C 2

Db 3 C 3

RESULT 8
US-07-791-213D-62/c
; Sequence 62, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 9
US-08-268-679B-7/c
; Sequence 7, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD; MULLA,
; APPLICANT: AKHTERUZZAMAN; PAUL, ANIRO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; TITLE OF INVENTION: SYNTHESIS PICO RNA VIRUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,679B
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07\846,914
FILING DATE: 06-MAR-1992
CLASSIFICATION: 435
APPLICATION NUMBER: 07\719,761
FILING DATE: 24-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C.H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 0887-4095 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE: N.A.
POSITION IN GENOME: N.A.
US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 3 C 3

RESULT 10
US-08-602-036A-2
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Podstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 3 C 3

RESULT 11
US-08-602-036A-2/c
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Podstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 C 1
Db 3 C 3

RESULT 17
US-08-502-374A-2/C
Sequence 2, Application US/08502374A
Patent No. 5872007
GENERAL INFORMATION:
APPLICANT: Fodstad, Oeystein
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,374A
FILING DATE: 14-Jul-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO

ANTI-SENSE: YES
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 18
US-08-642-407A-2
Sequence 2, Application US/08642407A
Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 3 C 3

RESULT 19
US-08-642-407A-2/C
Sequence 2, Application US/08642407A

Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Eivind
APPLICANT: Engebraten, Olav
APPLICANT: Maelandmo, Gunnild H.
APPLICANT: Agraewal, Sudhir
TITLE OF INVENTION: CARL SPECIFIC OLIGONUCLEOTIDES AND
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Keirner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 20
US-08-873-709-9/c
Sequence 9, Application US/08873709
Patent No. 6037126
GENERAL INFORMATION:
APPLICANT: Grossman, Abraham
TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND
TITLE OF INVENTION: APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF
TITLE OF INVENTION: PROTEIN COMPONENT OF TELOMERASE ENZYME
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abraham Grossman
STREET: 666 Washington Avenue
CITY: Pleasantville
STATE: NY
COUNTRY: USA
ZIP: 10570
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,709
FILING DATE: 12-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Janluk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: 0001/002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-747-9108
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-873-709-9

Query Match 100.0%; Score 1; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 3 C 3

RESULT 21
US-09-032-365A-36/c
Sequence 36, Application US/09032365A
Patent No. 6114502
GENERAL INFORMATION:
APPLICANT: No. 6114502th, Michael
APPLICANT: Nishina, Patsy
APPLICANT: Nagart, Juergen
APPLICANT: No. 6114502en-Trauth, Konrad
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
TITLE OF INVENTION: NEUROSENSORY DEFECTS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-2C1P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:

LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-032-365A-36

Query Match 100.0%: Score 1; DB 3; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 3 C 3

RESULT 22
US-08-793-634B-12/C
Sequence 12, Application US/08793634B
Patent No. 6211431
GENERAL INFORMATION:
APPLICANT: Boevink, Petra C.
APPLICANT: Surin, Brian P.
APPLICANT: Keese, Paul K.
APPLICANT: Chu, Paul W.G.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Khen, Rafiqul I.
APPLICANT: Larkin, Phillip J.
APPLICANT: Taylor, William C.
APPLICANT: Marshall, Jerry S.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,634B
FILING DATE: June 9, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10530
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-793-634B-12

Query Match 100.0%: Score 1; DB 4; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 C 1
DB 2 C 2

RESULT 23
US-08-973-568-55/C
Sequence 55, Application US/08973568B
Patent No. 6277634
GENERAL INFORMATION:
APPLICANT: McCall, Maxine J.
APPLICANT: Hendry, Phillip
APPLICANT: Lockett, Trevor
TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF
FILE REFERENCE: 47203bpcus
CURRENT APPLICATION NUMBER: US/08/973,568B
CURRENT FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 3
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
FEATURE:
OTHER INFORMATION: Synthetic Ribozyme or portion thereof
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
US-08-973-568-55

Query Match 100.0%: Score 1; DB 4; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 24
US-07-755-462-2
Sequence 2, Application US/07755462
Patent No. 5273881
GENERAL INFORMATION:
APPLICANT: Seng, Elissa P.
APPLICANT: Calhoun, Cornelia J.
APPLICANT: Zarling, David A.
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,462
FILING DATE: 19910904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4255-0001.30
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 4 C 4

RESULT 25
US-07-755-462-2/c
Sequence 2, Application US/07755462
Patent No. 5273881
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calhoun, Cornelia J.
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
TITLE OF INVENTION: Formation
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755.462
FILING DATE: 19910904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4255-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 26
US-08-169-950-6
Sequence 6, Application US/08169950
Patent No. 5366882
GENERAL INFORMATION:
APPLICANT: LUNNEN, KEITH D.
APPLICANT: WILSON, GEOFFREY G.
TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI
TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,950
FILING DATE: 17-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 3 C 3

RESULT 27
US-08-169-950-6/c
Sequence 6, Application US/08169950
Patent No. 5366882
GENERAL INFORMATION:
APPLICANT: LUNNEN, KEITH D.
APPLICANT: WILSON, GEOFFREY G.
TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI
TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,950
FILING DATE: 17-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 2 C 2

RESULT 28
US-07-630-288A-7/C
Sequence 7, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-7

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 29
US-07-630-288A-11
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 4 C 4

RESULT 30
US-07-630-288A-11/C
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Giesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Giesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 4 C 4

Db 1 C 1

RESULT 31
US-07-630-288A-13/C
Sequence 13, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Giesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Giesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-13

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 4 C 4

RESULT 32
US-07-630-288A-14
Sequence 14, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Giesser

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 3 C 3

RESULT 33
US-07-630-288A-14/C
Sequence 14, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 2 C 2

RESULT 34
US-07-630-288A-34
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1
Db 4 C 4

RESULT 35
US-07-630-288A-34/C
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glessner
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glessner, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1
Db 2 C 2

RESULT 36
US-08-126-594-25
Sequence 25, Application US/08126594
Patent No. 5482845
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Estratiadis, Algis
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1
Db 1 C 1

RESULT 37
US-08-126-594-25/C
Sequence 25, Application US/08126594
Patent No. 5482845
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Estratiadis, Algis
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 3 C 3

RESULT 38
US-08-188-943-1
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudbande, Satyanarayana R.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 4 C 4

RESULT 39
US-08-188-943-1/C
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudbande, Satyanarayana R.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 C 1
1
Db 3 C 3

RESULT 40

US-08-188-943-2
Sequence 2, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-2

Query Match 100.0%; Score 1: DB 1: Length 4:
Best Local Similarity 100.0%; Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 C 1
1
Db 2 C 2

RESULT 41

US-08-188-943-2/C
Sequence 2, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-2

Query Match 100.0%; Score 1: DB 1: Length 4:
Best Local Similarity 100.0%; Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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Db 1 C 1

RESULT 42
US-08-465-811A-25
Sequence 25, Application US/08465811A
Patent No. 5637685
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstratiadis, Argiris
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,811A
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JPM/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 43
US-08-465-811A-25/C
Sequence 25, Application US/08465811A
Patent No. 5637685
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Estratiadis, Argiris
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,811A
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPM/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 C 3

RESULT 44
US-08-199-317-2
Sequence 2, Application US/08199317
Patent No. 5670316
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calhoun, Cornelia J.
APPLICANT: Zarling, David A.
TITLE OF INVENTION: Diagnostic Applications of Double D-loop
TITLE OF INVENTION: Formation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,317
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,791
FILING DATE: 09-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,462
FILING DATE: 04-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 9150-0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for Dpn I
US-08-199-317-2

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-08-199-317-2/C
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: Patent No. 5670316
: GENERAL INFORMATION:
: APPLICANT: Sena, Elissa P.
: APPLICANT: Calhoun, Cornelia J.
: APPLICANT: Zarling, David A.
: TITLE OF INVENTION: Diagnostic Applications of Double D-loop
: TITLE OF INVENTION: Formation
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Ave., Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/199,317
: FILING DATE: 25-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/910,791
: FILING DATE: 09-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/755,462
: FILING DATE: 04-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/520,321
: FILING DATE: 07-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Stratford, Carol A.
: REGISTRATION NUMBER: 34,444
: REFERENCE/DOCKET NUMBER: 9150-0004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-324-0880
: TELEFAX: 415-324-0960
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Cleavage site for Dpn I
: US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 C 1
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Search completed: July 15, 2002, 23:07:38
Job time: 22991 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:25 ; Search time 12941.8 Seconds
(without alignments)
1.672 Million cell updates/sec

Title: US-09-375-248-1-COPY_3360_3360
Sequence: 1 c 1

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Word size : 0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	100.0	1	2	16 US-09-284-725-201	Sequence 201, App
6	100.0	1	2	17 US-09-306-333A-32	Sequence 32, App1
7	100.0	1	2	17 US-09-387-777-2	Sequence 2, App1
8	100.0	1	2	17 US-09-387-777-3	Sequence 3, App1
9	100.0	1	2	17 US-09-387-777-5	Sequence 5, App1
10	100.0	1	2	17 US-09-387-777-6	Sequence 6, App1
11	100.0	1	2	17 US-09-387-777-7	Sequence 7, App1
12	100.0	1	2	17 US-09-387-777-8	Sequence 8, App1
13	100.0	1	2	17 US-09-387-777-9	Sequence 9, App1
14	100.0	1	2	17 US-09-387-777-10	Sequence 10, App1
15	100.0	1	2	17 US-09-387-777-11	Sequence 11, App1
16	100.0	1	2	17 US-09-387-777-12	Sequence 12, App1
17	100.0	1	2	17 US-09-387-777-13	Sequence 13, App1
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C 36 1 100.0 2 24 US-09-634-306B-175426 Sequence 175426,
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C 39 1 100.0 2 24 US-09-634-306B-175449 Sequence 175449,
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ALIGNMENTS

RESULT 1
US-07-934-385-14/C
; Sequence 14, Application US/07934385
; GENERAL INFORMATION:
; APPLICANT: LATNAM, JOHN
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES
; CONTAINING MODIFIED NUCLEOTIDE RESIDUES
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,385
; FILING DATE: 19920821
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 24610-20022.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc,difference
; LOCATION: replace(1, "")
; OTHER INFORMATION: /note= "This position is a
; OTHER INFORMATION: biotin-17 nucleotide stretch of random sequences."
US-07-934-385-14

Query Match 100.0%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 c 1
Db 2 c 2

RESULT 2
US-08-107-721-46/C
; Sequence 46, Application US/08107721
; GENERAL INFORMATION:
; APPLICANT: TOOLE, JOHN J.
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: BOCK, LOUIS C.
; APPLICANT: LATNAM, JOHN A.
; APPLICANT: MUENCHAU, DARYL D.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; METHODS OF MAKING
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GILEAD SCIENCES, INC.
; STREET: 344 LAKEVIEW DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,721
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28216
; REFERENCE/DOCKET NUMBER: 24610-20022.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)574-3000
; TELEFAX: (415)578-9264
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc,feature
; LOCATION: 1
; OTHER INFORMATION: /note= "This is a biotin-17
; OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-107-721-46

Query Match 100.0%; Score 1; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 c 1
Db 2 c 2

RESULT 3
US-08-107-721B-46/C
; Sequence 46, Application US/08107721B
; GENERAL INFORMATION:
; APPLICANT: TOOLE, JOHN J.
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: BOCK, LOUIS C.
; APPLICANT: LATNAM, JOHN A.
; APPLICANT: MUENCHAU, DARYL D.
; APPLICANT: KRAMCZYK, STEVEN
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; METHODS OF MAKING

```

: NUMBER OF SEQUENCES: 109
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GILEAD SCIENCES, INC.
: STREET: 344 LAKESIDE DRIVE
: CITY: FOSTER CITY
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94404
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/08/107,721B
: FILING DATE: 20-AUG-1993
: CLASSIFICATION: 415
: ATTORNEY/AGENT INFORMATION:
: NAME: GRACEY, NANCY J.
: REGISTRATION NUMBER: 28216
: REFERENCE/DOCKET NUMBER: 24610-20022.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)574-3000
: TELEFAX: (415)578-9264
: INFORMATION FOR SEQ ID NO: 46:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1
: OTHER INFORMATION: /note="This is a biotin-17
: OTHER INFORMATION: nucleotide stretch of abasic residues."
:
: US-08-107-721B-46

```

```

Query Match          100.0%; Score 1; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 c 1
Db 2 c 2

RESULT 4
US-09-172-828-15/c
: Sequence 15, Application US/09172828
: GENERAL INFORMATION:
: APPLICANT: Children's Medical Center Corporation
: APPLICANT: Klagsbrun, Michael
: APPLICANT: Elenius, Klaus
: APPLICANT: Corfas, Gabriel
: TITLE OF INVENTION: Novel Human EGF Receptors and Use
: FILE REFERENCE: 47758-PCT
: CURRENT APPLICATION NUMBER: US/09/172,828
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 15
: LENGTH: 2
: TYPE: DNA
: ORGANISM: mouse
:
: US-09-172-828-15

```

```

Query Match          100.0%; Score 1; DB 15; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 c 1
Db 1 c 1

```

```

RESULT 5
US-09-284-725-201
: Sequence 201, Application US/09284725
: GENERAL INFORMATION:
: APPLICANT: Quint, Wilhelmus
: APPLICANT: Van Doorn, Leenderl
: TITLE OF INVENTION: Probes, methods and kits for detection and
: TITLE OF INVENTION: typing of Helicobacter pylori nucleic acids in biological
: TITLE OF INVENTION: samples.
: NUMBER OF SEQUENCES: 280
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
: STREET: 620 Newport Center Drive, 16th floor
: CITY: Newport Beach
: STATE: CA
: COUNTRY: USA
: ZIP: 92660
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/284,725
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: EP96/870131.8
: FILING DATE: 16-OCT-1996
: APPLICATION NUMBER: PCT/EP97/05614
: FILING DATE: 10-OCT-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Altman, Daniel E.
: REGISTRATION NUMBER: 34,115
: REFERENCE/DOCKET NUMBER: INNOG2.001APC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (949) 760-0404
: TELEFAX: (949) 760-9395
: INFORMATION FOR SEQ ID NO: 201:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
:
: US-09-284-725-201

```

```

Query Match          100.0%; Score 1; DB 16; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 c 1
Db 2 c 2

```

```

RESULT 6
US-09-306-333A-32
: Sequence 32, Application US/09306333A
: GENERAL INFORMATION:
: APPLICANT: Academy of Applied Science
: TITLE OF INVENTION: BRCA1 and hMLH1 Gene Primer Sequences and Method for
: TITLE OF INVENTION: Testing
: FILE REFERENCE: BRCA1
: CURRENT APPLICATION NUMBER: US/09/306,333A
: CURRENT FILING DATE: 1999-05-06

```


PRIOR APPLICATION NUMBER: PCT/1B00/01607
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 2
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-333A-32

Query Match 100.0% Score 1: DB 17: Length 2:
Best Local Similarity 100.0% Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
Db 1 c 1

RESULT 7
US-09-306-333A-32/C
Sequence 32, Application US/09306333A
GENERAL INFORMATION:
APPLICANT: Academy of Applied Science
TITLE OF INVENTION: BRCAL and hMLH1 Gene Primer Sequences and Method for
TITLE OF INVENTION: Testing
FILE REFERENCE: BRCAL
CURRENT APPLICATION NUMBER: US/09/306.333A
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: PCT/1B00/01607
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 122
SUBTITLE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 2
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-333A-32

Query Match 100.0% Score 1: DB 17: Length 2:
Best Local Similarity 100.0% Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
Db 2 c 2

RESULT 8
US-09-387-777-2
Sequence 2, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kiess
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman C/O Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead-Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-2

Query Match 100.0% Score 1: DB 17: Length 2:
Best Local Similarity 100.0% Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
Db 2 c 2

RESULT 9
US-09-387-777-3/C
Sequence 3, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kiess
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman C/O Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead-Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-1

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 2 C 2

RESULT 10
US-09-387-777-5
Sequence 5, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimole-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-5

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 11

US-09-387-777-6
Sequence 6, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimole-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-6

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 12
US-09-387-777-7
Sequence 7, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Klees
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

```
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-7

Query Match      100.0%  Score 1: DB 17: Length 2:
Best local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 1 C 1
Db 1 C 1

RESULT 13
US-09-387-777-7/C
: Sequence 7, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Klees
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-387-777-7

Computer Readable Form:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-7

Query Match      100.0%  Score 1: DB 17: Length 2:
Best local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Caps 0:
```

```
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-7

Query Match      100.0%  Score 1: DB 17: Length 2:
Best local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 1 C 1
Db 2 C 2

RESULT 14
US-09-387-777-8
: Sequence 8, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Klees
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-387-777-8

Computer Readable Form:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-8

Query Match      100.0%  Score 1: DB 17: Length 2:
Best local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Caps 0:
```

Db 1 C 1

RESULT 15

US-09-387-777-9/c

Sequence 9, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESS: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-562553

TELEFAX: 972-3-562554

TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-9

Query Match

Best Local Similarity 100.0%; Score 1; DB 17; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

Db 1 C 1

RESULT 16

US-09-387-777-10

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESS: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-562553

TELEFAX: 972-3-562554

TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-9

Query Match

Best Local Similarity 100.0%; Score 1; DB 17; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

Db 1 C 1

RESULT 17

US-09-387-777-10/c

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESS: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-562553

TELEFAX: 972-3-562554

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-10

Query Match

Best Local Similarity 100.0%; Score 1; DB 17; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

Db 2 C 2

ATTORNEY/AGENT INFORMATION:
NAME: Friedmann, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-10

Query Match
Best Local Similarity 100.0%; Score 1: DB 17; Length 2:
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 18
US-09-387-777-11/C
SEQUENCE 11, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedmann C/O Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedmann, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-11

Query Match
Best Local Similarity 100.0%; Score 1: DB 17; Length 2:
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 2 C 2

RESULT 19
US-09-387-777-12/C
SEQUENCE 12, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedmann C/O Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedmann, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-12

Query Match
Best Local Similarity 100.0%; Score 1: DB 17; Length 2:
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 20
US-09-387-777-14
SEQUENCE 14, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-14

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 21
US-09-387-777-15/C
Sequence 15, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-15

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 22
US-09-472-035A-19/C
Sequence 19, Application US/09472035A
GENERAL INFORMATION:
APPLICANT: Yechezkel Kashi et al.
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
SOFTWARE: an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472,035A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 74/77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-472-035A-19

Query Match
Best Local Similarity 100.0%; Score 1: DB 18: Length 2:
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 C 1
Db 1 C 1

RESULT 23
US-09-472-035A-20
Sequence 20, Application US/09472035A
GENERAL INFORMATION:
APPLICANT: Yechezkel Kashi et al.
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
NUMBER OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
CORRESPONDENCE ADDRESS: 42
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead Slimote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472,035A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 74/77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-472-035A-20

Query Match
Best Local Similarity 100.0%; Score 1: DB 18: Length 2:
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 C 1
Db 2 C 2
RESULT 24

US-09-634-306B-51869
Sequence 51869, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51869
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-51869

Query Match
Best Local Similarity 100.0%; Score 1: DB 24: Length 2:
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 C 1
Db 2 C 2

RESULT 25
US-09-634-306B-52280
Sequence 52280, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52280
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-52280

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 c 1
Db 2 c 2

RESULT 26
US-09-634-306B-52357
; Sequence 52357, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 52357
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52357

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 c 1
Db 2 c 2

RESULT 27
US-09-634-306B-53003
; Sequence 53003, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 53003
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-53003

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 c 1
Db 1 c 1

RESULT 28
US-09-634-306B-58305
; Sequence 58305, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 58305
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58305

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 c 1
Db 1 c 1

RESULT 29
US-09-634-306B-175312/c
; Sequence 175312, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21


```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175312
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```

RESULT 30
US-09-634-306B-175337/c
; Sequence 175337, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175337
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```

RESULT 31
US-09-634-306B-175354/c
; Sequence 175354, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175354
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```

RESULT 32
US-09-634-306B-175401/c
; Sequence 175401, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
```

US-09-634-306B-175401

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 33

US-09-634-306B-175403/c
; Sequence 175403, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175403

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 34

US-09-634-306B-175415/c
; Sequence 175415, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175415

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 35

US-09-634-306B-175419/c
; Sequence 175419, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175419

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 36

US-09-634-306B-175426/c
; Sequence 175426, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

```

: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175426
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175426
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```

RESULT 37
US-09-634-306B-175433/c
: Sequence 175433, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175433
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175433
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```

Db 1 c 1
RESULT 38
US-09-634-306B-175849/c
: Sequence 175849, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175849
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 2 c 2
```

```

RESULT 39
US-09-634-306B-176848/c
: Sequence 176848, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176848
: LENGTH: 2
```

TYPE: DNA
ORGANISM: Human
US-09-634-306B-176848

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 40
US-09-634-306B-176849/c
Sequence 176849, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176849
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-176849

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 41
US-09-634-306B-176880/c
Sequence 176880, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176880
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-176880

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 42
US-09-634-306B-178420/c
Sequence 178420, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 178420
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-178420

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 1 C 1

RESULT 43
US-09-634-306B-178440
Sequence 178440, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

1  TITLE OF INVENTION: Polymorphisms in the Human Genome
2  FILE REFERENCE: 108827.129
3  CURRENT APPLICATION NUMBER: US/09/634,306B
4  PRIOR FILING DATE: 2002-02-21
5  PRIOR APPLICATION NUMBER: US 60/218,006
6  PRIOR FILING DATE: 2000-07-12
7  PRIOR APPLICATION NUMBER: US 60/198,676
8  PRIOR FILING DATE: 2000-04-20
9  PRIOR APPLICATION NUMBER: US 60/193,483
10 PRIOR FILING DATE: 2000-03-29
11 PRIOR APPLICATION NUMBER: US 60/185,218
12 PRIOR FILING DATE: 2000-02-24
13 PRIOR APPLICATION NUMBER: US 60/167,363
14 PRIOR FILING DATE: 1999-11-23
15 PRIOR APPLICATION NUMBER: US 60/156,358
16 PRIOR FILING DATE: 1999-09-28
17 PRIOR APPLICATION NUMBER: US 60/146,002
18 PRIOR FILING DATE: 1999-08-09
19 NUMBER OF SEQ ID NOS: 325720
20 SOFTWARE: FastSPU for Windows Version 4.0
21 SEQ ID NO 178440
22 LENGTH: 2
23 TYPE: DNA
24 ORGANISM: Human
US-09-634-306B-178440

```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Gaps 0;
```

```

RESULT 44
US-09-634-3068-178440/C
: Sequence 178440, Application US/096343068
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634, 3068
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-26
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178440
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-3068-178440

```

Qy	1	c	1
		1	
Db	1	c	1

```

RESULT 45
US-09-634-3068-178617/c
: Sequence 178617, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: POLYMORPHISMS IN THE HUMAN GENOME
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634.306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178617
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-3068-178617

```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches      1; Conservative 0; Mismatches 0; Indels 0; Caps 0
```

Search completed: July 16, 2002, 02:50:26
Job time: 31279 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:10:11 ; Search time 932.4 Seconds

(without alignments)
1.841 Million cell updates/sec

Title: US-09-375-248-1_COPY_3150_3150
Perfect score: 1

Sequence:

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

word size : 0

Total number of hits satisfying chosen parameters: 3472872

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

```

Maximum DB seq length: 20000000000

post-processing: Listing first 45 summaries

Database :

```
1: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseqn -emb1/NA2002.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	1	100.0	3	17	AAT33326	CAPL trinucleotide repeat expansion
	2	1	100.0	3	22	AAI20244	Human breast cancer gene expression profile
c	3	1	100.0	3	22	AAI20244	Human breast cancer gene expression profile
	4	1	100.0	4	16	AAO81664	BEGF binding oligo probe for target n immunostimulatory protein
c	5	1	100.0	4	16	AAO81665	BEGF binding oligo probe for target n immunostimulatory protein
c	6	1	100.0	4	18	AAT86385	Immunostimulatory peptide sequence derived from human breast cancer tissue
	7	1	100.0	4	18	AAT77252	Immunostimulatory peptide sequence derived from human breast cancer tissue
c	8	1	100.0	4	18	AAT77252	Immunostimulatory peptide sequence derived from human breast cancer tissue
	9	1	100.0	4	22	AAI17191	Human Breast Cancer Gene Expression Profile

C	10	1	100.0	4	22	AA117191	Human breast cancer
C	11	1	100.0	4	22	AA124357	Human breast cancer
C	12	1	100.0	4	22	AA161450	Cyclin binding ham
C	13	1	100.0	5	10	AA193676	Synthetic probe fo
C	14	1	100.0	5	10	AA193676	Synthetic probe fo
C	15	1	100.0	5	15	AA068752	CHAZ25 heavy chain
C	16	1	100.0	5	16	AA081667	bcrf binding oligo
C	17	1	100.0	5	16	AA081667	bcrf binding oligo
C	18	1	100.0	5	16	AA081666	bcrf binding oligo
C	19	1	100.0	5	16	AA081666	bcrf binding oligo
C	20	1	100.0	5	17	AA112043	Cleavable replicab
C	21	1	100.0	5	19	AA161663	Fusarium sp. 18S r
C	22	1	100.0	5	19	AA161663	Fusarium sp. 18S r
C	23	1	100.0	5	19	AA196299	Fungal telomeric n
C	24	1	100.0	5	20	AA210695	Oligonucleotide se
C	25	1	100.0	5	20	AA210695	Oligonucleotide se
C	26	1	100.0	5	20	AA210696	Oligonucleotide se
C	27	1	100.0	5	20	AA210696	Oligonucleotide se
C	28	1	100.0	5	20	AA211611	DNA enhancer sequ
C	29	1	100.0	5	20	AA211611	DNA enhancer sequ
C	30	1	100.0	5	20	AA172347	US5008745 primer #
C	31	1	100.0	5	20	AA172348	US5008745 primer #
C	32	1	100.0	5	20	AA172349	US5008745 primer #
C	33	1	100.0	5	20	AA172350	US5008745 primer #
C	34	1	100.0	5	20	AA156964	US5008745 primer #
C	35	1	100.0	5	20	AA156964	Ras gene modulat
C	36	1	100.0	5	21	AA156981	Mutant H-ras speci
C	37	1	100.0	5	21	AA293601	Human colon cancer
C	38	1	100.0	5	21	AA293602	Transcription fact
C	39	1	100.0	5	21	AA293602	Transcription fact
C	40	1	100.0	5	21	AA293603	Transcription fact
C	41	1	100.0	5	21	AA293603	Transcription fact
C	42	1	100.0	5	21	AA289330	Human UCP3 promote
C	43	1	100.0	5	21	AA289330	Human UCP3 promote
C	44	1	100.0	5	21	AA289331	Human UCP3 promote
C	45	1	100.0	5	21	AA289331	Human UCP3 promote

ALIGNMENTS

RESULT 1
AAT33326

ID	AAAT33326 standard; RNA; 3 BP.
XX	

AC AAT33326;

DT 12-NOV-1996 (first entry)
XX

DE CAPL trinucleotide.

KW CAPL; antisense oligonucle

osteosarcoma; therapy; ss.

OS v/v	Synthetic
-----------	-----------

PN W09625499-A1.

PD 22-AUG-1996.

PF 16-FEB-1996; 96WO-US02108.

PR 17-FEB-1995; 95US-0391375.
.....

PA (HYBR-) HYBRIDON INC.

AMERICAN MONTESSORI HOSPITAL RES. FOUND.

	Eingezeichnet O,	Fodstad O,	Hovig E,	Maelandsmo GJ;
Pf	Von Hofe E;			

WPI; 1996-393400/39.

Synthetic oligo:nuc1

Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -

ID AA081664 standard; RNA; 4 BP.
 XX
 AC AA081664:
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #1.
 XX
 KW Basic: fibroblast growth factor: bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;
 KW metastasis; diagnosis; gene therapy; ss.
 XX
 CS Synthetic.
 XX
 PN MO9500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI: 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 PT factor - modulating, esp. inhibiting, its activity; useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp; English.
 XX
 CC The sequences given in AA081642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC with its receptor and heparin. These oligonucleotides may inhibit
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; length 4;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 ;
 Db 2 u 2

RESULT 5
 ID AA081665 standard; RNA; 4 BP.
 XX
 AC AA081665:
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #2.

XX
 KW Basic: fibroblast growth factor: bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;
 KW metastasis; diagnosis; gene therapy; ss.
 XX
 CS Synthetic.
 XX
 PN MO9500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI: 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 PT factor - modulating, esp. inhibiting, its activity; useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp; English.
 XX
 CC The sequences given in AA081642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC with its receptor and heparin. These oligonucleotides may inhibit
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; length 4;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 ;
 Db 2 u 2

RESULT 6
 ID AAT86385/C
 XX
 AC AAT86385:
 XX
 DT 23-APR-1998 (first entry)
 XX
 DE Probe for target nucleic acid sequence P0.
 XX
 KW Point mutation detection; nucleic acid sequence analysis; probe;
 KW viral disease diagnosis; genetic disease diagnosis; ss.
 XX
 OS Synthetic.
 XX
 FH Key location/Qualifiers

PF	28-JAN-1997;	97WO-US01277.
XX		
PR	30-JAN-1996;	96US-0593554.
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Carson DA, Raz E;	
XX		
DR	WPI: 1997-402613/37.	
XX		
PT	Recombinant vector containing immunostimulatory palindromic	
PT	polynucleotide - useful for selectively enhancing the TH1 immune	
PT	response in a host, whilst reducing the risk of anaphylaxis	
PS	Claim 16; Page 15; 102pp; English.	
CC		
CC	This sequence represents a non-coding immunostimulatory polynucleotide	
CC	(15') comprised of at least one strand of a palindrome, which includes	
CC	at least one dinucleotide consisting of adjacent, unethylated cytosine	
CC	and guanine residues. ISP's could be used used in vaccination methods	
CC	for enhancing the immune response of a host to an antigen. Administration	
CC	of naked gene expression vectors which encode antigens or their	
CC	immunostimulatory fragments suppresses IgE antibody production	
CC	reducing the risk of anaphylaxis posed by conventional immunotherapy.	
XX		
XX		
SQ	Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;	
	Query Match	100.0%; Score 1; DB 18; Length 4;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 t 1	
Db	4 t 4	
	RESULT 8	
ID	AAT77252/C	
XX	AAT77252 standard; DNA; 4 BP.	
XX		
AC	AAT77252;	
XX		
DT	18-MAR-1998 (first entry)	
XX		
DE	Immunostimulatory polynucleotide 11.	
XX		
KW	Immunostimulatory polynucleotide; ISP; palindrome; vaccine;	
KW	immune response; antigen; naked gene expression vector; IgE;	
XX	antibody; immunotherapy; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO9728259-A1.	
XX		
PD	07-AUG-1997.	
XX		
PF	28-JAN-1997; 97WO-US01277.	
XX		
PR	30-JAN-1996; 96US-0593554.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Carson DA, Raz E;	
XX		
DR	WPI: 1997-402613/37.	
XX		
PT	Recombinant vector containing immunostimulatory palindromic	
PT	polynucleotide - useful for selectively enhancing the TH1 immune	
PT	response in a host, whilst reducing the risk of anaphylaxis	
PS	Claim 16; Page 15; 102pp; English.	

CC This sequence represents a non-coding immunostimulatory polynucleotide
CC (ISP) comprised of at least one strand of a palindromic, which includes
CC at least one dinucleotide consisting of adjacent, unmethylated cytosine
CC and guanine residues. ISP's could be used in vaccination methods
CC for enhancing the immune response of a host to an antigen. Administration
CC of naked gene expression vectors which encode antigens or their
CC immunostimulatory fragments suppresses IgE antibody production
CC reducing the risk of anaphylaxis posed by conventional immunotherapy.
X

SU Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 18; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
UB 1 T 1

RESULT 9

AA17191
ID AA17191 standard; cDNA; 4 BP.

XX AA17191;

DT 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 9648.

KW Human; breast cancer; cell marker; cytostatic; ss.

OS Homo sapiens.

PN W0200151628-A2.

PR 19-JUL-2001.

PF 10-JAN-2001; 2001WO-US00798.

PR 14-JAN-2000; 2000US-0176077.

PR 14-MAR-2000; 2000US-0189167.

PR 24-MAR-2000; 2000US-0192099.

PR 29-MAR-2000; 2000US-0193480.

PR 15-MAY-2000; 2000US-0205230.

PR 09-JUN-2000; 2000US-0211315.

PR 25-JUL-2000; 2000US-0220534.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Lillie J, Xu Y, Wang Y, Steinmann K;

DR WPI: 2001-451856/48.

XX New peptide useful as a marker for the diagnosis of breast cancer -

PS Claim 1; Page 1720; 3655pp; English.

CC The invention relates to human breast cancer expressed polynucleotides
CC (AA107544-AA126789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.

SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 4 t 4

RESULT 10

AA17191/c
ID AA17191 standard; cDNA; 4 BP.

XX AA17191;

DT 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 9648.

KW Human; breast cancer; cell marker; cytostatic; ss.

OS Homo sapiens.

PN W0200151628-A2.

PR 19-JUL-2001.

PF 10-JAN-2001; 2001WO-US00798.

PR 14-JAN-2000; 2000US-0176077.

PR 14-MAR-2000; 2000US-0189167.

PR 24-MAR-2000; 2000US-0192099.

PR 29-MAR-2000; 2000US-0193480.

PR 15-MAY-2000; 2000US-0205230.

PR 09-JUN-2000; 2000US-0211315.

PR 25-JUL-2000; 2000US-0220534.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Lillie J, Xu Y, Wang Y, Steinmann K;

DR WPI: 2001-451856/48.

XX New peptide useful as a marker for the diagnosis of breast cancer -

PS Claim 1; Page 1720; 3655pp; English.

CC The invention relates to human breast cancer expressed polynucleotides
CC (AA107544-AA126789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.

SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 2 T 2

RESULT 11

AA124357
ID AA124357 standard; cDNA; 4 BP.

AC AA124357;

XX 07-DEC-2001 (first entry)
DT
XX
DE Human breast cancer expressed polynucleotide 16814.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PP 10-JAN-2001: 2001WO-US00798.
XX
PR 14-JAN-2000: 2000US-0176077.
PR 14-MAR-2000: 2000US-0189167.
PR 24-MAR-2000: 2000US-0192099.
PR 29-MAR-2000: 2000US-0193480.
PR 15-MAY-2000: 2000US-0205230.
PR 09-JUN-2000: 2000US-0211315.
PR 25-JUL-2000: 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI: 2001-451656/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS
XX
PS Claim 1: Page 3087: 3695pp: English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AA107544-AA126789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 4 BP: 0 A; 1 C; 0 G; 3 T; 0 other:

Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 1 t 1

RESULT 12
AAAF61450/c
ID AAF61450 standard; RNA; 4 BP.
XX
AC AAF61450:
XX
DT 18-JUN-2001 (first entry)
XX
DE Cyclin binding hammerhead ribozyme 3' catalytic fragment SEQ ID 19.
XX
KW Hammerhead ribozyme; cyclin E; restenosis; catalytic; angioplasty;
XX cyclin E2F1; vasotropic; gene therapy; cell cycle arrest; ss.
OS Synthetic.
XX
PN WO200121789-A1.
XX
PD 29-MAR-2001.

XX 22-SEP-1999; 99WO-EP07049.
PF
XX
PR 22-SEP-1999; 99WO-EP07049.
XX
PA (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.
XX
PI Grassi G, Kuhn AC, Kandolf R;
XX
DR WPI: 2001-257985/26.
XX
PT New catalytically acting RNA molecule comprising hammerhead ribozyme
PT directed against mRNA molecules encoding cyclin E or E2F1, useful for
PT inhibiting vascular smooth muscle cell proliferation and restenosis -
XX
PS Claim 12: Page 28; 40pp: German.
XX
CC This invention describes a novel catalytic RNA molecule which is directed
CC against mRNA molecules (11) which encode the cell-relevant protein cyclin
CC E or E2F1. The products of the invention have vasotropic activity and can
CC be used for gene therapy. The use of (11), or a DNA molecule or a plasmid
CC of the invention is claimed for obtaining a vector for gene therapy and
CC for inhibiting restenosis of blood vessel after angioplasty; therapeutic
CC compositions containing these components are also claimed. (1)
CC efficiently induces cell cycle arrest by combined inactivation of cyclin
CC E and E2F1.
XX
SQ Sequence 4 BP: 2 A; 0 C; 1 G; 0 U; 1 other:

Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 4 T 4

RESULT 13
AAN93676
ID AAN93676 standard; DNA; 5 BP.
XX
AC AAN93676;
XX
DT 24-JUN-1990 (first entry)
XX
DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber
DE variant (HSV-c) and HSV grape variant (HSV-g).
XX
KW Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.
XX
OS Hop growth retarding viroid.
XX
PN JP01040000-A.
XX
PD 10-FEB-1989.
XX
PF 05-AUG-1987; 87JP-0194377.
XX
PR 05-AUG-1987; 87JP-0195377.
XX
PA (YUKI) YUKI GOSEI YAKUHIN.
XX
DR WPI: 1989-089715/12.
XX
PT Fractionating and detecting hop growth retarding viroids -
PT using synthetic DNA probe contg. specific base sequence
XX
PS Disclosure; page 3; 5pp: Japanese.
XX
CC The synthetic probes is complementary to the RNA of HSV-g bases 53-59.
CC HSV, HSV-c and HSV-g are fractionated and detected using the synthetic

CC probe. The probe is 15-25mer. The probe can be used to diagnose HSV
CC infections in plants.
XX
SQ Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 4 t 4

RESULT 14
AA068752
ID AA068752 standard; DNA: 5 BP.
XX
AC AA068752;

XX 24-JUN-1990 (first entry)

DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber
DE variant (HSV-C) and HSV grape variant (HSV-G).

XX Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.

XX Hop growth retarding viroid.

XX JP01040000-A.

XX 10-FEB-1989.

XX 05-AUG-1987; 87JP-0194377.

XX 05-AUG-1987; 87JP-0195377.

XX (YUKI) YUKI GOSHI YAKUHIN.

XX WPI: 1989-089715/12.

XX Fractionating and detecting hop growth retarding viroids -
XX using synthetic DNA probe contg. specific base sequence

XX Disclosure: page 3; 5pp; Japanese.

XX The synthetic probes is complementary to the RNA of HSV-g bases 53-59.
CC HSV, HSV-C and HSV-G are fractionated and detected using the synthetic
CC probe. The probe is 15-25mer. The probe can be used to diagnose HSV
CC infections in plants.
XX

SQ Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 1 t 1

RESULT 15
AA068752
ID AA068752 standard; DNA: 5 BP.
XX
AC AA068752;

XX 22-FEB-1995 (first entry)

XX CHA255 heavy chain CDR1 clone 3.3.3. coding sequence.

XX Polymerase chain reaction; primer; PCR; amplify; heavy; light;
XX chain; complementarity determining region; CDR; variable; constant;
XX region; monoclonal antibody; Mab; binding affinity; EDTA; DOTA;
XX tumour; cancer; colorectal; breast; metal chelate; hapten; ss.

OS Synthetic.

XX AU9350602-A.

XX 26-MAY-1994.

XX 10-NOV-1993; 93AU-0050602.

XX 12-NOV-1992; 92US-0975230.

XX (HYBR-) HYBRITTECH INC.

XX Ahweiler PM, Moore MD;

XX WPI: 1994-209063/26.

XX P-PSDB: AAR54150.

XX Polypeptide used in imaging and treatment of carcinomas and
XX tumours - comprising substd antibody CDR having binding affinity
XX for metal chelate of EDTA or DETA or analogues

XX Claim 25; Fig 3a; 61pp; English.

XX The sequences given in AA068747-57 encode the wild type and mutagenised
XX versions of the complementarity determining region 1 (CDR1) of the
XX antibody designated CHA255. CHA255 is a murine monoclonal antibody
XX (Mab) which is capable of binding complexes. Mutagenesis of these
XX CDRs, causes the production of polypeptides with a particularly
XX high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3
XX of the heavy chain, and CDR2 and -3 of the light chain were targeted
XX for mutagenesis. Five residues of both CDR1 and -3 of the CHA255
XX heavy chain, five of seven residues of light chain CDR and six of
XX nine light chain CDR3 residues were specifically targeted for
XX codon-based mutagenesis. The mutagenised Mab's can be used in
XX compositions for in vivo imaging of malignant tissues or tumours. They
XX are also useful for the treatment of malignant tissues or tumours eg.
XX colorectal or breast cancer. Both methods involve the use of
XX radionuclides which bind to metal chelates or haptens which are
XX specifically delivered to the target site by a targeting molecule. CDR
XX derived peptides may be used to construct bi-functional antibodies
XX having dual specificities, or as donor or recipients of CDR sequences.

SQ Sequence 5 BP; 0 A; 0 C; 1 G; 1 T; 3 other;

Query Match 100.0%; Score 1; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 3 t 3

RESULT 16
AA081667
ID AA081667 standard; RNA: 5 BP.
XX
AC AA081667;

XX 29-SEP-1995 (first entry)

XX bFGF binding oligomer core sequence #4.

XX Basic: fibroblast growth factor; bFGF; stem-loop structure;
XX bubble structure; pseudoknot; receptor; heparin; competition;
XX inhibition; enhance; neovascularisation; solid tumour; cancer;
XX

KW metastasis; diagnosis; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO9500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI: 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 PT factor - modulating, esp. inhibiting, its activity, useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp: English.
 XX
 CC The sequences given in AA081642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC with its receptor and heparin. These oligonucleotides may inhibit
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SO Sequence 5 BP; 2 A; 2 C; 0 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 Db 2 u 2

RESULT 17
 AA081667/c
 ID AA081667 standard; RNA: 5 BP.
 XX
 AC AA081667;
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #4.
 XX
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;
 KW metastasis; diagnosis; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO9500528-A.
 XX
 PR 05-JAN-1995.
 XX

XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI: 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 PT factor - modulating, esp. inhibiting, its activity, useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp: English.
 XX
 CC The sequences given in AA081642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC with its receptor and heparin. These oligonucleotides may inhibit
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SO Sequence 5 BP; 2 A; 2 C; 0 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
 Db 3 t 3

RESULT 18
 AA081666
 ID AA081666 standard; RNA: 5 BP.
 XX
 AC AA081666;
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #3.
 XX
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;
 KW metastasis; diagnosis; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO9500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.

CC to (11) and forms a cleavage site between p1 and p3; p3 (AA112043)
CC is an inhibitory element that binds to x2 and interacts with a
CC region of p1 corresp. to nucleotides 81-126 of MDV-1. p4 contributes
CC nucleotides to form the ribozyme with x1 and p2, or is the terminal
CC nucleotide of p1; x1 is a target region of (11); x2 and x3 are
CC terminal nucleotides or second or third target regions of (11); R1
CC is a ribozyme-forming area of (11); and R2 is a terminal nucleotide
CC of R1 or an area of (11) that binds to (11). x1 and R1 are
CC mutually exclusive and are represented by the sequences of AA112040 and
CC AA112041. For hairpin ribozymes, p2 is AA112045 and R1 is AA112046.
CC Probes bearing ribozymes are produced in a single step by transcription
CC of DNA of appropriate sequence, thereby reducing costs. The ribozymes
CC produce specific cleavage events, leading to a product RNA with
CC defined replication properties.
XX
SO Sequence 5 BP; 1 A; 1 C; 0 G; 2 U; 2 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 17; Length 5;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 u 1

RESULT 21

AAV61663
ID AAV61663 standard; DNA; 5 BP.

AC AAV61663;

XX 03-DEC-1998 (first entry)

DE Fusarium sp. 18S rRNA DNA fragment #7.

XX 18S rRNA; detection; identification; fungus; ss.

OS Fusarium sp.

XX JP10234380-A.

PD 08-SEP-1998.

PF 28-FEB-1997; 97JP-0062104.

PR 28-FEB-1997; 97JP-0062104.

XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

PA WPI; 1998-535034/46.

XX
XX
XX Use of oligo:nucleotide for detecting and identification of fungus
PT of Fusarium genus - as primer or probe to detect of identify
PT microbes rapidly and exactly

PS Claim 1; Page 7; 20pp; Japanese.

XX
XX AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are
CC used in a method for the detection and identification of a fungus of
CC Fusarium genus. The process can be used to detect or identify microbes
CC rapidly and exactly.

SO Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 19; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1

Db 1 t 1

RESULT 22

AAV61663/C
ID AAV61663 standard; DNA; 5 BP.

XX AAV61663;

XX 03-DEC-1998 (first entry)

DE Fusarium sp. 18S rRNA DNA fragment #7.

XX 18S rRNA; detection; identification; fungus; ss.

XX Fusarium sp.

XX JP10234380-A.

PD 08-SEP-1998.

PF 28-FEB-1997; 97JP-0062104.

PR 28-FEB-1997; 97JP-0062104.

XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

PA WPI; 1998-535034/46.

XX
XX Use of oligo:nucleotide for detecting and identification of fungus
PT of Fusarium genus - as primer or probe to detect of identify
PT microbes rapidly and exactly

PS Claim 1; Page 7; 20pp; Japanese.

XX
XX AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are
CC used in a method for the detection and identification of a fungus of
CC Fusarium genus. The process can be used to detect or identify microbes
CC rapidly and exactly.

SO Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 19; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 2 t 2

RESULT 23

AA196299
ID AA196299 standard; DNA; 5 BP.

XX AA196299;

XX 08-APR-1998 (first entry)

DE Fungal telomeric nucleic acid sequence.

XX
XX Detection; eukaryotic pathogen; telomeric nucleic acid sequence;
KW telomerase activity; diagnosis; fungal infection; fungus; fungi;
XX malarial infection; malaria; ss.

XX Saccharomyces cerevisiae.

XX US5695932-A.

PD 09-DEC-1997.

PF 13-MAY-1993; 93US-0060952.

DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative disease

Query Match	Score 1;	DB 20;	Length 5
100.0%			

Query Match	Score 1;	DB 20;	Length 5
100.0%			

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 3 t 3

RESULT 26

AA210696
ID AA210696 standard; DNA: 5 BP.

AC AA210696;

DT 23-NOV-1999 (first entry)

XX Oligonucleotide sequence that increases p53 activity in a cell.

XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;

XX UV-induced hyperproliferative disease; psoriasis; vitiligo;

XX atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;

XX skin cancer; ss.

XX Synthetic.

XX GB2336157-A.

XX 13-OCT-1999.

XX 24-MAR-1999; 99GB-0006758.

XX 26-MAR-1998; 98US-0048927.

XX (UYBO-) UNIV BOSTON.

XX Gilchrist BA, Yaar M, Eller M;

XX WPI: 1999-543520/46.

XX DNA fragments useful for increasing p53 activity in a cell and reducing

XX susceptibility to UV-induced hyperproliferative diseases .

XX Claim 11: Page 30; 44pp; English.

XX AA210692-97 represent DNA fragments that are used for increasing p53

XX activity in a cell. The oligonucleotides are are UV mimetics and

XX protect cells against subsequent exposure to UV-irradiation or

XX chemicals. The oligonucleotides are useful for increasing p53 activity

XX in a cell, reducing the susceptibility to UV-induced hyperproliferative

XX diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic

XX rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging

XX and reducing susceptibility to skin cancer.

XX Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

XX Query Match

XX Best Local Similarity 100.0%; Score 1; DB 20; Length 5;

XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 t 1

XX DB 3 t 3

DE Oligonucleotide sequence that increases p53 activity in a cell.
XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
XX UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
XX skin cancer; ss.

XX Synthetic.

XX GB2336157-A.

XX 13-OCT-1999.

XX 24-MAR-1999; 99GB-0006758.

XX 26-MAR-1998; 98US-0048927.

XX (UYBO-) UNIV BOSTON.

XX Gilchrist BA, Yaar M, Eller M;

XX WPI: 1999-543520/46.

XX DNA fragments useful for increasing p53 activity in a cell and reducing

XX susceptibility to UV-induced hyperproliferative diseases .

XX Claim 11: Page 30; 44pp; English.

XX AA210692-97 represent DNA fragments that are used for increasing p53

XX activity in a cell. The oligonucleotides are are UV mimetics and

XX protect cells against subsequent exposure to UV-irradiation or

XX chemicals. The oligonucleotides are useful for increasing p53 activity

XX in a cell, reducing the susceptibility to UV-induced hyperproliferative

XX diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic

XX rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging

XX and reducing susceptibility to skin cancer.

XX Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

XX Query Match

XX Best Local Similarity 100.0%; Score 1; DB 20; Length 5;

XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 t 1

XX DB 4 t 4

XX RESULT 28

XX AA211611

XX ID AA211611 standard; DNA: 5 BP.

XX AC AA211611;

XX 16-NOV-1999 (first entry)

XX DNA enhancer sequence present in an upstream element.

XX Plant promoter; TATA motif; transcription start site; upstream element;

XX gene expression; oxidate oxidase; plant resistance; pathogen; maize;

XX Ubl-1 promoter; Syn II core promoter; ss.

XX Synthetic.

XX WO9943838-A1.

XX 02-SEP-1999.

XX 23-FEB-1999; 99WO-US03863.

XX 24-FEB-1998; 98US-0028819.

XX

PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;
 XX
 DR WPI: 1999-540601/45.
 XX
 PT New synthetic promoter functional in plants to provide non-tissue
 PT specific, constitutive expression, particularly of oxalate oxidase for
 PT increased resistance to pathogens
 XX
 PS Claim 39; Page 47; 61pp; English.
 XX
 CC The invention provides a new synthetic plant promoter that comprises a
 CC TATA motif; a transcription start site (TSS) and a region between TATA
 CC and TSS containing at least 64 percent GC content. The synthetic core
 CC promoter, optionally containing additional upstream elements are used to
 CC increase expression, provides non-tissue specific, constitutive
 CC transcription of heterologous genes in any sort of plant, especially the
 CC gene for oxalate oxidase for increasing plant resistance to pathogens.
 CC The upstream activating elements can be used to increase transcription
 CC from any promoter. A combination of the synthetic core promoter with
 CC synthetic upstream elements can induce expression 10 times greater than
 CC that provided by the maize Ubi-1 promoter. The present sequence
 CC represents a DNA enhancer OSC-like motif present in an upstream element
 CC sequence.
 CC
 SO Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;
 XX
 Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 t 1
 Db 1 t 1
 XX
 RESULT 29
 AA21611/C
 ID AA21611 standard; DNA; 5 BP.
 XX
 AC AA21611;
 XX
 DT 16-NOV-1999 (first entry)
 XX
 DE DNA enhancer sequence present in an upstream element.
 XX
 KW Plant promoter; TATA motif; transcription start site; upstream element;
 KW gene expression; oxalate oxidase; plant resistance; pathogen; maize;
 KW Ubi-1 promoter; Syn II core promoter; ss.
 XX
 OS Synthetic.
 XX
 PN WO943838-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 23-FEB-1999; 99WO-US03863.
 XX
 PR 24-FEB-1998; 98US-0028819.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;
 XX
 DR WPI: 1999-540601/45.
 XX
 PT New synthetic promoter functional in plants to provide non-tissue
 PT specific, constitutive expression, particularly of oxalate oxidase for
 PT increased resistance to pathogens
 XX
 PS Claim 39; Page 47; 61pp; English.

XX
 CC The invention provides a new synthetic plant promoter that comprises a
 CC TATA motif; a transcription start site (TSS) and a region between TATA
 CC and TSS containing at least 64 percent GC content. The synthetic core
 CC promoter, optionally containing additional upstream elements are used to
 CC increase expression, provides non-tissue specific, constitutive
 CC transcription of heterologous genes in any sort of plant, especially the
 CC gene for oxalate oxidase for increasing plant resistance to pathogens.
 CC The upstream activating elements can be used to increase transcription
 CC from any promoter. A combination of the synthetic core promoter with
 CC synthetic upstream elements can induce expression 10 times greater than
 CC that provided by the maize Ubi-1 promoter. The present sequence
 CC represents a DNA enhancer OSC-like motif present in an upstream element
 CC sequence.
 CC
 SO Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;
 XX
 Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 t 1
 Db 3 t 3
 XX
 RESULT 30
 AAV72347/C
 ID AAV72347 standard; DNA; 5 BP.
 XX
 AC AAV72347;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE US5908745 primer #4.
 XX
 KW DNA sequencing; disease-associated allele; polyacrylamide matrix;
 KW continuous/contiguous stacking hybridization technique; detection;
 KW mutation; diagnosis; primer; ss.
 XX
 OS Synthetic.
 XX
 PN US5908745-A.
 XX
 PD 01-JUN-1999.
 XX
 PF 16-JAN-1996; 96US-0587332.
 XX
 PR 16-JAN-1996; 96US-0587332.
 XX
 PA (UYCH-) UNIV CHICAGO.
 XX
 PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
 PI Parinov SV, Yershov GM;
 XX
 DR WPI: 1999-347002/29.
 XX
 PT Detecting disease-associated alleles using continuous/contiguous
 PT stacking hybridization as a diagnostic tool
 XX
 PS Example 1; Column 9; 16pp; English.
 XX
 CC This invention describes novel methods for sequencing and analyzing DNA
 CC samples to detect disease-associated alleles, by continuous/contiguous
 CC stacking hybridization techniques (utilizing universal bases) with
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
 CC be used to detect multiple DNA base mutations which are specific for
 CC certain diseases. The methods of the invention provide accurate and
 CC efficient and sensitive methods for diagnosing disease by detecting
 CC multiple mutation sequences in patient DNA. The method require the
 CC minimum number of oligonucleotides and few stacking hybridization steps
 CC than prior art methods. The methods are also efficient enough to

CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.
XX
SQ Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 4 T 4

RESULT 31
AAV72348/C
ID AAV72348 standard; DNA: 5 BP.

XX AAV72348;

XX 28-JUL-1999 (first entry)

XX US5908745 primer #5.

DE DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
KW mutation; diagnosis; primer; ss.

XX Synthetic.

XX US5908745-A.

XX 01-JUN-1999.

XX 16-JAN-1996; 96US-0587332.

XX 16-JAN-1996; 96US-0587332.

XX (UYCH-) UNIV CHICAGO.

XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

XX Parinov SV, Yershov GM;

XX WPI: 1999-347002/29.

PT Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool

XX Example 1: Column 9; 16pp; English.

CC This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.

XX Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

OY 1 t 1
|
Db 4 T 4

RESULT 32
AAV72349/C
ID AAV72349 standard; DNA: 5 BP.

XX AAV72349;

XX 28-JUL-1999 (first entry)

XX US5908745 primer #6.

DE DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
KW mutation; diagnosis; primer; ss.

XX Synthetic.

XX US5908745-A.

XX 01-JUN-1999.

XX 16-JAN-1996; 96US-0587332.

XX 16-JAN-1996; 96US-0587332.

XX (UYCH-) UNIV CHICAGO.

XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

XX Parinov SV, Yershov GM;

XX WPI: 1999-347002/29.

PT Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool

XX Example 1: Column 9; 16pp; English.

CC This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.

XX Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 3 T 3

RESULT 33
AAV72350/C
ID AAV72350 standard; DNA: 5 BP.

XX AAV72350;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 28-JUL-1999 (first entry)

XX US5908745 primer #7.

DE DNA sequencing; disease-associated allele; polyacrylamide matrix;
 KM continuous/contiguous stacking hybridization technique; detection;
 mutation; diagnosis; primer; ss.

XX Synthetic.

PN US5908745-A.

XX 01-JUN-1999.

PF 16-JAN-1996: 96US-0587332.

PK 16-JAN-1996: 96US-0587332.

XX (UYCH-) UNIV CHICAGO.

PI Baraki VE, Kirillov EV, Lysov YP, Mirzabekov AD;

PI Parinov SV, Yershov GM;

DR WPI: 1999-347002/29.

XX Detecting disease-associated alleles using continuous/contiguous
 PT stacking hybridization as a diagnostic tool

PS Example 1: Column 9; 16pp: English.

CC This invention describes novel methods for sequencing and analysing DNA
 CC samples to detect disease-associated alleles, by continuous/contiguous
 CC stacking hybridization techniques (utilizing universal bases) with
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
 CC be used to detect multiple DNA base mutations which are specific for
 CC certain diseases. The methods of the invention provide accurate and
 CC efficient mutation sequences in patient DNA. The method require the
 CC minimum number of oligonucleotides and few stacking hybridization steps
 CC than prior art methods. The methods are also efficient enough to
 CC discriminate between perfect and imperfect duplexes. The methods also
 CC obviate the need for the fabrication and array placement of large numbers
 CC of immobilized oligomers.

SO Sequence 5 BP; 3 A; 2 C; 0 G; 0 U; 0 other:

Query Match

Best Local Similarity 100.0%; Score 1; DB 20; Length 5;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

DB 3 T 3

RESULT 34

AA56964/c

XX AAX56964 standard; DNA; 5 BP.

AC AAX56964;

DT 16-JUL-1999 (first entry)

XX Ras gene modulating liposomal entrapped oligonucleotide primer 8.

KM Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
 KM cell growth inhibitor; treatment; cancer; ras protein; ss.

OS Synthetic.

PN WO9922772-A1.

PD 14-MAY-1999.

XX 28-OCT-1998: 98WO-US22821.

PR 31-OCT-1997: 97US-0961469.

PA (ISIS-) ISIS PHARM INC.

PI Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;

PI Templin MV;

DR WPI: 1999-313181/26.

XX Liposome-encapsulated oligonucleotides useful for treating or
 PT preventing cancers associated with ras gene activation

PS Example 1: Page 107; 120pp: English.

CC This invention describes novel compositions comprising oligonucleotides
 CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
 CC ras protein. The products of the invention have anticancer activity and
 CC specifically bring about the antisense inhibition of ras genes or mRNA.
 CC The products of the invention are used to modulate expression of a ras
 CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
 CC growth and especially to treat or prevent cancers associated with
 CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
 CC rate at which it is cleared from the blood when compared with
 CC non-encapsulated material, and the oligonucleotides become distributed to
 CC practically all parts of the body.

SO Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other:

Query Match

Best Local Similarity 100.0%; Score 1; DB 20; Length 5;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

DB 3 T 3

RESULT 35

AA521608/c

XX AAX21608 standard; DNA; 5 BP.

AC AAX21608;

DT 14-MAY-1999 (first entry)

XX Mutant H-ras specific antisense oligo ISIS #2563.

KM Human; N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
 KM diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.

OS Synthetic.

PN WO9902732-A1.

XX 21-JAN-1999.

PF 06-JUL-1998: 98WO-US13966.

PR 08-JUL-1997: 97US-0889296.

PA (ISIS-) ISIS PHARM INC.

PI Cowsett LM, Manoharan M, Monia BP;

DR WPI: 1999-120932/10.

XX New oligonucleotide targeting human N-ras nucleic acid - is

PT capable of inhibiting human N-ras expression, useful for preventing
PT or treating conditions arising from the activation of a human N-ras
XX oncogene
XX
PS Disclosure: Page 22: 97pp: English.
XX
CC The invention relates to oligonucleotides, which target a nucleic acid
CC encoding human N-ras, and are capable of inhibiting human N-ras
CC expression. The antisense oligonucleotides form a pharmaceutical
CC composition, which is useful for modulating the expression of human
CC N-ras, inhibiting the proliferation of cancer cells, and preventing or
CC treating conditions arising from the activation of a human N-ras
CC oncogene. The oligonucleotides are also useful in diagnostics,
CC therapeutics, and as research reagents and kits. The oligonucleotides
CC enable the specific modulation of activated human N-ras expression,
CC which is associated with tumour formation. Sequences AA21601-619
CC represent antisense oligonucleotides targeted to mutant H-ras.
XX
SQ Sequence 5 BP: 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 3 T 3

RESULT 36
AA56981
ID AA56981 standard; CDNA: 5 BP.
XX
AC AA56981;
XX
DT 14-NOV-2000 (first entry)
XX
DE Human colon cancer cell CDNA sequence #109.
XX
XX Human: arbitrary primer; CDNA synthesis: contig sequence construction;
XX open reading frame; ORF: low stringency; CDNA sequencing: ss.
OS Homo sapiens.
XX
XX MO20001299-A2.
XX
PD 02-JUN-2000.
XX
PF 19-NOV-1999; 99MO-US27430.
XX
XX 20-NOV-1998; 98US-0196716.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
PI Simpson AJG, Dias Neto E, Brentani RR;
XX
DR WPI: 2000-400100/34.
XX
PT Method for determining open reading frames of the genome of an organism
PT using primers at low stringency conditions, useful in the construction
XX of contigs or constructs of sequenced nucleic acid molecules -
XX
XX Example 6: Page 47: 113pp: English.
XX
CC The present sequence is a CDNA sequence obtained using a method for
CC determining open reading frames (ORFs) of the genome of an
CC organism. An aliquot of mRNA from human colon cancer cells was mixed
CC with a single, arbitrary primer, Moloney murine leukemia virus reverse
CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
CC incubated under low stringency conditions to yield single stranded
CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
CC than providing nucleotide sequence information from the non-coding

CC termini of nucleic acid molecules, the method provides information on
CC the more interesting and relevant internal portions, such as ORFs. The
CC method also permits the construction of contigs of sequenced nucleic
CC acid molecules.
XX
SQ Sequence 5 BP: 0 A; 3 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 t 2

RESULT 37
AA293601/c
ID AA293601 standard; DNA: 5 BP.
XX
AC AA293601;
XX
DT 24-JUL-2000 (first entry)
XX
DE Transcription factor binding site of tobacco gene promoter sequence.
XX
DE Regulatory sequence; meristem; genetic engineering;
XX gene expression; crop protection; transgenic plant; resistance;
XX tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.
OS Synthetic.
OS Nicotiana glauca.
XX
OS WO200012713-A1.
XX
PN 09-MAR-2000.
XX
PD 26-AUG-1999; 99MO-AU00692.
XX
PF 26-AUG-1998; 98AU-0005498.
XX
PR (UYOU) UNIV QUEENSLAND.
XX
PA Mudge SR, Birch RG;
XX
PI WPI: 2000-237875/20.
XX
DR Meristem-expressible nucleic acid sequences, useful for producing
XX transgenic plants with improved characteristics such as resistance to
XX pathogens
XX
PS Example 9: Page 51: 102pp: English.
XX
CC Isolated regulatory sequences of plants that are operable in
CC dividing cells, in particular the meristem cells of plants are useful
CC in the genetic engineering of plants. The regulatory sequences can
CC be used to control the expression of foreign genes placed under their
CC control. Such methods are useful for producing transgenic plants with
CC altered shape and/or size. The sequences are also useful for
CC producing transgenic plants capable of rapid regeneration following
CC harvest or plants having improved resistance to pathogens. This
CC sequence has been shown to bind a factor involved in the activation
CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three
CC times in the meristem regulatory sequence of tobacco described in
CC GENESEQ record AA293567.
XX
SQ Sequence 5 BP: 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 3 T 3

RESULT 38

ID AA293602 standard; DNA: 5 BP.

XX AA293602;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KM gene expression; crop protection; transgenic plant; resistance;

KW tobacco; transcription factor; NIT2; nitrate; ss.

XX

OS Synthetic.

XS Nicotiana acuminata.

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU000692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYQU) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

XX

PT Meristem-expressible nucleic acid sequences, useful for producing

transgenic plants with improved characteristics such as resistance to

pathogens

XX Example 9; Page 51; 102pp; English.

PS Isolated regulatory sequences of plants that are operable in

dividing cells, in particular the meristem cells of plants are useful

in the genetic engineering of plants. The regulatory sequences can

be used to control the expression of foreign genes placed under their

control. Such methods are useful for producing transgenic plants with

altered shape and/or size. The sequences are also useful for

producing transgenic plants capable of rapid regeneration following

harvest or plants having improved resistance to pathogens. This

sequence has been shown to regulate nitrate metabolism in the

fungus Neurospora crassa. It occurs multiple times in the meristem

regulatory sequence of tobacco described in GENESEQ record AA293567.

CC Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

XX

SO

Query Match 100.0%; Score 1; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

DB 1 t 1

RESULT 39

AA293602/c

ID AA293602 standard; DNA: 5 BP.

XX AA293602;

AC

XX

XX

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KM gene expression; crop protection; transgenic plant; resistance;

KW tobacco; transcription factor; NIT2; nitrate; ss.

XX

OS Synthetic.

XS Nicotiana acuminata.

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU000692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYQU) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

XX

PT Meristem-expressible nucleic acid sequences, useful for producing

transgenic plants with improved characteristics such as resistance to

pathogens

XX Example 9; Page 51; 102pp; English.

PS Isolated regulatory sequences of plants that are operable in

dividing cells, in particular the meristem cells of plants are useful

in the genetic engineering of plants. The regulatory sequences can

be used to control the expression of foreign genes placed under their

control. Such methods are useful for producing transgenic plants with

altered shape and/or size. The sequences are also useful for

producing transgenic plants capable of rapid regeneration following

harvest or plants having improved resistance to pathogens. This

sequence has been shown to regulate nitrate metabolism in the

fungus Neurospora crassa. It occurs multiple times in the meristem

regulatory sequence of tobacco described in GENESEQ record AA293567.

CC Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

XX

SO

Query Match 100.0%; Score 1; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

DB 2 T 2

RESULT 40

AA293603

ID AA293603 standard; DNA: 5 BP.

XX AA293603;

AC

XX

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KM gene expression; crop protection; transgenic plant; resistance;

KW tobacco; transcription factor; yeast; ss.

XX Synthetic.

OS Nicotiana acuminata.

PN WO200012713-A1.

```

XX 09-MAR-2000.
PD
XX
XX 26-AUG-1999; 99WO-AU00692.
PT
XX
XX 26-AUG-1998; 98AU-0005498.
PH
XX
XX (UYOU ) UNIV QUEENSLAND.
PA
XX
XX Mudge SR, Birch RG;
PI
XX WPI: 2000-237875/20.
DK
XX
XX Meristem-expressible nucleic acid sequences, useful for producing
PT transgenic plants with improved characteristics such as resistance to
PT pathogens
XX
XX Example 9; Page 51; 102pp; English.
PS
XX
XX Isolated regulatory sequences of plants that are operable in
CC dividing cells, in particular the meristem cells of plants are useful
CC in the genetic engineering of plants. The regulatory sequences can
CC be used to control the expression of foreign genes placed under their
CC control. Such methods are useful for producing transgenic plants with
CC altered shape and/or size. The sequences are also useful for
CC producing transgenic plants capable of rapid regeneration following
CC harvest or plants having improved resistance to pathogens. This
CC sequence has been shown to activate yeast amino acid biosynthetic
CC enzymes. It occurs multiple times in the meristem regulatory sequence
CC of Tobacco described in GENESFO record AA293567.
XX
SQ Sequence 5 BP; 1 A; 0 C; 0 G; 2 T; 2 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 1 1
DB 1 1 1

RESULT 41
AA293603/C
ID AA293603 standard; DNA; 5 BP.
XX
XX AA293603;
AC
XX
XX 24-JUL-2000 (first entry)
DT
XX
XX Transcription factor binding site of tobacco gene promoter sequence.
DE
XX
XX Regulatory sequence; meristem; genetic engineering;
KW gene expression; crop protection; transgenic plant; resistance;
KW tobacco; transcription factor; yeast; ss.
XX
XX Synthetic.
OS Nicotiana glauca.
XX
XX WO200012713-A1.
PN
XX
XX 09-MAR-2000.
PD
XX
XX 26-AUG-1999; 99WO-AU00692.
PF
XX
XX 26-AUG-1998; 98AU-0005498.
PR
XX
XX (UYOU ) UNIV QUEENSLAND.
PA
XX
XX Mudge SR, Birch RG;
PI
XX
XX WPI: 2000-237875/20.

```

```

XX Meristem-expressible nucleic acid sequences, useful for producing
PT transgenic plants with improved characteristics such as resistance to
PT pathogens
XX
XX Example 9; Page 51; 102pp; English.
PS
XX
XX Isolated regulatory sequences of plants that are operable in
CC dividing cells, in particular the meristem cells of plants are useful
CC in the genetic engineering of plants. The regulatory sequences can
CC be used to control the expression of foreign genes placed under their
CC control. Such methods are useful for producing transgenic plants with
CC altered shape and/or size. The sequences are also useful for
CC producing transgenic plants capable of rapid regeneration following
CC harvest or plants having improved resistance to pathogens. This
CC sequence has been shown to activate yeast amino acid biosynthetic
CC enzymes. It occurs multiple times in the meristem regulatory sequence
CC of Tobacco described in GENESFO record AA293567.
XX
SQ Sequence 5 BP; 1 A; 0 C; 0 G; 2 T; 2 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 1 1
DB 3 1 3

RESULT 42
AA289330
ID AA289330 standard; DNA; 5 BP.
XX
XX AA289330;
AC
XX
XX 13-JUN-2000 (first entry)
DT
XX
XX Human UCP3 promoter fragment #10.
DE
XX
XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
KW fat metabolism; ss.
XX
XX Homo sapiens.
OS
XX
XX DE19838837-A1.
PN
XX
XX 02-MAR-2000.
PD
XX
XX 27-AUG-1998; 98DE-1038837.
PF
XX
XX 27-AUG-1998; 98DE-1038837.
PR
XX
XX (BOEH ) BOEHRINGER INSELHEIM INT GMBH.
PA
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Esterbauer H, Oberkofler H, Patsch W;
PI
XX
XX WPI: 2000-272214/24.
DR
XX
XX Recombinant fat and muscle tissue specific uncoupling protein 3
PT promoters useful for identifying UCP3 modulators
XX
XX Claim 25; Page 12; 38pp; German.
PS
XX
XX This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases

```


CC With inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.

XX
SU Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 5 t 5

RESULT 43
AA289330/C
ID AA289330 standard; DNA; 5 BP.

XX
AC AA289330;

XX DT 13-JUN-2000 (first entry)

XX DE Human UCP3 promoter fragment #10.

XX KM UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
XX KW fat metabolism; ss.

XX OS Homo sapiens.

XX PN DE19838837-A1.

XX PD 02-MAR-2000.

XX PF 27-AUG-1998; 98DE-1038837.

XX PK 27-AUG-1998; 98DE-1038837.

XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX PI (NOVO) NOVO-NORDISK AS.

XX PI Esterbauer H, Oberkofler H, Patsch W;

XX DR WPI: 2000-272214/24.

XX PT Recombinant fat and muscle tissue specific uncoupling protein 3
XX PT promoters useful for identifying UCP3 modulators -

XX PS Claim 25; Page 12; 38pp; German.

XX CC This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases
CC with inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.

XX XX Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 4 t 4

RESULT 44
AA289331
ID AA289331 standard; DNA; 5 BP.

XX
AC AA289331;

XX DT 13-JUN-2000 (first entry)

XX DE Human UCP3 promoter fragment #11.

XX KM UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
XX KW fat metabolism; ss.

XX OS Homo sapiens.

XX PN DE19838837-A1.

XX PD 02-MAR-2000.

XX PF 27-AUG-1998; 98DE-1038837.

XX PR 27-AUG-1998; 98DE-1038837.

XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX PI (NOVO) NOVO-NORDISK AS.

XX PI Esterbauer H, Oberkofler H, Patsch W;

XX DR WPI: 2000-272214/24.

XX PT Recombinant fat and muscle tissue specific uncoupling protein 3
XX PT promoters useful for identifying UCP3 modulators -

XX PS Claim 28; Page 12; 38pp; German.

XX CC This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases
CC with inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.

XX SU Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 2 t 2

RESULT 45
AA289331/C
ID AA289331 standard; DNA; 5 BP.

XX
AC AA289331;

XX DT 13-JUN-2000 (first entry)

XX DE Human UCP3 promoter fragment #11.

XX KM UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
XX KW fat metabolism; ss.

XX OS Homo sapiens.

XX DE1983837-A1.
PN
XX
PD 02-MAR-2000.
XX
PF 27-AUG-1998; 98DE-1038837.
XX
PR 27-AUG-1998; 98DE-1038837.
XX
PA (BOEHI) BOEHRINGER INGELHEIM INT GMBH.
XX (NOVO) NOVO-NORDISK AS.
XX
PI Esterbauer H, Oberkofler H, Patsch W;
XX
DK WPI: 2000-272214/24.
XX
PT Recombinant fat and muscle tissue specific uncoupling protein 3
XX promoters useful for identifying UCP3 modulators -
XX
PS Claim 28; Page 12; 38pp; German.
XX
CC This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcripition of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases
CC with inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.
XX
SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 21; length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
1
Db 1 T 1

Search completed: July 15, 2002, 23:10:11
Job time: 18429 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:56:59 ; Search time 808.35 Seconds

(Without alignments)
2.105 Million cell updates/sec

Title: US-09-375-248-1_COPY_3360_3360

Perfect score: 1

Sequence: 1 c 1

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

Pending_Patents_MA_New:*
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2: /cgn2_6/ptodata/2/pna/US06_NEM_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEM_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEM_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEM_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEM_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEM_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	1	2	US-10-027-632-51869	Sequence 51869, A
2	100.0	1	2	US-10-027-632-52280	Sequence 52280, A
3	100.0	1	2	US-10-027-632-52357	Sequence 52357, A
4	100.0	1	2	US-10-027-632-53003	Sequence 53003, A
5	100.0	1	2	US-10-027-632-58305	Sequence 58305, A
6	100.0	1	2	US-10-027-632-175312	Sequence 175312, A
7	100.0	1	2	US-10-027-632-175337	Sequence 175337, A
8	100.0	1	2	US-10-027-632-175354	Sequence 175354, A
9	100.0	1	2	US-10-027-632-175401	Sequence 175401, A
10	100.0	1	2	US-10-027-632-175419	Sequence 175419, A
11	100.0	1	2	US-10-027-632-175426	Sequence 175426, A
12	100.0	1	2	US-10-027-632-175433	Sequence 175433, A
13	100.0	1	2	US-10-027-632-175449	Sequence 175449, A
14	100.0	1	2	US-10-027-632-175456	Sequence 175456, A
15	100.0	1	2	US-10-027-632-175463	Sequence 175463, A
16	100.0	1	2	US-10-027-632-175470	Sequence 175470, A
17	100.0	1	2	US-10-027-632-175477	Sequence 175477, A
18	100.0	1	2	US-10-027-632-175484	Sequence 175484, A
19	100.0	1	2	US-10-027-632-175491	Sequence 175491, A
20	100.0	1	2	US-10-027-632-175498	Sequence 175498, A
21	100.0	1	2	US-10-027-632-175505	Sequence 175505, A
22	100.0	1	2	US-10-027-632-175512	Sequence 175512, A
23	100.0	1	2	US-10-027-632-175519	Sequence 175519, A
24	100.0	1	2	US-10-027-632-175526	Sequence 175526, A
25	100.0	1	2	US-10-027-632-175533	Sequence 175533, A
26	100.0	1	2	US-10-027-632-175540	Sequence 175540, A

27	1	100.0	3	US-10-027-632-52403	Sequence 52403, A
28	1	100.0	3	US-10-027-632-52404	Sequence 52404, A
29	1	100.0	3	US-10-027-632-52410	Sequence 52410, A
30	1	100.0	3	US-10-027-632-52417	Sequence 52417, A
31	1	100.0	3	US-10-027-632-52418	Sequence 52418, A
32	1	100.0	3	US-10-027-632-52419	Sequence 52419, A
33	1	100.0	3	US-10-027-632-52425	Sequence 52425, A
34	1	100.0	3	US-10-027-632-52491	Sequence 52491, A
35	1	100.0	3	US-10-027-632-52495	Sequence 52495, A
36	1	100.0	3	US-10-027-632-52496	Sequence 52496, A
37	1	100.0	3	US-10-027-632-52508	Sequence 52508, A
38	1	100.0	3	US-10-027-632-52512	Sequence 52512, A
39	1	100.0	3	US-10-027-632-52513	Sequence 52513, A
40	1	100.0	3	US-10-027-632-52615	Sequence 52615, A
41	1	100.0	3	US-10-027-632-52633	Sequence 52633, A
42	1	100.0	3	US-10-027-632-52651	Sequence 52651, A
43	1	100.0	3	US-10-027-632-52753	Sequence 52753, A
44	1	100.0	3	US-10-027-632-52758	Sequence 52758, A
45	1	100.0	3	US-10-027-632-52761	Sequence 52761, A

ALIGNMENTS

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RESULT 1
US-10-027-632-51869
: Sequence 51869, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027, 632
: PRIOR FILING DATE: 2002-04-10
: PRIOR APPLICATION NUMBER: US 60/218, 006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198, 676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193, 483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185, 218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167, 363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156, 358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146, 002
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 51869
: TYPE: DNA
: ORGANISM: Human
: US-10-027-632-51869

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 2 c 2

RESULT 2
US-10-027-632-52280
: Sequence 52280, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
```

```
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52280
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52280
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Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 c 1
DB 2 c 2
```

```
RESULT 3
US-10-027-632-52357
SEQUENCE 52357, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52357
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52357
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 c 1
```

```
DB 2 c 2
```

```
RESULT 4
US-10-027-632-53003
SEQUENCE 53003, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53003
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-53003
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Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 c 1
DB 1 c 1
```

```
RESULT 5
US-10-027-632-58305
SEQUENCE 58305, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58305
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; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58305
```

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Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 1 c 1
db 1 c 1
```

RESULT 6

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US-10-027-632-175312/c
; Sequence 175312, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175312
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
db 1 c 1
```

RESULT 7

```
US-10-027-632-175337/c
; Sequence 175337, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175337
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
db 1 c 1
```

RESULT 8

```
US-10-027-632-175354/c
; Sequence 175354, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175354
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
db 1 c 1
```

RESULT 9

```
US-10-027-632-175401/c
; Sequence 175401, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175401
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175401

```

```

Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Oy      1 c 1
Db      1 c 1

```

```

RESULT 10
US-10-027-632-175403/c
: Sequence 175403, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175403
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175403

```

```

Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Oy      1 c 1
Db      1 c 1

```

```

RESULT 11
US-10-027-632-175415/c
: Sequence 175415, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175415
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175415

```

```

Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Oy      1 c 1
Db      1 c 1

```

```

RESULT 12
US-10-027-632-175419/c
: Sequence 175419, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720

```

```
SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175419
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175419
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 C 1
Db 1 C 1
```

```
RESULT 13
US-10-027-632-175426/c
: Sequence 175426, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175426
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175426
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 C 1
Db 1 C 1
```

```
RESULT 14
US-10-027-632-175433/c
: Sequence 175433, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
```

```
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175433
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175433
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 C 1
Db 1 C 1
```

```
RESULT 15
US-10-027-632-175849/c
: Sequence 175849, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175849
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 C 1
Db 2 C 2
```

```
RESULT 16
US-10-027-632-176848/c
: Sequence 176848, Application US/10027632
```

```

: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 176848
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176848

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 c 1
Db 1 c 1
```

```

RESULT 17
US-10-027-632-176849/c
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 176849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176849
```

Query Match 100.0%: Score 1; DB 6; Length 2;

```

Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 c 1
Db 1 c 1
```

```

RESULT 18
US-10-027-632-176880/c
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 176880
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176880
```

```

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 c 1
Db 1 c 1
```

```

RESULT 19
US-10-027-632-178420/c
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
```



```
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178420
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178420
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 C 1
        |
Db       1 C 1
```

```
RESULT 20
US-10-027-632-178440
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 C 1
        |
Db       2 C 2
```

```
RESULT 21
US-10-027-632-178440/c
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 C 1
        |
Db       1 C 1
```

```
RESULT 22
US-10-027-632-178617/c
; Sequence 178617, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178617
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 C 1
        |
Db       2 C 2
```

RESULT 23

```
US-10-027-632-178640/C
; Sequence 178640, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178640
```

Query Match

Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1

Db 2 c 2

RESULT 24

```
PCT-US02-00351-20
; Sequence 20, Application PC/TUS0200351
; GENERAL INFORMATION:
; APPLICANT: Chet, Ilan
; APPLICANT: Viterbo, Ada
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING
; FILE REFERENCE: 02/23682
; CURRENT APPLICATION NUMBER: PCT/US02/00351
; CURRENT FILING DATE: 2002-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: motif found in the URSS of both ech42 and prb1 genes
PCT-US02-00351-20
```

Query Match

Best Local Similarity 100.0%; Score 1; DB 1; Length 3;
Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1

Db 3 c 3

RESULT 25

```
US-10-027-632-52136/C
; Sequence 52136, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52136
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52136
```

Query Match

Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1

Db 3 c 3

RESULT 26

```
US-10-027-632-52402
; Sequence 52402, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52402
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52402
```

```
Query Match          100.0%: Score 1: DB 6: Length 3:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
OY      1 c 1
db      1 c 1

RESULT 27
US-10-027-632-52403
: Sequence 52403, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52403
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52403
```

```
Query Match          100.0%: Score 1: DB 6: Length 3:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
OY      1 c 1
db      1 c 1
```

```
RESULT 28
US-10-027-632-52404
: Sequence 52404, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
```

```
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52404
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52404
```

```
Query Match          100.0%: Score 1: DB 6: Length 3:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
OY      1 c 1
db      1 c 1
```

```
RESULT 29
US-10-027-632-52410
: Sequence 52410, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52410
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52410
```

```
Query Match          100.0%: Score 1: DB 6: Length 3:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
OY      1 c 1
db      1 c 1
```

```
RESULT 30
US-10-027-632-52417
: Sequence 52417, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
```

```

: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52417
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52417
```

```

Query Match          100.0%: Score 1; DB 6; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
   |
Db 1 c 1
```

```

RESULT 31
US-10-027-632-52418
: Sequence 52418, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52418
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52418
```

```

Query Match          100.0%: Score 1; DB 6; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
   |
Db 1 c 1
```

```

RESULT 32
US-10-027-632-52419
: Sequence 52419, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52419
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52419
```

```

Query Match          100.0%: Score 1; DB 6; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
   |
Db 1 c 1
```

```

RESULT 33
US-10-027-632-52425
: Sequence 52425, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52425
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
```

US-10-027-632-52425

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 1 c 1

RESULT 34
US-10-027-632-52491/c
; Sequence 52491, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52491
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52491

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 2 c 2

RESULT 35
US-10-027-632-52495
; Sequence 52495, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52495
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52495

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 3 c 3

RESULT 36
US-10-027-632-52496/c
; Sequence 52496, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52496
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52496

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
|
Db 2 c 2

RESULT 37
US-10-027-632-52508/c
; Sequence 52508, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

```

: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52508
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52508
```

```

Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 2 C 2
```

```

RESULT 38
US-10-027-632-52512
: Sequence 52512, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52512
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52512
```

```

Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1
```

```
Db 3 C 3
```

```

RESULT 39
US-10-027-632-52513/C
: Sequence 52513, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52513
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52513
```

```

Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 2 C 2
```

```

RESULT 40
US-10-027-632-52615/C
: Sequence 52615, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52615
: LENGTH: 3
```

TYPE: DNA
ORGANISM: Human
US-10-027-632-52615

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 2 C 2

RESULT 41
US-10-027-632-52633/C
; Sequence 52633, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52633
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52633

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 2 C 2

RESULT 42
US-10-027-632-52651/C
; Sequence 52651, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52651
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52651

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 2 C 2

RESULT 43
US-10-027-632-52753/C
; Sequence 52753, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52753
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52753

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
1
Db 2 C 2

RESULT 44
US-10-027-632-52758
; Sequence 52758, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 52758
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52758
```

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 c 1
        |
Db       1 c 1
```

```

RESULT 45
: Sequence 52761, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 52761
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52761
```

```
Oy      1 c 1
        |
Db       1 c 1
```

Search completed: July 16, 2002, 02:57:00
Job time: 24558 sec

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Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

XX  [1]
RN  Koehrer K., Beyer A., Mewes W., Cassenhuber J., Wiemann S.;
RP  1-2
KI  ;
KL  Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX  MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC  clone from S. Wiemann, sequenced by MIPS within the cDNA
CC  sequencing consortium of the German Genome Project
CC  No sl sequence available
CC  This clone is available at the RZPD in Berlin
CC  Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC  Berlin-Charlottenburg, GERMANY. Email: clone@rzpd.de
XX
FH  Key
FH  location/Qualifiers
FT  source
FT  1..2
FT  /db_xref="taxon:9606"
FT  /organism="Homo sapiens"
FT  /clone="DKFZP586P0517"
FT  /clone_lib="586 (synonym: butel). Vector pSPORT1; host
FT  DH10B; sites NotI + SalI/MluI"
FT  /dev_stage="adult"
FT  /tissue_type="uterus"
XX
SO  Sequence 2 BP; 0 A; 1 G; 0 C; 1 T; 0 other;

Query Match
Host Local Similarity 100.0%; Score 1; DB 2; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 g 1
DB  2 G 2

RESULT  5
Locus B1817789/c 2 bp mRNA linear EST 04-OCT-2001
DEFINITION G3-C22 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
to Putative ribosomal protein S2, mRNA sequence.
ACCESSION B1817789
VERSION B1817789.1 GI:35951401
KEYWORDS EST.
SOURCE axolotl.
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
Ambystoma.
REFERENCE 1 (bases 1 to 2)
AUTHORS Voss,S.K., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,
Gardiner,D.M. and Parichy,D.M.
TITLE Expressed sequence tags from an axolotl limb regeneration library
JOURNAL Unpublished (2001)
COMMENT Contact: Voss SR
Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel: 970 491 4869
Fax: 970 491 0649
Email: srvoos@lamar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate ~ 5%). Trace file available:
srvoos@lamar.colostate.edu.
Location/Qualifiers
1..2
/organism="Ambystoma mexicanum"
/db_xref="taxon:8296"
/clone_lib="Axolotl Lambda Zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

FEATURES
source

```

```

BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN
Query Match
Host Local Similarity 100.0%; Score 1; DB 10; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 g 1
DB  1 G 1

RESULT  6
Locus C55081
DEFINITION C55081 Yui Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone YK350C9 3', mRNA sequence.
ACCESSION C55081
VERSION C55081.1 GI:2399682
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea
REFERENCE 1 (bases 1 to 2)
AUTHORS Kohara,Y., Motoshashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yui Kohara
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1..2
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="YK350C9"
/clone_lib="Yui Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT 1 a 1 c 0 g 0 t
ORIGIN
Query Match
Host Local Similarity 100.0%; Score 1; DB 10; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 g 1
DB  2 G 2

RESULT  7
Locus BE351920
DEFINITION BE351920 2 bp mRNA linear EST 18-JUL-2000
CHlamydomonas reinhardtii CC-1690, normalized, lambda zap II
CHlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE351920
VERSION BE351920.1 GI:9263773
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE 1 (bases 1 to 2)

```

AUTHORS
 Grossman, A., Davies, J., Federspiel, N., Harris, E., Lebevre, P.,
 McJermott, J. P., Sillfow, C., Stern, D., and Surzycki, R.
TITLE
 Analyses of the Chlamydomonas reinhardtii Genome: A Model,
 Unicellular System for Analyzing Gene Function and Regulation in
 Vascular Plants: project phase 2
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Elizabeth H. Harris
 ICMR Box 91000
 Duke University
 Durham, NC 27708-1000, USA
 Tel: 919 613 8164
 Fax: 919 613 8177
 Email: eharris@duke.edu

FEATURES
 source
 1. .2
 /organism "Chlamydomonas reinhardtii"
 /strain "CC-1690 wild type mt+ 21gr"
 /db_xref "taxon:3055"
 /clone_11b "C. reinhardtii CC-1690, normalized, lambda Zap
 11"
 /note "Vector: Bluescript II SK-; Site 1: EcoRI; Site 2:
 XhoI; This library, constructed by John Davies and Jeffrey
 McJermott, combines cDNAs from CC-1690 cells grown to
 mid-log phase in YAP (acetate-containing) medium to the
 light, YAP medium in the dark, HS (minimal) medium in
 ambient levels of CO2 and HS medium bubbled with 5% CO2.
 PolyA mRNA was purified from each sample, pooled and cDNA
 synthesized. The cDNA was directionally cloned into lambda
 Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
 plasmid script II SK- plasmids were excised from the lambda
 Zap clones by superinfection with ExAssist (Stratagene)
 phage. The library was normalized using method 4 described
 in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT
 origin 0 a 0 c 2 g 0 t

Query Match
 Best Local Similarity 100.0%; Score 1: DB 10; Length 2;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 1
 Db 1 g 1

RESULT 8
 A2463604 2 bp DNA linear GSS 04-OCT-2000
LOCUS
 1M0272J05R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION
 clone UUCG1M0272J05 R, DNA sequence.
ACCESSION
 A2463604
VERSION
 A2463604.1 GI:10621729
KEYWORDS
 GSS.
SOURCE
 house mouse.
ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

FEATURES
 source
 1. .2
 /organism "Mus musculus"
 /strain "C57BL/6J"
 /db_xref "taxon:10090"
 /clone "UUCG1M0272J05"
 /clone_11b "Mouse 10kb plasmid UUCG1M library"
 /sex "Male"
 /lab_host "E. coli strain XL10-Gold, T1-resistant, F-"
 /note "Vector: PMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from The Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1473211419b1AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 origin 0 a 0 c 1 g 1 t

Query Match
 Best Local Similarity 100.0%; Score 1: DB 12; Length 2;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 1
 Db 1 g 1

RESULT 9
 AM672605 3 bp mRNA linear EST 26-SEP-2001
LOCUS
 2XA Explanted metanephric mesenchyme induced to differentiate into
DEFINITION
 epithelial structures of the nephron ex vivo. Rattus norvegicus
 cDNA similar to: gb|AF022811.1|AF022811 Mus musculus
 cornichon mRNA, mRNA sequence.
ACCESSION
 AM672605
VERSION
 AM672605.1 GI:7541085
KEYWORDS
 EST.
SOURCE
 Norway rat.
ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 3)
 Plisov, S. Y., Ivanov, S. V., Yoshino, K., Dove, L. F., Plisova, T. M.,
 Higginbotham, K. G., Karavanova, I., Lerman, M., and Perantoni, A. O.
TITLE
 Kidney: gene expression transition in the developing metanephric
JOURNAL
 Genesis 27 (1), 22-31 (2000)
COMMENT
 Contact: Plisov S. Y.
 Laboratory of Comparative Carcinogenesis
 National Cancer Institute
 FCRC, Bldg. 538, Room 205, Frederick, MD 21702, USA

Tel: 301 846 1242
 Fax: 301 846 4956
 Email: plisov@mail.ncifcrf.gov
 PCR Primers
 FORWARD: ctccagctccgctc
 BAC/KMARD: ttaagcttttttttc
 Insert Length: 350 Std Error: 0.00
 Seq primer: Sp6
 High quality sequence stop: 261.
 Location/Qualifiers
 1..3
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /clone_lib="Explicated metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo."
 /tissue_type="Metanephric mesenchyme"
 /cell_type="Mesenchymal/Epithelial"
 /dev_stage="13 dpc-16dpc"
 /lab_host="JMI09"
 /note="Organ: Kidney; Vector: pGEM-Teasy (Promega).; Restriction Enzymes 1: AclI, AclII, SphI, NcoI, BstXI, NotI, SacII, and EcoRI SpeI, EcoRI, NotI, BstXI, PstI, SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pGEM-Teasy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."
 BASE COUNT
 ORIGIN 1 a 0 c 2 g 0 t
 Query Match 100.0%; Score 1: DB 9; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 Oy 1 g 1
 Db 1 c 1
 RESULT 10
 A2438202/c 3 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0228108F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 LOCUS A2438202
 ACCESSION A2438202
 VERSION A2438202.1 GI:10562215
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Mus.
 1 (bases 1 to 3)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0228 row: 1 column: 08
 Seq primer: CGTTGTAACACGACGCCACGT
 Class: plasmid ends

High quality sequence stop: 302.
 Location/Qualifiers
 1..3
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0228108"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydridynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT
 ORIGIN 1 a 1 c 0 g 1 t
 Query Match 100.0%; Score 1: DB 12; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 Oy 1 g 1
 Db 1 c 1
 RESULT 11
 CNS00KCV 3 bp DNA linear GSS 03-JUN-1999
 LOCUS CNS00KCV
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR17D19 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 ACCESSION AL077515
 VERSION AL077515.1 GI:4956992
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 3)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using the BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's

PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
Source
Location/Qualifiers

1.3
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCT-98"
/clone="BACR17D19"
/note="end : TET3"

BASE COUNT 0 a 0 c 3 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 G 1

RESULT 12

BC926576 standard: RNA; EST: 4 BP.

AC BC926576;

SV BC926576.1

09-JUN-2001 (Rel. 68, Created)

14-NOV-2001 (Rel. 69, Last updated, Version 2)

HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

DE EST.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

XX [1]

RP 1-4

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J., Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries";

RL Osteoarthritic Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay_kumar-1@gsk.com

CC Seq primer: T7.

XX Key Location/Qualifiers

PH source

FT 1..4 /db_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

FT Directional"

FT /organism="Homo sapiens"

FT /clone_lib="HNC (Human Normal Cartilage)"

FT /tissue_type="Cartilage"

FT /lab_host="E.coli DH10 B"

XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

SO Query Match

Best Local Similarity 100.0%; Score 1; DB 2; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 4 G 4

RESULT 13

BC926576/C standard: RNA; EST: 4 BP.

XX BC926576;

SV BC926576.1

09-JUN-2001 (Rel. 68, Created)

14-NOV-2001 (Rel. 69, Last updated, Version 2)

HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

DE EST.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

XX [1]

RP 1-4

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J., Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries";

RL Osteoarthritic Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay_kumar-1@gsk.com

CC Seq primer: T7.

XX Key

PH Location/Qualifiers

FT source

FT 1..4 /db_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

FT Directional"

FT /organism="Homo sapiens"

FT /clone_lib="HNC (Human Normal Cartilage)"

FT /tissue_type="Cartilage"

FT /lab_host="E.coli DH10 B"

XX Seq primer: T7.

XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

SO Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 3 G 3

RESULT 14
ID HSM001901
X X HSM003901 standard; RNA; EST: 4 BP.

AC AL039425;
X X
SV AL039425.1

DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434L0810_s1 (from clone DKFZp434L0810)
X X
X X EST: expressed sequence tag.

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

KN 11
RP 1-4
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

PH source

FT 1. .4
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"

SO Sequence 4 BP; 2 A; 0 C; 1 G; 0 T; 1 other;

Query Match 100.0%; Score 1; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1
Db 4 G 4

RESULT 15
ID HSM010467
X X HSM010467 standard; RNA; EST: 4 BP.

AC AL045617;
X X
SV AL045617.1

DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434O245_r1 (from clone DKFZp434O245)

XX EST: expressed sequence tag.

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

KN 11
RP 1-4

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

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CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

PH source

FT 1. .4
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"

SO Sequence 4 BP; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1
Db 4 G 4

RESULT 16
ID HSM010467/c
X X HSM010467 standard; RNA; EST: 4 BP.

AC AL045617;
X X
SV AL045617.1

DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434O245_r1 (from clone DKFZp434O245)
X X
X X EST: expressed sequence tag.

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

KN 11
RP 1-4

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project

CC No s1 sequence available
CC This clone is available at the RZPD in Berlin


```
/dev_stage="13 dpc-16dpc"
```

```

Query Match      100.0%; Score 1; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Indels 0; Gaps 0.

```

Db 4 C 4

RESULT 19
HSM007310
ID HSM007310 standard; RNA; EST: 5 BP.

XX AL042460;

SV AL042460.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434E1821_r1 (from clone DKFZp434E1821)

XX EST: expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC No s1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

FT Key Location/Qualifiers

FT

FT source 1..5

FT /db_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434E1821"

FT /clone_id="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev_stage="adult"

FT /tissue_type="testis"

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

FT Key Location/Qualifiers

FT source 1..5

FT /db_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434N1522"

FT /clone_id="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev_stage="adult"

FT /tissue_type="testis"

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

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FT

FT

FT

FT

FT

```

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT source
FT 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434D137"
FT /clone_lib="434 (synonym: htes3). Vector pSPORT1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
FT
XX
SQ Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 g 1

RESULT 22
BG927410/c standard; RNA; EST; 6 BP.
XX
AC BG927410;
XX
SV BG927410.1
XX
DT 09-JUN-2001 (Rel. 68, Created)
DT 14-NOV-2001 (Rel. 69, last updated, Version 2)
XX
DE HNC1-1-G7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
XX
KM EST.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
XX
KN [1]
KP 1-6
XX MEDLINE: 21482651.
XX PUBMED: 11597177.
RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
RT "Identification and initial characterization of 5000 expressed sequenced
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
RT libraries";
RL Osteoarthritis Cartilage 9(7):641-653(2001).
XX
XX Contact: Sanjay Kumar
XX UW2109
XX GlaxoSmithKline
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
CC Tel: 610-270-7245
CC Fax: 610-270-5598
CC Email: sanjay.kumar-1@gsk.com
CC Seq primer: 77.
XX
XX
FH key Location/Qualifiers
FH
FH source
FH 1..6
FH /db_xref="taxon:9606"
FH /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
FH Directional!"
FH /organism="Homo sapiens"
FH /clone_lib="HNC (Human Normal Cartilage)"
FH /tissue_type="cartilage"

```

```

FT
XX /lab_host="E.coli DH10 B"
XX
SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 6 G 6

RESULT 23
HSM003844 standard; RNA; EST; 6 BP.
XX
AC HSM003844;
XX
SV AL039368.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX
XX EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
XX
KN [1]
KP 1-6
XX
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX
FH key Location/Qualifiers
FH
FH source
FH 1..6
FH /db_xref="taxon:9606"
FH /organism="Homo sapiens"
FH /clone="DKFZp434I0110"
FH /clone_lib="434 (synonym: htes3). Vector pSPORT1; host
FH DH10B; sites NotI + SalI"
FH /dev_stage="adult"
FH /tissue_type="testis"
FH
XX
XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 G 1

RESULT 24
HSM004423 standard; RNA; EST; 6 BP.
ID HSM004423

```

```

XX AC AL039947;
XX SV AL039947.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX RN [1]
XX RP 1-6
XX RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone_id="DKFZp434J0112"
XX FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 25
HSM007334 standard; RNA; EST; 6 BP.
XX ID HSM007334
XX AC AL042484;
XX SV AL042484.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434F0321_r1 (from clone DKFZp434F0321)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX RN [1]

```

```

RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone_id="DKFZp434F0321"
XX FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 26
HSM007683/C
XX ID HSM007683
XX AC AL042833;
XX SV AL042833.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX RN [1]
XX RP 1-6
XX RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source 1..6
XX FT /db_xref="taxon:9606"

```

```

FT      /organism="Homo sapiens"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
XX
SQ      Sequence 6 BP: 2 A; 2 C; 0 G; 2 T; 0 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
        |
DB      6 G 6

```

```

RESULT 27
HSM008014/c
ID      HSM008014 standard; RNA; EST: 6 BP.
XX
XX      AL043164;
AC
XX      AL043164.1
SV
XX
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFZp434F1123_s1 (from clone DKFZp434F1123)
DE
XX      EST: expressed sequence tag.
XX
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
XX      sequencing consortium of the German Genome Project
XX      r1 sequence also available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX
XX      source      1..6
XX                  /db_xref="taxon:9606"
XX                  /organism="Homo sapiens"
XX                  /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX                  DH10B; sites NotI + SalI"
XX                  /dev_stage="adult"
XX                  /tissue_type="testis"
XX
XX      Sequence 6 BP: 1 A; 2 C; 0 G; 3 T; 0 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
        |
DB      5 G 5

```

```

RESULT 28
HSM010918
ID      HSM010918 standard; RNA; EST: 6 BP.
XX
XX      AL046068;
AC
XX      AL046068.1
SV
XX      AL046068.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFZp434F1672_r1 (from clone DKFZp434F1672)
DE
XX      EST: expressed sequence tag.
XX
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by DKFZ within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No s1 sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX
XX      source      1..6
XX                  /db_xref="taxon:9606"
XX                  /organism="Homo sapiens"
XX                  /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX                  DH10B; sites NotI + SalI"
XX                  /dev_stage="adult"
XX                  /tissue_type="testis"
XX
XX      Sequence 6 BP: 0 A; 2 C; 2 G; 0 T; 2 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
        |
DB      1 G 1

```

```

RESULT 29
HSM010918/c
ID      HSM010918 standard; RNA; EST: 6 BP.
XX
XX      AL046068;
AC
XX      AL046068.1
SV
XX      AL046068.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFZp434F1672_r1 (from clone DKFZp434F1672)
DE
XX      EST: expressed sequence tag.
XX
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by DKFZ within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No s1 sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX
XX      source      1..6
XX                  /db_xref="taxon:9606"
XX                  /organism="Homo sapiens"
XX                  /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX                  DH10B; sites NotI + SalI"
XX                  /dev_stage="adult"
XX                  /tissue_type="testis"
XX
XX      Sequence 6 BP: 0 A; 2 C; 2 G; 0 T; 2 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
        |
DB      1 G 1

```

```

DEFINITION 128628 MARC 1pIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE030526
VERSION BE030526.1 GI:8325535
KEYWORDS EST.
SOURCE plg.
ORGANISM Sus scrofa
            Fukarya: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 546)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
        Sloane,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
        and Keele,J.W.
        Design and use of two pooled tissue normalized cDNA libraries for
        EST discovery in swine
        Unpublished (2000)
        Contact: Smith TPJ
        USDA, ARS, US Meat Animal Research Center
        PO Box 166, Clay Center, NE 68933-0166, USA
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smithemail.marc.usda.gov
        Single pass sequencing. Bases called and alt trimmed with phred
        v0.980904.e. Vector identified by cross_match with the -minscore 18
        and -minmatch 12 options.
        PCR primers
        FORWARD: AGCAACACCTATGACCAT
        BACKWARD: GTTTCCTCCAGTCACGACG
        Plate: 62 row: F column: 16
        Seq primer: ATTAGTGACACTATAC.
FEATURES
    source
        1..546
        /organism="Sus scrofa"
        /db_xref="taxon:9823"
        /clone_id="MARC 1pIG"
        /rissue_type="pooled"
        /lab_host="DH10B"
        /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
        library made from pooled tissue from day 11, 13, 15, 20,
        and 30 embryos."
BASE COUNT 120 a 164 c 149 g 113 t
ORIGIN
Query Match 5.1%; Score 24; DB 9; Length 546;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 139 gacttggccttgcgggacatc 162
    |||||||||||||||||||
Db 83 CACTTGGCCTTGCCCGGACATC 106
RESULT 20
A1556371/c 357 bp mRNA linear EST 23-MAR-1999
LOCUS UI-R-C2p-rg-f-10-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone
DEFINITION UI-R-C2p-rg-f-10-0-UI 3', mRNA sequence.
ACCESSION A1556371
VERSION A1556371.1 GI:4488734
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
            Eukarya: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 357)
REFERENCE Bernaldo,M.F., Lennon,G. and Soares,M.B.
AUTHORS Normalization and subtraction: two approaches to facilitate gene
TITLE discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
        Program for Rat Gene Discovery and Mapping

```

```

University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mscoare@blue.weeg.uiowa.edu
CDNA Library Preparation: M. Fatima Bernaldo, Ph.D. Clone
distribution: clones will be available through Research Genetics
(www.resgen.com)
Seq primer: M13 Forward.
FEATURES
    source
        1..357
        /organism="Rattus norvegicus"
        /strain="Sprague-Dawley"
        /db_xref="taxon:10116"
        /clone="UI-R-C2p-rg-f-10-0-UI"
        /clone_id="UI-R-C2p"
        /dev_stage="adult"
        /lab_host="DH10B (Life Technologies)"
        /note="Vector: p775D-Pac (Pharmacia) with a modified
        polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
        library is a subtracted library derived from the UI-R-C1
        library, which is a subtracted library derived from the
        UI-R-C0 library. The UI-R-C0 library consisted of a
        mixture of individually tagged normalized libraries
        constructed from rat placenta, adult lung, brain, liver,
        kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
        embryo. The tag is a string of 3-5 nucleotides present
        between the Not I site and the oligo-dT track which allows
        identification of the library of origin of a clone within
        the mixture. The subtracted library (UI-R-C2p) was
        constructed as follows: PCR amplified cDNA inserts from
        UI-R-C1 clones from which 3' ESTs had been derived was
        used as a driver in a hybridization with the UI-R-C1
        library in the form of single-stranded circles. The
        remaining single-stranded circles (subtracted library) was
        purified by hydroxyapatite column chromatography,
        converted to double-stranded circles and electroporated
        into DH10B bacteria (Life Technologies) to generate the
        UI-R-C2p library. This procedure has been previously
        described (Bernaldo, Lennon and Soares, Genome Research 6:
        791-806, 1996)."
BASE COUNT 82 a 103 c 66 g 106 t
ORIGIN
Query Match 4.9%; Score 23; DB 9; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 124 gtggtgaagactgtgacttgg 146
    |||||||||||||||||||
Db 130 GTGCTGAAGATCTGTGACTTTGG 108
RESULT 21
A0136157/c 409 bp DNA linear GSS 24-SEP-1998
LOCUS HS_3060_B1.G08_MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate-3060 Col-15 Row-N, DNA sequence.
ACCESSION A0136157
VERSION A0136157.1 GI:3527493
KEYWORDS GSS.
SOURCE Homo sapiens
ORGANISM Homo sapiens
            Eukarya: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 409)
REFERENCE Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
AUTHORS Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
TITLE Hood,L.
JOURNAL Sequence-tagged connectors: A sequence approach to mapping and
        scanning the human genome
        Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

```

MEDLINE 99380589
COMMENT Contact: Mahatras CG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3060 Row: N Column: 15
Class: BAC ends
High quality sequence stop: 409.

FEATURES
source
1. 409
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIR Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT 124 a 96 c 96 g 92 t 1 others
ORIGIN

Query Match 4.9%; Score 23; DB 12; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gTgaagatctgtgacttgacct 149
|||||
Db 359 GTGAAGATCTGTGACTTGCGCT 337

RESULT 22
AA709653 455 bp mRNA linear EST 24-DEC-1997
LOCUS UVAL105.r1 Soares_thymus_2NBMT Mus musculus cDNA clone
DEFINITION IMAGE:1224993 5' similar to gb:X58712 Mouse MAPK mRNA for
mitogen-activated protein kinase (MOUSE);, mRNA sequence.
ACCESSION AA709653
VERSION AA709653.1 GI:2719571
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 455)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelning,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu

FEATURES
source
1. 455
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1224993"

/clone_lib="Soares_thymus_2NBMT"
/sex="male"
/tissue_type="thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: p7773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAGTGGAGCGCGCGTTTGTGTGTGTGTGTGTGTGT
3'); double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7773 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 120 a 117 c 95 g 123 t
ORIGIN

Query Match 4.9%; Score 23; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtgacttgacctgc 152
|||||
Db 191 AAGATCTGTGACTTGCGCTTGC 213

RESULT 23
A1092636 461 bp mRNA linear EST 23-OCT-1998
LOCUS qa35d08.x1 Soares_NbHMPu.S1 Homo sapiens cDNA clone IMAGE:1688751
DEFINITION 3' similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR
RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION A1092636
VERSION A1092636.1 GI:3431612
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 461)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR Gene Index
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 677 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 435.

FEATURES
source
1. 461
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1688751"

/clone_lib="Soares_NbHMPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: p7773D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."


```

sequence.
AL272456
VERSION AL272456.1 GI:7994531
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 1003)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1003)
AUTHORS Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brotlier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
HUMAN Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 1003)
Genoscope.
DIRECT Direct Submission
SUBMITTED Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
LOCATION/Qualifiers
1..1003
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone.lib="G"
/note="Genoscope sequence ID : C0BG079AE06SP1-end :
PUC-Or1"

BASE COUNT 264 a 174 c 239 g 291 t 35 others
ORIGIN

Query Match 4.9% Score 23; DB 12; Length 1003;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 gtgaagatcctgacttgccct 149
|||||
Db 727 GTCAAGATCTGCACTTGCCCT 705

RESULT 27
CNS03S1B 1099 bp DNA linear GSS 17-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 050010 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL257960
VERSION AL257960.1 GI:7978972
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 1099)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the

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```

freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 1099)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brotlier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
HUMAN Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 1099)
Genoscope.
DIRECT Direct Submission
SUBMITTED Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
LOCATION/Qualifiers
1..1099
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone.lib="G"
/note="Genoscope sequence ID : C0BG050DB05SP1-end : T7"

BASE COUNT 226 a 322 c 324 g 216 t 11 others
ORIGIN

Query Match 4.9% Score 23; DB 12; Length 1099;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 gcccgagacatcacaaagacc 173
|||||
Db 882 GCCCGACACTCTACCAAGACCC 860

RESULT 28
AL642415 658 bp mRNA EST 12-DEC-2001
LOCUS AL642415 XGC-neurula Slurana tropicalis cDNA clone TNeu025K14 5',
DEFINITION mRNA sequence.
AL642415
VERSION AL642415.1 GI:16794540
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Slurana tropicalis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
Xenopodinae; Slurana.
1 (bases 1 to 658)
Huckie,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckie E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu025K14.sp6
Sequencing primer: Sp6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
LOCATION/Qualifiers
1..658
/organism="Slurana tropicalis"
/db_xref="taxon:8364"
/clone.lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from sug of poly A+ RNA from neurula.

```

ECORI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
BASE COUNT 149 a 192 c 178 g 138 t 1 others
ORIGIN

Query Match 4.7% Score 22; DB 9; Length 658;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 128 tgaagatcgtgacttgacct 149
|||||
Db 428 tcgaagatcgtgacttgacct 449

RESULT 29
LOCUS B1556970 743 bp mRNA linear EST 05-SEP-2001
DEFINITION 603238431p1 NIH-CGAP_Mam3 Mus musculus cDNA clone IMAGE:5291694 5',
B1556970
ACCESSION mRNA sequence.
VERSION B1556970
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 743)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM1737 row: m column: 07
High quality sequence stop: 700.

FEATURES
source Location/Qualifiers
1..743

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5291694"
/clone_1lb="NIH-CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert 2 kb. Library constructed by Life
Technologies, catalog #12017-018. Investigators providing
samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
for transgenic model; Xu et al., Nature Genetics 22, 37-43
(1999). Note: this is a NCI-CGAP Library."
BASE COUNT 154 a 215 c 214 g 160 t
ORIGIN

Query Match 4.7% Score 22; DB 10; Length 743;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 gagacctgctgctcggaacat 104
|||||
Db 141 GAGACCTGCTGCTCGAACAT 162

RESULT 30
BFI36721
LOCUS BFI36721 793 bp mRNA linear EST 24-OCT-2000

DEFINITION 601780488F1 NCI-CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008812 5',
mRNA sequence.
ACCESSION BFI36721
VERSION BFI36721.1 GI:10975761
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 793)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9243 row: o column: 21
High quality sequence stop: 654.

FEATURES
source Location/Qualifiers
1..793

/organism="Mus musculus"
/strain="C2ECB II"
/db_xref="taxon:10090"
/clone="IMAGE:4008812"
/clone_1lb="NCI-CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; transgenic model MMT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 158 a 227 c 232 g 175 t 1 others
ORIGIN

Query Match 4.7% Score 22; DB 10; Length 793;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 gagacctgctgctcggaacat 104
|||||
Db 119 GAGACCTGCTGCTCGAACAT 140

RESULT 31
B1686934 834 bp mRNA linear EST 18-SEP-2001
LOCUS B1686934
DEFINITION 603313809F1 NCI-CGAP_Mam6 Mus musculus cDNA clone IMAGE:5351635 5',
mRNA sequence.
ACCESSION B1686934
VERSION B1686934.1 GI:15649562
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 834)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.

Db 236 ACTGCATCCACAGACCTGGC 215

RESULT 34
CNS02YAK/C
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone 180A18 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL219413
VERSION AL219413.1 GI:7878232
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis

REFERENCE 1 (bases 1 to 967)
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL 2 (bases 1 to 967)
REFERENCE Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
AUTHORS Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

TITLE Unpublished
JOURNAL 3 (bases 1 to 967)
REFERENCE Genoscope.
AUTHORS Direct Submission
COMMENT Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
Location/Qualifiers
1..967
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="180A18"
/note="Genoscope sequence ID : C0AG180BA09SP1-end : PUC-Or1"

BASE COUNT 253 a 252 c 247 g 211 t 4 others

ORIGIN

Query Match 4.7%; Score 22; DB 12; Length 967;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 tctgtctacagctccaggtgac 41
|||||
Db 229 TCTGCTACAGCTTCCAGGTGGC 208

RESULT 35
CNS02SAS/C
LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 236D19 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL181837
VERSION AL181837.1 GI:7819921
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 978)
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL 2 (bases 1 to 978)
REFERENCE Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
AUTHORS Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

TITLE Unpublished
JOURNAL 3 (bases 1 to 978)
REFERENCE Genoscope.
AUTHORS Direct Submission
COMMENT Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
Location/Qualifiers
1..978
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="236D19"
/note="Genoscope sequence ID : C0AG236CB10LP1-end : T7"

BASE COUNT 239 a 260 c 265 g 210 t 4 others

ORIGIN

Query Match 4.7%; Score 22; DB 12; Length 978;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 tctgtctacagctccaggtgac 41
|||||
Db 605 TCTGCTACAGCTTCCAGGTGGC 584

RESULT 36
CNS01UBA
LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone 196I14 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL167598
VERSION AL167598.1 GI:7805656
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 1023)
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL 2 (bases 1 to 1023)
REFERENCE Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
AUTHORS Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1023)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the tetradon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetradon>.

FEATURES
source Location/Qualifiers
1..1023
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="196114"
/clone_1lb="G"
/note="Genoscope sequence ID : C0AG196BE07SP1-end : PUC-ori"

BASE COUNT 205 a 305 c 290 g 218 t 5 others
ORIGIN

Query Match 4.7%; Score 22; DB 12; Length 1023;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 71 agtgcattccacagagactgcg 92
|||||
Db 695 agtcattccacagagactgcg 716

RESULT 37
LOCUS BC013342 3397 bp mRNA linear HTC 04-SEP-2001
DEFINITION Mus musculus, clone IMAGE:4013934, mRNA.
ACCESSION BC013342
VERSION BC013342.1 GI:15426477
KEYWORDS HTC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3397)
REFERENCE 1 (bases 1 to 3397)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbioology.org>
Contact: amadansystemsbioology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Ketteman and Anuradha Madan

REMARK
COMMENT
FEATURES
source
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 18 Row: f Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1089897
This clone has the following problem: frame shifted.
Location/Qualifiers
1..3397

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4013934"
/tissue-type="Mammary tumor metastasized to lung."
MTV-LTR/Mtl model. Expression driven by an MTV-LTR

enhancer."
/clone_1lb="NCI CGAP_Lu30"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"
BASE COUNT 728 a 970 c 1014 g 685 t
ORIGIN

Query Match 4.7%; Score 22; DB 11; Length 3397;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 83 gagacgtgctgcgcgaacat 104
|||||
Db 2393 gagactgctgcgcgaacat 2414

RESULT 38
LOCUS AA895295 359 bp mRNA linear EST 06-APR-1998
DEFINITION vx49609.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1278568 5' similar to gb:U10717 TYROSINE-PROTEIN KINASE LYK I (HUMAN); gb:X55663 Mouse mRNA for protein-tyrosine kinase, tec type I (MOUSE);, mRNA sequence.
ACCESSION AA895295
VERSION AA895295.1 GI:3031714
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 359)
REFERENCE 1 (bases 1 to 359)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:670368
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 200.

FEATURES
source Location/Qualifiers
1..359

/organism="Mus musculus"
/strain="C57BL/6 x CBA"
/db_xref="taxon:10090"
/clone="IMAGE:1278568"
/clone_1lb="Stratagene mouse lung 937302"
/sex="female"
/tissue-type="lung"
/dev_stage="6-8 month old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: lung; Vector: pluscript SK-; Site_1: ECORI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. 6-8 month old female lung and 1.5 year old male lung
were source of mRNA. Average insert size: 1.5 kb; Uni-2AP
XR Vector: -5' adaptor sequence: 5' CAATCGGACGAG 3' -3'
adaptor sequence: 5' CACGAGTTTTTTTTTTTTTT 3' "

BASE COUNT 94 a 76 c 97 g 92 t
ORIGIN

Query Match 4.5%; Score 21; DB 9; Length 359;

Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 catcacagagacctgctgc 95
|||||
Db 111 CATCCACAGACCTGCTGCTC 131

RESULT 39
BF147285
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF147285 458 bp mRNA linear EST 26-OCT-2000
uw64d05.y1 Soares.mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:3467145.5. similar to SW:TEC_MOUSE P24604 TYROSINE-PROTEIN
KINASE TEC ; mRNA sequence.
BF147285
BF147285.1 GI:11026680
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 458)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1386505
Seq primer: -40RP from Glibco
High quality sequence stop: 381.
Location/Qualifiers
1..458
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3467145"
/clone_lib="Soares.mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonatido."
BASE COUNT 120 a 99 c 125 g 113 t 1 others
ORIGIN

Query Match 4.5%; Score 21; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 catcacagagacctgctgc 95
|||||
Db 161 CATCCACAGACCTGCTGCTC 181

RESULT 40
AG094291/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AG094291 711 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-095A06.F, genomic survey sequence.
AG094291
AG094291.1 GI:16646093
GSS: GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-095A06.F.
Pan troglodytes

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (sites)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totohi,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of library PTB
Unpublished
2 (bases 1 to 711)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totohi,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimps@gsc.riken.go.jp, URL: <http://hgsc.riken.go.jp/>,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..711
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-095A06.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 147 a 260 c 158 g 146 t
ORIGIN

Query Match 4.5%; Score 21; DB 12; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 ggttgccagagagatgagtt 56
|||||
Db 502 GGTGCCACAGCGATGCGATT 482

RESULT 41
B1111982
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

B1111982 845 bp mRNA linear EST 26-JUN-2001
602901317F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5031052.5',
mRNA sequence.
B1111982
B1111982.1 GI:14562883
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 845)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1087 row: a column: 05
High quality sequence stop: 837.

FEATURES

Location/Qualifiers

1. 845
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:5031052"
/clone_1lb="NCI CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT

211 a 188 c 238 g 208 t

ORIGIN

Query Match 4.5%; Score 21; DB 10; Length 845;
Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 75 catccacagagactgctgc 95
|||||

Db 88 CATCCACAGACCTGCTGC 108

RESULT 42

LOCUS

Bf119392 945 bp mRNA linear EST 24-OCT-2000
DEFINITION 60175815f1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3992642 5',
mRNA sequence.

ACCESSION Bf119392
VERSION Bf119392.1 GI:10958432

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 945)
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/

JOURNAL

Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9207 row: n column: 03
High quality sequence stop: 661.

FEATURES

Location/Qualifiers

source

1. 945

/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:3992642"
/clone_1lb="NCI CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT

255 a 235 c 237 g 217 t 1 others

ORIGIN

Query Match

4.5%; Score 21; DB 10; Length 945;
Best Local Similarity 100.0%; Pred. No. 8.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgacct 150
|||||

Db 452 AAGATCTGTGACTTGGCCTT 472

RESULT 43

LOCUS

B1153717 1019 bp mRNA linear EST 05-JUL-2001
DEFINITION 60287135f1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5003055 5',
mRNA sequence.

ACCESSION B1153717
VERSION B1153717.1 GI:14613718

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 1019)
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/

JOURNAL

Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11039 row: b column: 16
High quality sequence start: 2
High quality sequence stop: 442.

FEATURES

Location/Qualifiers

source

1. 1019

/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5003055"
/clone_1lb="NCI CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Gilbert Smith, NIH"

BASE COUNT

308 a 294 c 276 g 141 t

ORIGIN

Query Match 4.5%; Score 21; DB 10; Length 1019;
Best Local Similarity 100.0%; Pred. No. 8.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 83 gaacacgagctgctggaaca 103
|||||

Db 318 GAACACCTGCTCGCAACA 338

RESULT 44

LOCUS

BC018230 2564 bp mRNA linear HTC 06-DEC-2001
DEFINITION Mus musculus, similar to cytoplasmic tyrosine kinase, Dscr28C
related (Drosophila), clone IMAGE:4484096, mRNA.

ACCESSION BC018230
VERSION BC018230.1 GI:17390527

KEYWORDS

HTC.

SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus. 1 (bases 1 to 2564)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: vllation@bcm.tmc.edu
Villation, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 31 Row: 1 Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA ql: 7305568
This clone has the following problem: frame shifted.
FEATURES
source
1..2564
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4484096"
/tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."
/clone_1lb="NCI_CGAP_Mam1"
/lab_host="DH108"
/note="Vector: pCMV-SPORT6"
BASE COUNT 789 a 521 c 656 g 598 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 75 catccacagagacctgctgc 95
|||||
Db 1538 CATCCACAGAGACTTGGCTGC 1558
RESULT 45
AUI29676 253 bp mRNA linear EST 24-OCT-2000
LOCUS AUI29676 NT2RP2 Homo sapiens cDNA clone NT2RP2006021 5', mRNA
DEFINITION sequence.
ACCESSION AUI29676
VERSION AUI29676.1 GI:10990030
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 253)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Makamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
REFERENCE HRI human cDNA project
AUTHORS HRI human cDNA project
TITLE HRI human cDNA project
JOURNAL unpublished (2000)

COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES
source
1..253
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP2006021"
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BASE COUNT 63 a 64 c 58 g 65 t 3 others
ORIGIN
Query Match 4.2%; Score 20; DB 9; Length 253;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 130 aaguctctgtgacttgct 149
|||||
Db 32 AAGATCTGTGACTTTGGCCT 51

Search completed: July 15, 2002, 20:07:35
Job time: 14493 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:56:48 ; Search time 808.35 Seconds
(without alignments)
991.681 Million cell updates/sec

Title: US-09-375-248-1_COPY_3044_3514

Perfect score: 471

Sequence: 1 ctgaccatggaagatctgtg.....gacctgcatctcgagctg 471

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/prodata/2/pna/US06_NEW_COMB.seq:*
2: /cgn2_6/prodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/prodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/prodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/prodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	471	100.0	4416	US-09-053-375B-132	Sequence 132, App
2	471	100.0	4416	US-09-442-384B-447	Sequence 447, App
3	96	20.4	476	US-09-539-331D-34177	Sequence 34177, A
4	23	4.9	476	US-09-539-331D-34177	Sequence 34177, A
5	23	4.9	6373	US-10-027-400-1	Sequence 1, App11
6	23	4.9	6373	US-09-053-375B-419	Sequence 419, App
7	22	4.7	22	US-09-704-167A-8	Sequence 8, App11
8	22	4.7	4479	US-09-053-375B-724	Sequence 724, App
9	21	4.5	744	US-10-027-632-15064	Sequence 15064, A
10	21	4.5	997	US-10-027-632-30946	Sequence 30946, A
11	21	4.5	2574	US-10-045-428A-2	Sequence 2, App11
12	20	4.2	366	US-09-721-544-17950	Sequence 17950, A
13	20	4.2	461	US-09-721-544-17950	Sequence 17950, A
14	20	4.2	462	US-09-918-995-24204	Sequence 24204, A
15	20	4.2	484	US-09-721-544-17950	Sequence 17950, A
16	20	4.2	698	US-10-027-632-148136	Sequence 148136, App
17	20	4.2	1611	US-09-053-375B-130	Sequence 130, App
18	20	4.2	1611	US-09-053-375B-130	Sequence 130, App
19	20	4.2	1611	US-10-171-311-126	Sequence 126, App
20	20	4.2	1611	US-10-171-311-126	Sequence 126, App
21	20	4.2	5279	US-10-105-299-752	Sequence 752, App
22	20	4.2	5427	US-09-053-375B-420	Sequence 420, App
23	20	4.2	5427	US-09-442-384B-437	Sequence 437, App11
24	20	4.2	5427	US-10-027-400-3	Sequence 209, App
25	20	4.2	5570	US-10-007-926A-209	Sequence 17143, A
26	19	4.0	303	US-09-539-331D-17143	

ALIGNMENTS

27	19	4.0	465	5	US-09-442-384B-358	Sequence 358, App
28	19	4.0	466	5	US-09-442-366A-66	Sequence 66, App1
29	19	4.0	504	5	US-09-911-904-130	Sequence 130, App
30	19	4.0	1063	6	US-10-106-698-2068	Sequence 2068, App
31	19	4.0	1706	5	US-09-937-060A-17	Sequence 17, App
32	19	4.0	1939	6	US-10-104-047-1465	Sequence 1465, App
33	19	4.0	1948	6	US-10-027-632-97991	Sequence 97991, A
34	19	4.0	1948	6	US-10-027-632-97992	Sequence 97992, A
35	19	4.0	2344	5	US-09-053-375B-907	Sequence 907, App
36	19	4.0	2526	5	US-09-053-375B-1006	Sequence 1006, App
37	19	4.0	3949	5	US-09-442-384B-773	Sequence 773, App
38	19	4.0	3949	5	US-09-721-544-12422	Sequence 12422, A
39	18	3.8	340	5	US-10-121-925-5	Sequence 5, App11
40	18	3.8	361	6	US-10-121-925-5	Sequence 5, App11
41	18	3.8	361	6	US-09-918-995-1503	Sequence 1503, App
42	18	3.8	449	5	US-09-918-995-11621	Sequence 31621, A
43	18	3.8	738	6	US-10-027-632-15007	Sequence 15007, A
44	18	3.8	738	6	US-10-027-632-15008	Sequence 15008, A
45	18	3.8	738	6	US-10-027-632-15008	

RESULT

1
US-09-053-375B-132
Sequence 132, Application US/09053375B
GENERAL INFORMATION:
APPLICANT: Chemchik, Alex
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053, 375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 132
LENGTH: 4416
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: 4243
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc-feature
LOCATION: 4243
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc-feature
LOCATION: 4243
OTHER INFORMATION: n = A,T,C or G
US-09-053-375B-132

Query Match 100.0%; Score 471; DB 5; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.6e-246;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ctgaccatggaagatctgtgctgctcaagcttgcggaagggatgagcttcg 60
DB	3044	ctgaccatggaagatctgtgctgctcaagcttgcggaagggatgagcttcg 3103
QY	61	gtctccggaagatgcatccacagaagctgtgctgctggaacatctgctgcggaagc 120
DB	3104	gtctccggaagatgcatccacagaagctgtgctgctggaacatctgctgcggaagc 3163
QY	121	gacgtgtggaagatctgtgacttgccttgcggaagatctggaacatctggaac 180
DB	3164	gacgtgtggaagatctgtgacttgccttgcggaagatctggaacatctggaac 3223
QY	181	gtccggaagggcagtgccggtgctgcccctgaagtgtatgagccctgaagatctgcgac 240

```
Db 3224 gtcgcaagggcagtgcccgctgcccctgaagtgtgatgtgcccctgaagaacatcttcgac 3283
Oy 241 aaggtgtacacacacagacagatgacgtgtgtcttctgtgggtgtcttctctcggagagatcttc 300
Db 3284 aaggtgtacacacacacagacagatgacgtgtgtcttctgtgggtgtcttctcggagagatcttc 3343
Oy 301 tctctgtgggtgtccctcccgtaacctgtgggtgtcagatcaatgaagaagttctcggacagcgctg 360
Db 3344 tctctgtgggtgtccctcccgtaacctgtgggtgtcagatcaatgaagaagttctcggacagcgctg 3403
Oy 361 aagacgcgcacagaagatgtgagggcccgagctgtgcacatcccgccatacgcgcgacatcgt 420
Db 3404 aagacgcgcacagaagatgtgagggcccgagctgtgcacatcccgccatacgcgcgacatcgt 3463
Oy 421 ctgaactgtgtgtccggagaccccaagggacacgtgacatctcggagctg 471
Db 3464 ctgaactgtgtgtccggagaccccaagggacacgtgacatctcggagctg 3514
```

RESULT 2

```
US-09-442-384B-447
: Sequence 447, Application US/09442384B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Lukashov, Matvey
: TITLE OF INVENTION: Hematology/Immunology Array
: FILE REFERENCE: CLON-006C1P15
: CURRENT APPLICATION NUMBER: US/09/442, 384B
: PRIORITY FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: 09/053, 375
: NUMBER OF SEQ ID NOS: 830
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 447
: LENGTH: 4416
: TYPE: DNA
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 4243
: OTHER INFORMATION: n = A,T,C or G
: OTHER INFORMATION: n = A,T,C or G
US-09-442-384B-447
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Query Match 100.0%; Score 471; DB 5; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3 6e-246;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 ctgacctgtgaagaatctgtctgtctacagcttcccaagtgccagagagatgtgagtttctg 60
Db 3044 ctgacctgtgaagaatctgtctgtctacagcttcccaagtgccagagagatgtgagtttctg 3103
Oy 61 gcttcccgaaagtgcatccacagagacctgtgctcgcgcgaacatcttgcgtctcggaaagc 120
Db 3104 gcttcccgaaagtgcatccacagagacctgtgctcgcgcgaacatcttgcgtctcggaaagc 3163
Oy 121 gacgtgtgtgaagaatctgtgacttctgacctgtcccgagacatctcaaaagacctgactac 180
Db 3164 gacgtgtgtgaagaatctgtgacttctgacctgtcccgagacatctcaaaagacctgactac 3223
Oy 181 gtcgcaagggcagtgcccgctgcccctgaagtgtgagtgccctgtgaaagacatcttcgac 240
Db 3224 gtcgcaagggcagtgcccgctgcccctgaagtgtgagtgccctgtgaaagacatcttcgac 3283
Oy 241 aaggtgtacacacacagacagatgacgtgtgtcttctgtgggtgtcttctcggagagatcttc 300
Db 3284 aaggtgtacacacacagacagatgacgtgtgtcttctgtgggtgtcttctcggagagatcttc 3343
Oy 301 tctctgtgggtgtccctcccgtaacctgtgggtgtcagatcaatgaagaagttctcggacagcgctg 360
```

```
Db 3344 tctctgtgggtgtccctcccgtaacctgtgggtgtcagatcaatgaagaagttctcggagagatcttc 3403
Oy 361 aagacgcgcacagaagatgtgagggcccgagctgtgcacatcccgccatacgcgcgacatcgt 420
Db 3404 aagacgcgcacagaagatgtgagggcccgagctgtgcacatcccgccatacgcgcgacatcgt 3463
Oy 421 ctgaactgtgtgtccggagaccccaagggacacgtgacatctcggagctg 471
Db 3464 ctgaactgtgtgtccggagaccccaagggacacgtgacatctcggagctg 3514
```

RESULT 3

```
US-09-539-331D-34177
: Sequence 34177, Application US/09539331D
: GENERAL INFORMATION:
: APPLICANT: Seilhamer, Jeffrey J.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Mullany, Sara J.
: APPLICANT: Naughton, Rebecca E.
: TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
: FILE REFERENCE: PD-1022 CIP
: CURRENT APPLICATION NUMBER: US/09/539, 331D
: PRIORITY FILING DATE: 2000-03-30
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 40961
: SOFTWARE: PERL Program
: SEQ ID NO 34177
: LENGTH: 476
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: hu01173578
US-09-539-331D-34177
```

Query Match 20.4%; Score 96; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.4e-42;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 42 cagagagatgagttctgtgtcttcccgaaagtgcacccacagagagactgtgtctggaa 101
Db 24 cagagagatgagttctgtgtcttcccgaaagtgcacccacagagagactgtgtctggaa 83
Oy 102 catctgtgttcggaagcgagctgtgtgaagatctg 137
Db 84 catctgtgttcggaagcgagctgtgtgaagatctg 119

RESULT 4
US-09-539-331D-34177/C
: Sequence 34177, Application US/09539331D
: GENERAL INFORMATION:
: APPLICANT: Seilhamer, Jeffrey J.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Mullany, Sara J.
: APPLICANT: Naughton, Rebecca E.
: TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
: FILE REFERENCE: PD-1022 CIP
: CURRENT APPLICATION NUMBER: US/09/539, 331D
: PRIORITY FILING DATE: 2000-03-30
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 40961
: SOFTWARE: PERL Program
: SEQ ID NO 34177
: LENGTH: 476
: TYPE: DNA
: ORGANISM: Homo sapiens
```

FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO: hu01173578
US-09-539-331D-34177

Query Match 4.9%; Score 23; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 tctgtacagcttccagtgcc 42
|||||
DB 27 tctgtacagcttccagtgcc 5

RESULT 5
US-10-027-400-1
Sequence 1, Application US/10027400
GENERAL INFORMATION:
APPLICANT: WILLIAMS, Lewis T.
ESCHEDO, Jaime A.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market, Steuart Street Tower, 20th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,400
FILING DATE: 19-Dec-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/461,917
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-267-2-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
TELEFAX: 415/326-2422

SEQUENCE CHARACTERISTICS:
LENGTH: 6373 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 129..3398
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-027-400-1

Query Match 4.9%; Score 23; DB 6; Length 6373;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtaagatctgtacttgcc 149
|||||
DB 2622 gtaagatctgtacttgcc 2644

RESULT 6
US-09-053-375B-419
Sequence 419, Application US/09053375B
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Bibilashvili, Robert
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 419
LENGTH: 6378
TYPE: DNA
ORGANISM: Homo sapiens
US-09-053-375B-419

Query Match 4.9%; Score 23; DB 5; Length 6378;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtaagatctgtacttgcc 149
|||||
DB 2633 gtaagatctgtacttgcc 2655

RESULT 7
US-09-704-167A-8/C
Sequence 8, Application US/09704167A
GENERAL INFORMATION:
APPLICANT: Havemann, Klaus
TITLE OF INVENTION: Production and Use of Endothelial-like Cells
FILE REFERENCE: BPD-100
CURRENT APPLICATION NUMBER: US/09/704,167A
CURRENT FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent version 3.1
SEQ ID NO 8
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: VEGFR-3 3'-primer for RT-PCR, VEGFR-3 GenBank accession no. NM
US-09-704-167A-8

Query Match 4.7%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 117 aagcagctgtgaagatctgt 138
|||||
DB 22 AAGCAGCTGTGACGATCTGT 1

RESULT 8
US-09-053-375B-724
Sequence 724, Application US/09053375B
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Bibilashvili, Robert
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 724

LENGTH: 4479
TYPE: DNA
ORGANISM: Mus musculus
US-09-053-375B-724

Query Match
Best Local Similarity 100.0%; Score 22; DB 5; Length 4479;
Pred. No. 0.11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 gagacctgctgcgcgaacat 104
|||||
DB 2309 gagacctgctgcgcgaacat 2330

RESULT 9
US-10-027-632-15064/C

Sequence 15064, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 15064

LENGTH: 744

TYPE: DNA

ORGANISM: Human

US-10-027-632-15064

Query Match

Best Local Similarity 100.0%; Score 21; DB 6; Length 744;
Pred. No. 0.37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ggtggccagagagatgagtt 56
|||||

DB 275 GGTGCCAGAGATGAGTT 255

RESULT 10
US-10-027-632-30946/C

Sequence 30946, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30946
LENGTH: 997
TYPE: DNA
ORGANISM: Human
US-10-027-632-30946

Query Match
Best Local Similarity 100.0%; Score 21; DB 6; Length 997;
Pred. No. 0.37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ggtggccagagagatgagtt 56
|||||

DB 604 GGTGCCAGAGATGAGTT 584

RESULT 11
US-10-045-428A-2

Sequence 2, Application US/10045428A

GENERAL INFORMATION:

APPLICANT: Mano, Hiroyuki

APPLICANT: Sakata, Tsuneaki

APPLICANT: Hasegawa, Mamoru

APPLICANT: Tabata, Toshiaki

TITLE OF INVENTION: Promoter

FILE REFERENCE: 50026/011003

CURRENT APPLICATION NUMBER: US/10/045,428A

PRIOR FILING DATE: 2002-04-15

PRIOR APPLICATION NUMBER: 09/735,103

PRIOR FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: 09/142,529

PRIOR FILING DATE: 1999-08-12

PRIOR APPLICATION NUMBER: PCT/JP97/00741

PRIOR FILING DATE: 1997-03-10

PRIOR APPLICATION NUMBER: JP 8/54294

PRIOR FILING DATE: 1996-03-12

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 2574

TYPE: DNA

ORGANISM: Mus musculus

US-10-045-428A-2

Query Match

Best Local Similarity 100.0%; Score 21; DB 6; Length 2574;
Pred. No. 0.38;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 catccacagagacgtgctgc 95
|||||

DB 1566 catccacagagacgtgctgc 1586

RESULT 12
US-09-721-544-17950

Sequence 17950, Application US/09721544

GENERAL INFORMATION:

APPLICANT: Arterburn, Matthew

APPLICANT: Asghari, Vida

APPLICANT: Damavandi, Simin

APPLICANT: Dickson, Mark

APPLICANT: Drake, Jim

```

: APPLICANT: Drmanac, Radoje
: APPLICANT: Engleman, Carrie
: APPLICANT: Faulkner, Brandy
: APPLICANT: Garcia, Veronica
: APPLICANT: Gledt, Gretchen
: APPLICANT: Hunter, Kelly
: APPLICANT: Jessen, Aaron
: APPLICANT: Jones, Lee
: APPLICANT: Kita, David
: APPLICANT: Labat, Ivan
: APPLICANT: Laroya, Mimi
: APPLICANT: Lomelli, Michelle
: APPLICANT: Nguyen, Phuong
: APPLICANT: Nogra, Margie
: APPLICANT: Palencia, Servando
: APPLICANT: Raistl, Farida
: APPLICANT: Smith, Benjamin
: APPLICANT: Tkach, Joe
: APPLICANT: Tran, Lien
: APPLICANT: Verna, Ron
: APPLICANT: Yang, Fel
: APPLICANT: Yim, Kenneth
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
: FILE REFERENCE: From a cDNA Library of Fetal Liver-Spleen
: CURRENT APPLICATION NUMBER: US/09/721,544
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 09/515,128
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: 09/034,341
: PRIOR FILING DATE: 1998-02-13
: NUMBER OF SEQ ID NOS: 24489
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 17950
: LENGTH: 366
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-721-544-17950

```

```

Query Match      4.2%: Score 20; DB 5; Length 366;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY 130 aagatctgtgacttgacct 149
      |||
Db 73 aagatctgtgacttgacct 92

```

```

RESULT 13
US-09-721-544-7766
: Sequence 7766, Application US/09721544
: GENERAL INFORMATION:
: APPLICANT: Arteburn, Matthew
: APPLICANT: Asghari, Vida
: APPLICANT: Damavandi, Smln
: APPLICANT: Dickson, Mark
: APPLICANT: Drake, Jim
: APPLICANT: Drmanac, Radoje
: APPLICANT: Engleman, Carrie
: APPLICANT: Faulkner, Brandy
: APPLICANT: Garcia, Veronica
: APPLICANT: Gledt, Gretchen
: APPLICANT: Hunter, Kelly
: APPLICANT: Jessen, Aaron
: APPLICANT: Jones, Lee
: APPLICANT: Kita, David
: APPLICANT: Labat, Ivan
: APPLICANT: Laroya, Mimi
: APPLICANT: Lomelli, Michelle
: APPLICANT: Nguyen, Phuong
: APPLICANT: Nogra, Margie
: APPLICANT: Palencia, Servando

```

```

: APPLICANT: Raistl, Farida
: APPLICANT: Smith, Benjamin
: APPLICANT: Tkach, Joe
: APPLICANT: Tran, Lien
: APPLICANT: Verna, Ron
: APPLICANT: Yang, Fel
: APPLICANT: Yim, Kenneth
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
: FILE REFERENCE: From a cDNA Library of Fetal Liver-Spleen
: CURRENT APPLICATION NUMBER: US/09/721,544
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 09/515,128
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: 09/034,341
: PRIOR FILING DATE: 1998-02-13
: NUMBER OF SEQ ID NOS: 24489
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 7766
: LENGTH: 461
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(461)
: OTHER INFORMATION: n = A,T,C or G
: US-09-721-544-7766

```

```

Query Match      4.2%: Score 20; DB 5; Length 461;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY 130 aagatctgtgacttgacct 149
      |||
Db 170 aagatctgtgacttgacct 189

```

```

RESULT 14
US-09-918-995-24204
: Sequence 24204, Application US/09918995
: GENERAL INFORMATION:
: APPLICANT: Hysq, Inc.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
: FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
: CURRENT APPLICATION NUMBER: US/09/918,995
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: US/09/235,076
: PRIOR FILING DATE: 1999-01-20
: NUMBER OF SEQ ID NOS: 38054
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 24204
: LENGTH: 462
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(462)
: OTHER INFORMATION: n = A,T,C or G
: US-09-918-995-24204

```

```

Query Match      4.2%: Score 20; DB 5; Length 462;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY 130 aagatctgtgacttgacct 149
      |||
Db 91 aagatctgtgacttgacct 110

```

```
RESULT 15
```

```

US-09-721-544-7765
: Sequence 7765, Application US/09721544
: GENERAL INFORMATION:
: APPLICANT: Afterburn, Matthew
: APPLICANT: Asghari, Vida
: APPLICANT: Damavandi, Simin
: APPLICANT: Dickson, Mark
: APPLICANT: Drake, Jim
: APPLICANT: Drmanac, Radoje
: APPLICANT: Engleman, Carrie
: APPLICANT: Faulkner, Brandy
: APPLICANT: Garcia, Veronica
: APPLICANT: Giedt, Gretchen
: APPLICANT: Hunter, Kelly
: APPLICANT: Jensen, Aaron
: APPLICANT: Jones, Lee
: APPLICANT: Kila, David
: APPLICANT: Labat, Ivan
: APPLICANT: Laroya, Mimi
: APPLICANT: Lomelli, Michelle
: APPLICANT: Nguyen, Phuong
: APPLICANT: Nogra, Margie
: APPLICANT: Palencia, Servando
: APPLICANT: Raisl, Farida
: APPLICANT: Smith, Benjamin
: APPLICANT: Tkach, Joe
: APPLICANT: Tran, Lien
: APPLICANT: Verna, Ron
: APPLICANT: Yang, Fel
: APPLICANT: Yim, Kenneth
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
: TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
: FILE REFERENCE: 728CIP
: CURRENT APPLICATION NUMBER: US/09/721,544
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 09/515,128
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: 09/034,341
: PRIOR FILING DATE: 1998-02-13
: NUMBER OF SEQ ID NOS: 24489
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 7765
: LENGTH: 484
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(484)
: OTHER INFORMATION: n = A,T,C or G
US-09-721-544-7765

Query Match          4.2%; Score 20; DB 5; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aaagatctgtagcttgacct 149
Db 200 aaagatctgtagcttgacct 219

RESULT 16
US-10-027-632-148136
: Sequence 148136, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12

```

```

1 PRIOR APPLICATION NUMBER: US 60/198,676
2 PRIOR FILING DATE: 2000-04-20
3 PRIOR APPLICATION NUMBER: US 60/193,483
4 PRIOR FILING DATE: 2000-03-29
5 PRIOR APPLICATION NUMBER: US 60/185,218
6 PRIOR FILING DATE: 2000-02-24
7 PRIOR APPLICATION NUMBER: US 60/167,363
8 PRIOR FILING DATE: 1999-11-23
9 PRIOR APPLICATION NUMBER: US 60/156,358
10 PRIOR FILING DATE: 1999-09-28
11 PRIOR APPLICATION NUMBER: US 60/146,002
12 PRIOR FILING DATE: 1999-08-09
13 NUMBER OF SEQ ID NOS: 325720
14 SOFTWARE: FASTSEQ for Windows Version 4.0.
15 SEQ ID NO: 148136
16 LENGTH: 698
17 TYPE: DNA
18 ORGANISM: Human
19 US-10-027-632-148136

```

```

Query Match      4.2%  Score 20; DB 6; Length 698;
Best Local Similarity 100.0%; Pred. No. 1,3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 136 tttgacttgctgacctgccc 155
      |||
Db 579 tttgacttgctgacctgccc 598

```

```

RESULT 17
US-09-053-375B-130
? Sequence 130, Application US/09053375B
? GENERAL INFORMATION:
? APPLICANT: Chenchik, Alex
? TITLE OF INVENTION: Nucleic Acid Arrays
? FILE REFERENCE: CLON-006
? CURRENT APPLICATION NUMBER: US/09/053,375B
? CURRENT FILING DATE: 1998-08-31
? NUMBER OF SEQ ID NOS: 1543
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 130
? LENGTH: 1611
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-053-375B-130

```

Query Match	4.2%	Score 20	DB 5	Length 1611
Best Local Similarity	100.0%	Pred. No. 1,3		
Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	130	aaagatctgtgactcttgac	ct 149	
Db	817	aaagatctgtgactcttgac	ct 836	

```

1
2 RESULT 18
3 US-09-053-375B-130/c
4 : Sequence 130, Application US/09053375B
5 : GENERAL INFORMATION:
6 :
7 : APPLICANT: Chenchik, Alex
8 :
9 : TITLE OF INVENTION: Nucleic Acid Arrays
10 :
11 : FILE REFERENCE: CLON-006
12 :
13 : CURRENT APPLICATION NUMBER: US/09/053,375B
14 :
15 : CURRENT FILING DATE: 1998-08-31
16 :
17 : NUMBER OF SEQ ID NOS: 1543
18 :
19 : SOFTWARE: FastSeq for Windows Version 4.0
20 :
21 : SEQ ID NO 130
22 :
23 : LENGTH: 1611
24 :
25 : TYPE: DNA

```

ORGANISM: Homo sapiens
US-09-053-175B-130

Query Match 4.2%: Score 20; DB 5; Length 1611;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgacct 149
|||||
Db 109 AACATCTGACTTTGGCCT 90

RESULT 19
US-10-171-311-126
Sequence 126, Application US/10171311
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatz, Karen
APPLICANT: Gannavarapu, Manjula
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 126
LENGTH: 1611
TYPE: DNA
ORGANISM: Homo sapiens
US-10-171-311-126

Query Match 4.2%: Score 20; DB 6; Length 1611;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgacct 149
|||||
Db 817 aagatctgacttgacct 836

RESULT 20
US-10-171-311-126/c
Sequence 126, Application US/10171311
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatz, Karen
APPLICANT: Gannavarapu, Manjula
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12

PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 126
LENGTH: 1611
TYPE: DNA
ORGANISM: Homo sapiens
US-10-171-311-126

Query Match 4.2%: Score 20; DB 6; Length 1611;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgacct 149
|||||
Db 109 AACATCTGACTTTGGCCT 90

RESULT 21
US-10-105-299-752
Sequence 752, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: P5950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 752
LENGTH: 5279
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1371)..(1371)
OTHER INFORMATION: n equals a,t,g, or c
US-10-105-299-752

Query Match 4.2%: Score 20; DB 6; Length 5279;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgacct 149
|||||
Db 547 aagatctgacttgacct 566

RESULT 22
US-09-053-375B-420
Sequence 420, Application US/09053375B
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 420
LENGTH: 5427
TYPE: DNA
ORGANISM: Homo sapiens
US-09-053-375B-420

Query Match 4.2%: Score 20: DB 5: Length 5427;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 130 aagatctgtgacttggcct 149
|||||
Db 2707 aagatctgtgacttggcct 2726

RESULT 23
US-09-442-384B-437
Sequence 437, Application US/09442384B
GENERAL INFORMATION:
APPLICANT: Chemchik, Alex
APPLICANT: Lukashov, Matvey
TITLE OF INVENTION: Hematology/Immunology Array
FILE REFERENCE: CLON-006CIP15
CURRENT APPLICATION NUMBER: US/09/442,384B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 830
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 437
LENGTH: 5427
TYPE: DNA
ORGANISM: homo sapiens
US-09-442-384B-437

Query Match 4.2%: Score 20: DB 5: Length 5427;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 130 aagatctgtgacttggcct 149
|||||
Db 2707 aagatctgtgacttggcct 2726

RESULT 24
US-10-027-400-3
Sequence 3, Application US/10027400
GENERAL INFORMATION:
APPLICANT: WILLIAMS, Lewis T.
APPLICANT: ESCOBEDO, Jaime A.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market, Stewart Street Tower, 20th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/027,400
APPLICATION DATA:
FILING DATE: 19-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/461,917
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 2307K-267-2-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
TELEFAX: 415/326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5427 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 187..3507
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-027-400-3

Query Match 4.2%: Score 20: DB 6: Length 5427;
Best Local Similarity 100.0%: Pred. No. 1.3;
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 130 aagatctgtgacttggcct 149
|||||
Db 2707 AAGATCTGTGACTTTGGCCT 2726

RESULT 25
US-10-007-926A-209
Sequence 209, Application US/10007926A
GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOULGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 209
LENGTH: 5570
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: beta polypeptide (PDGFRB) gene.
US-10-007-926A-209

Query Match 4.2%: Score 20: DB 6: Length 5570;
Best Local Similarity 100.0%: Pred. No. 1.4;
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 130 aagatctgtgacttggcct 149
|||||
Db 2877 aagatctgtgacttggcct 2896

RESULT 26
US-09-538-331D-17143
Sequence 17143, Application US/09539331D
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleage, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.

```

; APPLICANT: Mullaby, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 17143
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incycle ID No: hu00007038
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3, 99, 284
; OTHER INFORMATION: d, t, c, g, or other
US-09-539-331D-17143
```

```

Query Match          4.0%: Score 19; DB 5; Length 303;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 128 tgaagatctgactctg 146
      |||
Db 112 tgaagatctgactctg 130
```

```

RESULT 27
; Sequence 358, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 358
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384B-358
```

```

Query Match          4.0%: Score 19; DB 5; Length 465;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 83 gagacctgctgctcgaa 101
      |||
Db 54 gagacctgctgctcgaa 72
```

```

RESULT 28
; Sequence 66, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey E.
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-006CIP13
; CURRENT APPLICATION NUMBER: US/09/442,366A
```

```

; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-66
```

```

Query Match          4.0%: Score 19; DB 5; Length 466;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 83 gagacctgctgctcgaa 101
      |||
Db 54 gagacctgctgctcgaa 72
```

```

RESULT 29
; Sequence 130, Application US/09911904
; GENERAL INFORMATION:
; APPLICANT: Farr, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 400742000200
; CURRENT APPLICATION NUMBER: US/09/911,904
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-911-904-130
```

```

Query Match          4.0%: Score 19; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 209 tgaagtgatgccccctga 227
      |||
Db 127 tgaagtgatgccccctga 145
```

```

RESULT 30
; Sequence 2068, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2068
```

LENGTH: 1063
TYPE: DNA
ORGANISM: Homo sapiens
US-10-106-698-2068

Query Match 4.0%; Score 19; DB 6; Length 1063;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 tgaagatctgacttgg 146
|||||
DB 454 TCACATCTGTACTTTCG 436

RESULT 31
US-09-937-060A-17
Sequence 17, Application US/09937060A
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: BANDMAN, Olga
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda
APPLICANT: LU, Dyung Alina M.
TITLE OF INVENTION: REGULATORS OF INTRACELLULAR PHOSPHORYLATION
FILE REFERENCE: PF-0683 PCT
CURRENT APPLICATION NUMBER: US/09/937,060A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/125,593; 60/135,049; 60/143,188
PRIOR FILING DATE: 1999-03-18; 1999-05-20; 1999-07-09
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 17
LENGTH: 1706
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 1425842CB1
US-09-937-060A-17

Query Match 4.0%; Score 19; DB 5; Length 1706;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 128 tgaagatctgacttgg 146
|||||
DB 577 tgaagatctgacttgg 595

RESULT 32
US-10-104-047-1465
Sequence 1465, Application US/10104047
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1465
LENGTH: 1939
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-1465

Query Match 4.0%; Score 19; DB 6; Length 1939;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 gtggccagagggatggagt 55
|||||
DB 1014 gtggccagagggatggagt 1032

RESULT 33
US-10-027-632-97991
Sequence 97991, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97991
LENGTH: 1948
TYPE: DNA
ORGANISM: Human
US-10-027-632-97991

Query Match 4.0%; Score 19; DB 6; Length 1948;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 acatctacaagaccctga 176
|||||
DB 958 acatctacaagaccctga 976

RESULT 34
US-10-027-632-97992
Sequence 97992, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23

```

: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 97992
: LENGTH: 1948
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-97992
```

```

Query Match          4.0%; Score 19; DB 6; Length 1948;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 158 acatctacaagaccctga 176
      |||||||
Db 958 acatctacaagaccctga 976
```

```

RESULT 35
US-09-053-375B-907/c
: Sequence 907, Application US/09053375B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Bibilashvili, Robert
: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053,375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 907
: LENGTH: 2344
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-053-375B-907
```

```

Query Match          4.0%; Score 19; DB 5; Length 2344;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 380 gggcccgagcgtgcgcac 398
      |||||||
Db 1579 GGGCCCCGAGCTGCCAC 1561
```

```

RESULT 36
US-09-053-375B-1006
: Sequence 1006, Application US/09053375B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Bibilashvili, Robert
: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053,375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1006
: LENGTH: 2526
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-053-375B-1006
```

```

Query Match          4.0%; Score 19; DB 5; Length 2526;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 209 tgaagtgatgccccctga 227
      |||||||
Db 2048 tgaagtgatgccccctga 2066
```

```

RESULT 37
US-09-053-375B-57
: Sequence 57, Application US/09053375B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Bibilashvili, Robert
: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053,375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 57
: LENGTH: 3949
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-053-375B-57
```

```

Query Match          4.0%; Score 19; DB 5; Length 3949;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 83 ggaacctgctgctcgaa 101
      |||||||
Db 2185 ggaacctgctgctcgaa 2203
```

```

RESULT 38
US-09-442-384B-773
: Sequence 773, Application US/09442384B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Lukashov, Matvey
: TITLE OF INVENTION: Hematology/Immunology Array
: FILE REFERENCE: CLON-006CIP15
: CURRENT APPLICATION NUMBER: US/09/442,384B
: CURRENT FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: 09/053,375
: PRIOR FILING DATE: 1998-03-31
: NUMBER OF SEQ ID NOS: 830
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 773
: LENGTH: 3949
: TYPE: DNA
: ORGANISM: homo sapiens
US-09-442-384B-773
```

```

Query Match          4.0%; Score 19; DB 5; Length 3949;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 83 ggaacctgctgctcgaa 101
      |||||||
Db 2185 ggaacctgctgctcgaa 2203
```

```

RESULT 39
US-09-721-544-12422/c
: Sequence 12422, Application US/09721544
: GENERAL INFORMATION:
: APPLICANT: Arterburn, Matthew
: APPLICANT: Asghari, Vida
: APPLICANT: Damavandi, Simin
: APPLICANT: Dickson, Mark
: APPLICANT: Drake, Jim
: APPLICANT: Drmanac, Radoje
```

```

: APPLICANT: Engleman, Carrie
: APPLICANT: Faulkner, Brandy
: APPLICANT: Garcia, Veronica
: APPLICANT: Giedt, Gretchen
: APPLICANT: Hunter, Kelly
: APPLICANT: Jones, Aaron
: APPLICANT: Jones, Lee
: APPLICANT: Kita, David
: APPLICANT: Labat, Ivan
: APPLICANT: Laroza, Mimi
: APPLICANT: Lomelli, Michelle
: APPLICANT: Nguyen, Phuong
: APPLICANT: Nogra, Margie
: APPLICANT: Palencia, Servando
: APPLICANT: Ralsi, Fariba
: APPLICANT: Smith, Benjamin
: APPLICANT: Tkach, Joe
: APPLICANT: Tran, Llen
: APPLICANT: Verna, Ron
: APPLICANT: Yang, Fei
: APPLICANT: Yim, Kenneth
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
: TITLE OF INVENTION: From a cDNA library of fetal liver-Spleen
: FILE REFERENCE: 728C1P
: CURRENT APPLICATION NUMBER: US/09/721,544
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 09/515,128
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: 09/034,341
: PRIOR FILING DATE: 1998-02-13
: NUMBER OF SEQ ID NOS: 24489
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 12422
: LENGTH: 340
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-721-544-12422

Query Match          3.8%; Score 18; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8  tgaagaatctgtctgct 25
      |||
Db 288  TCGAAGATCTTGTCTGCT 271

RESULT 40
: US-10-121-925-5
: Sequence 5, Application US/10121925
: GENERAL INFORMATION:
: APPLICANT: ROBINSON, KEITH E.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
: TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
: FILE REFERENCE: MNI-090
: CURRENT APPLICATION NUMBER: US/10/121,925
: CURRENT FILING DATE: 2002-04-12
: PRIOR APPLICATION NUMBER: US/09/948,802
: PRIOR FILING DATE: 2001-09-07
: PRIOR APPLICATION NUMBER: 09/387,212
: PRIOR FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 361
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: All occurrences of n indicate any nucleotide
: US-10-121-925-5
```

```

Query Match          3.8%; Score 18; DB 6; Length 361;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85  gacctggtctgcggaac 102
      |||
Db 244  gacctggtctgcggaac 261

RESULT 41
: US-10-121-995-5
: Sequence 5, Application US/10121995
: GENERAL INFORMATION:
: APPLICANT: ROBINSON, KEITH E.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
: TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
: FILE REFERENCE: MNI-090
: CURRENT APPLICATION NUMBER: US/10/121,995
: CURRENT FILING DATE: 2002-04-12
: PRIOR APPLICATION NUMBER: US/09/948,802
: PRIOR FILING DATE: 2001-09-07
: PRIOR APPLICATION NUMBER: 09/387,212
: PRIOR FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 361
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: All occurrences of n indicate any nucleotide
: US-10-121-995-5

Query Match          3.8%; Score 18; DB 6; Length 361;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85  gacctggtctgcggaac 102
      |||
Db 244  gacctggtctgcggaac 261

RESULT 42
: US-09-918-995-1503
: Sequence 1503, Application US/09918995
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
: TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
: FILE REFERENCE: 20411-756
: CURRENT APPLICATION NUMBER: US/09/918,995
: CURRENT FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: US/09/235,076
: PRIOR FILING DATE: 1999-01-20
: NUMBER OF SEQ ID NOS: 38054
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 1503
: LENGTH: 449
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(449)
: OTHER INFORMATION: n = A,T,C or G
: US-09-918-995-1503

Query Match          3.8%; Score 18; DB 5; Length 449;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85  gacctggtctgcggaac 102
```

Db 250 gaccgtgctgcgcgaac 267
|||||

RESULT 43
US-09-918-995-31621
; Sequence 31621, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31621
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(489)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31621

Query Match 3.8%; Score 18; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 262 gacgtgctgccttggg 279
|||||
Db 463 gacgtgctgccttggg 480

RESULT 44
US-10-027-632-15007
; Sequence 15007, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15007
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-15007

Query Match 3.8%; Score 18; DB 6; Length 738;
Best Local Similarity 100.0%; Pred. No. 16;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 23 gctacagcttcagtg 40
|||||
Db 460 gctacagcttcagtg 477

RESULT 45
US-10-027-632-15008
; Sequence 15008, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15008
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-15008

Query Match 3.8%; Score 18; DB 6; Length 738;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 23 gctacagcttcagtg 40
|||||
Db 460 gctacagcttcagtg 477

Search completed: July 16, 2002, 02:56:59
Job time: 24557 sec

GenCore version 4.5
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UM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:49:56 ; Search time 12941.8 Seconds
(without alignments)
787.375 Million cell updates/sec

Title: US-09-375-248-1_COPY_3044_3514
471
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Perfect score:

Sequence: OLIGO_NUC
Gap 60.0 , capext 60.0

Scoring table:

Searched: 21979536 seqs, 10817449327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Pending-Patents_NA_Main:*

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3: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
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5: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
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25: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*
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35: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US100_COMB.seq:*
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39: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
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41: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*

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45: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
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47: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
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58: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
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60: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
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62: /cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
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64: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6028_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6029_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6030_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6032_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6033_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6034_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	471	100.0	4111	1 PCT-US99-06133-1	Sequence 1, Appl1
2	471	100.0	4111	17 US-09-375-248-1	Sequence 1, Appl1
3	471	100.0	4195	3 US-07-959-951A-1	Sequence 1, Appl1
4	471	100.0	4195	6 US-08-257-754-1	Sequence 1, Appl1
5	471	100.0	4195	15 US-09-169-079-1	Sequence 36, Appl1
6	471	100.0	4416	10 US-08-601-132-36	Sequence 36, Appl1
7	471	100.0	4416	10 US-08-671-573A-36	Sequence 36, Appl1
8	471	100.0	4416	10 US-08-355-700-1	Sequence 1035, Ap
9	471	100.0	4416	17 US-09-440-302A-1035	Sequence 447, App
10	471	100.0	4416	18 US-09-442-384A-447	Sequence 636, App
11	471	100.0	4416	18 US-09-442-589B-636	Sequence 1, Appl1
12	471	100.0	4416	20 US-09-534-376A-1	Sequence 36, Appl1
13	471	100.0	4416	24 US-09-631-092-36	Sequence 31, Appl1
14	471	100.0	4425	8 US-08-446-648-31	Sequence 889, App
15	471	100.0	4425	11 US-08-770-449-31	Sequence 31, Appl1
16	471	100.0	4425	14 US-09-023-655-889	Sequence 101, App
17	471	100.0	4425	36 US-09-982-610-31	Sequence 15763, A
18	471	100.0	4425	56 US-60-167-943-103	Sequence 3, Appl1
19	471	100.0	4425	55 US-60-172-373-15763	Sequence 3, Appl1
20	471	100.0	4795	3 US-07-959-951A-3	Sequence 3, Appl1
21	471	100.0	4795	6 US-08-257-754-3	Sequence 45, Appl1
22	471	100.0	4795	15 US-09-169-079-3	Sequence 455, App
23	471	100.0	9108	8 US-08-446-648-45	Sequence 951, App
24	471	100.0	9108	36 US-09-209-009-455	Sequence 4300, Ap
25	471	100.0	3277	59 US-60-213-360-951	Sequence 4274, Ap
26	420	89.2	3277	71 US-60-324-185-4300	Sequence 19, Appl
27	420	89.2	3277	71 US-60-324-185-4274	Sequence 17, Appl
28	420	89.2	4459	71 US-08-256-769B-19	
29	420	89.2	6826	6 US-08-446-648-17	
30	420	89.2	6827	8 US-08-446-648-17	
31	420	89.2	6827	8 US-08-446-648-17	


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C 32 420 89.2 6827 11 US-08-770-449-17 Sequence 17, Appl
C 33 420 89.2 6827 36 US-09-982-610-17 Sequence 17, Appl
34 401 85.1 415 60 US-60-213-178-1247 Sequence 1247, Ap
35 405 64.8 4113 37 US-10-081-126-1 Sequence 1, Appl
36 405 64.8 4450 1 PCT-US99-08079-1 Sequence 1, Appl
37 405 64.8 4450 37 US-10-012-214-1 Sequence 1, Appl
38 189 40.1 443 28 US-09-710-286-674 Sequence 674, Appl
39 189 40.1 1046 28 US-09-710-286-2884 Sequence 2884, Ap
40 183 38.9 535 28 US-09-716-953-1245 Sequence 1245, Ap
C 41 126 26.8 610 56 US-60-170-374-1824 Sequence 1824, Ap
C 42 126 26.8 1077 60 US-60-213-178-297 Sequence 297, App
C 43 126 26.8 32768 60 US-60-213-178-954 Sequence 954, App
C 44 125 26.5 496 60 US-60-178-305-229 Sequence 229, App
C 45 113 24.0 516 56 US-60-178-305-229 Sequence 229, App
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ALIGNMENTS

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RESULT 1
PCT-US99-06133-1
: Sequence 1, Application PC/TUS9906133
: GENERAL INFORMATION:
: APPLICANT: Ferrell, Robert E
: APPLICANT: Alltalo, Karl
: APPLICANT: Finegold, David N
: APPLICANT: Karkkainen, Marika
: TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
: TITLE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
: FILE REFERENCE: 28967/35255
: CURRENT APPLICATION NUMBER: PCT/US99/06133
: CURRENT FILING DATE: 1999-03-26
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4111
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (20)..(4111)
: OTHER INFORMATION: Human FLT4 (VEGFR-3) Long form cDNA
PCT-US99-06133-1
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Query Match 100.0%; Score 471; DB 1; Length 4111;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3044 ctgacatggaagatctgtctgtctacagcttcccgagtggtgcagaggaatgagttcctg 60
QY 61 gcttccgaaagtgtacatccacagagacctgctgtcgcgaaacatctgtctcgaagaagc 120
Db 3104 gcttccgaaagtgtacatccacagagacctgctgtcgcgaaacatctgtctcgaagaagc 120
QY 121 gacgtggtggaagatctgtgacttggccttgcgcgggacatctacaagaagacctgtactac 180
Db 3164 gacgtggtggaagatctgtgacttggccttgcgcgggacatctacaagaagacctgtactac 180
QY 181 gtccgcaaggagcagtgcccggtgctgccttgaagtgtgagtgcccttgaagaatctctcgac 240
Db 3224 gtccgcaaggagcagtgcccggtgctgccttgaagtgtgagtgcccttgaagaatctctcgac 240
QY 241 aagtgtaacacacagcagagtgaagctgtgtctccttgggtgtcctctctcgtggagatcttc 300
Db 3284 aagtgtaacacacagcagagtgaagctgtgtctccttgggtgtcctctctcgtggagatcttc 300
QY 301 tctctgggggctcccgctacccctcgagggtgtcagatcaatgaaggatctctgcagcgtgctg 360
Db 3344 tctctgggggctcccgctacccctcgagggtgtcagatcaatgaaggatctctgcagcgtgctg 360
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QY 361 agagacggcacaaagatgagggcccgagtgctgacctcccgccatcagccgcatcatg 420
Db 3404 agagacggcacaaagatgagggcccgagtgctgacctcccgccatcagccgcatcatg 420
QY 421 ctgacctgtgtctcgagagaccacaaaggcagacctgtcatctctggagctg 471
Db 3464 ctgacctgtgtctcgagagaccacaaaggcagacctgtcatctctggagctg 471
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RESULT 2
US-09-375-248-1
: Sequence 1, Application US/09375248
: GENERAL INFORMATION:
: APPLICANT: Ferrell, Robert E.
: APPLICANT: Alltalo, Karl
: APPLICANT: Finegold, David N.
: APPLICANT: Karkkainen, Marika
: TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
: TITLE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
: FILE REFERENCE: 28967/35255A
: CURRENT APPLICATION NUMBER: US/09/375,248
: CURRENT FILING DATE: 1999-08-16
: EARLIER APPLICATION NUMBER: PCT/US99/06133
: EARLIER FILING DATE: 1999-03-26
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4111
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (20)..(4111)
: OTHER INFORMATION: Human FLT4 (VEGFR-3) Long form cDNA
US-09-375-248-1
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Query Match 100.0%; Score 471; DB 17; Length 4111;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3044 ctgacatggaagatctgtctgtctacagcttcccgagtggtgcagaggaatgagttcctg 60
QY 61 gcttccgaaagtgtacatccacagagacctgctgtcgcgaaacatctgtctcgaagaagc 120
Db 3104 gcttccgaaagtgtacatccacagagacctgctgtcgcgaaacatctgtctcgaagaagc 120
QY 121 gacgtggtggaagatctgtgacttggccttgcgcgggacatctacaagaagacctgtactac 180
Db 3164 gacgtggtggaagatctgtgacttggccttgcgcgggacatctacaagaagacctgtactac 180
QY 181 gtccgcaaggagcagtgcccggtgctgccttgaagtgtgagtgcccttgaagaatctctcgac 240
Db 3224 gtccgcaaggagcagtgcccggtgctgccttgaagtgtgagtgcccttgaagaatctctcgac 240
QY 241 aagtgtaacacacagcagagtgaagctgtgtctccttgggtgtcctctctcgtggagatcttc 300
Db 3284 aagtgtaacacacagcagagtgaagctgtgtctccttgggtgtcctctctcgtggagatcttc 300
QY 301 tctctgggggctcccgctacccctcgagggtgtcagatcaatgaaggatctctgcagcgtgctg 360
Db 3344 tctctgggggctcccgctacccctcgagggtgtcagatcaatgaaggatctctgcagcgtgctg 360
QY 361 agagacggcacaaagatgagggcccgagtgctgacctcccgccatcagccgcatcatg 420
Db 3404 agagacggcacaaagatgagggcccgagtgctgacctcccgccatcagccgcatcatg 420
QY 421 ctgacctgtgtctcgagagaccacaaaggcagacctgtcatctctggagctg 471
Db 3464 ctgacctgtgtctcgagagaccacaaaggcagacctgtcatctctggagctg 471
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```
RESULT 3
US-07-959-951A-1
: Sequence 1, Application US/0795951A
: GENERAL INFORMATION:
: APPLICANT: Alltalo, Karl, et al.
: TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/959,951A
: FILING DATE: 19921009
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Gruber, Lewis S.
: REGISTRATION NUMBER: 30,060
: REFERENCE/DOCKET NUMBER: 28113/31104
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4195 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..3916
: US-07-959-951A-1

Query Match          100.0%; Score 471; DB 3; Length 4195;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacacatgaagatctgtctacagctcccaagtgccagaggaatgagttcctg 60
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DB 3044 CTGACCATGGAAGATCTTGTCTCTACAGCTTCACAGTGGCCAGAGGAGATGAGTTCTCTG 3103

OY 61 gcttccgaagaagtgacacacacagagactgctgctcggaaacattcgtctggaagc 120
    |||||||
DB 3104 GCTTCCGAAAGTGACATCCACAGAGACTGGCTGCGAAGCATTTCTGCTGGGAAAGC 3163

OY 121 gaagtggagaaatctgtgacttgagccttgcgcggagacattcaaaagccctgactac 180
    |||||||
DB 3164 GAGCTGGTGAAGATCTGTGACTTTGGCCTTGCCTGGGACATCTTACAAAGACCTTGACTTAC 3223

OY 181 gtccgaagagcagtgcccgagctgccccttgaagtgatggcccttgaagacatcttcgac 240
    |||||||
DB 3224 GTCCGCAAGGAGAGTGGCCCGCTGCCCTGAAGTGATGGCCCTGTAAGACATCTTTCGAC 3283

OY 241 aagtggtacacacagcagagatgacgtgtgtccttgggggtgctctctctggaagatcttc 300
    |||||||
DB 3284 AAGGTGTACACACAGCAGAGATGAGCTGTGCTGCTTGGGGTCTTCTCTGGGAGATCTTTC 3343

OY 301 tctctggagagccctccctgacctgaggtgacagatcaatgaagagttctgcagagcgagctg 360
    |||||||
DB 3344 TCTCTGGGGCTCTCCCGTACCTCGGGGTGAGATCAATGAGAGTTTCTGCCAGCGGCTG 3403
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OY 361 agagacgcacaaagatgaagggcccgagacttggacactccgcacataccgcgcatcatg 420
    |||||||
DB 3404 AGAGACGCACAAAGATGAGGGCCCGAGCTGGCCACTCCGCCCATACCGGCATCATG 3463

OY 421 ctgaactgtgtgtcgcgagaccccaagcgagagactgtactctcggagctg 471
    |||||||
DB 3464 CTGAAGTGTGTGTCCGAGACCCCAAGGCGAGACCTGCAATCTCGGAGCTG 3514

RESULT 4
US-08-257-754-1
: Sequence 1, Application US/08257754
: GENERAL INFORMATION:
: APPLICANT: Alltalo, Karl
: APPLICANT: Kaipainen, Arja
: APPLICANT: Korhonen, Jaana
: APPLICANT: Mustonen, Tuja
: APPLICANT: Pajusola, Karl
: APPLICANT: Mäkeläinen, Marja-Terttu
: APPLICANT: Kärnä, Paivi
: TITLE OF INVENTION: FLT4 RECEPTOR TYROSINE KINASE AND ITS USE IN
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/257,754
: FILING DATE: 09-JUN-1994
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/959,951
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28344/32133
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4195 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..3916
: US-08-257-754-1

Query Match          100.0%; Score 471; DB 6; Length 4195;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacacatgaagatctgtctacagctcccaagtgccagaggaatgagttcctg 60
    |||||||
DB 3044 CTGACCATGGAAGATCTTGTCTCTACAGCTTCACAGTGGCCAGAGGAGATGAGTTCTCTG 3103

OY 61 gcttccgaagaatgacacacacagagactgctgctcggaaacattcgtctggaagc 120
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Db 3104 GCTTCCGAAGTGCATCCACAGACCTTGCTGCGAATCTGCTGCGAAGC 3163
OY 121 gacgtgtgaagatctgtgacttgccttgcgcggagacatctcaagaacctgtactac 180
Db 3164 GACCTGTGTAAGATCTGTGACTTTGGCTTGGCCGGACATCTACAAAGACCTGTGACTAC 3223
OY 181 gtccgaagggcagtgcccgctgcgcctccgaaagtgaatggccccctaaagacatcttcagc 240
Db 3224 GTCCCGAAGGCGCAGTCCCGGCTGCCCTGGAATGATGGCCCTTAAAGACATCTTGAC 3283
OY 241 aaggtttacaccacgacgagatgacgtgtgcttctgggtgcttctcctggagacatcttc 300
Db 3284 AAGGTTTAACACGACGACGAGTGTGCTGCTTGGGGTGTCTCTTGAGGATCTTC 3343
OY 301 tctctgggggctcccccgtaccctgggtgagtgatcaatgaagagttctgcgcagcgctc 360
Db 3344 TCTCTGGGGGCTCCCGTACCTTGAGGTGACAGATCAATGAAGAGATTCTGCGACGGCTG 3403
OY 361 agagacggcacaaagatgaaggcccgagctgcgcacatcccgacatacgccgacatcg 420
Db 3404 AGAGACGGCACAAAGATGAGGCGCCCGGAGCTGGCCACTCCGCCATACGCCATCATG 3463
OY 421 ctgaactgtgtgtccggagaccaccaagcgagacctgtcgtgagctg 471
Db 3464 CTGAACGTGCTGCTCCGAGACCCCAAGCGAGACCTGTGATCTCGAGCTG 3514
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RESULT 5
US-09-169-079-1

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: Sequence 1, Application US/09169079
: GENERAL INFORMATION:
: APPLICANT: Alltalo, Karl
: APPLICANT: Kaipainen, Arja
: APPLICANT: Valtola, Reija
: APPLICANT: Jussila, Lotta
: TITLE OF INVENTION: Fil4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therap
: FILE REFERENCE: 28113/34891
: CURRENT APPLICATION NUMBER: US/09/169,079
: EARLIER FILING DATE: 1998-10-09
: EARLIER APPLICATION NUMBER: 08/901,710
: EARLIER FILING DATE: 1997-07-28
: EARLIER APPLICATION NUMBER: 08/340,011
: EARLIER FILING DATE: 1994-11-14
: EARLIER APPLICATION NUMBER: 08/257,754
: EARLIER FILING DATE: 1994-07-09
: EARLIER APPLICATION NUMBER: 07/959,951
: EARLIER FILING DATE: 1992-10-09
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4195
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (20)..(3913)
: US-09-169-079-1
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Query Match 100.0%; Score 471; DB 15; Length 4195;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ctgaccatggaagatctgtctgtactaagcttcaggctggccgagagatgagttcccg 60
Db 3044 ctgaccatggaagatctgtctgtactaagcttcaggctggccgagagatgagttcccg 3103
OY 61 gcttcccgaaagtgcattccacagagacctgtgctccggaacaatctgtctgcgaaagc 120
Db 3104 gcttcccgaaagtgcattccacagagacctgtgctccggaacaatctgtctgcgaaagc 3163
OY 121 gacgtgtgaagatctgtgacttgccttgcgcggagacatctcaagaacctgtactac 180
```

```
Db 3164 gacgtgtgaagatctgtgacttgccttgcgcggagacatctcaagaacctgtactac 3223
OY 181 gtccgaagggcagtgcccgctgcgcctccgaaagtgaatggccccctaaagacatcttcagc 240
Db 3224 gtccgaagggcagtgcccgctgcgcctccgaaagtgaatggccccctaaagacatcttcagc 3283
OY 241 aaggtttacaccacgacgagatgacgtgtgcttctgggtgcttctcctggagacatcttc 300
Db 3284 aaggtttacaccacgacgagatgacgtgtgcttctgggtgcttctcctggagacatcttc 3343
OY 301 tctctgggggctcccccgtaccctgggtgagtgatcaatgaagagttctgcgcagcgctc 360
Db 3344 TCTCTGGGGGCTCCCGTACCTTGAGGTGACAGATCAATGAAGAGATTCTGCGACGGCTG 3403
OY 361 agagacggcacaaagatgaaggcccgagctgcgcacatcccgacatacgccgacatcg 420
Db 3404 agagacggcacaaagatgaaggcccgagctgcgcacatcccgacatacgccgacatcg 3463
OY 421 ctgaactgtgtgtccggagaccaccaagcgagacctgtcgtgagctg 471
Db 3464 CTGAACGTGCTGCTCCGAGACCCCAAGCGAGACCTGTGATCTCGAGCTG 3514
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RESULT 6
US-08-601-132-36

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: Sequence 36, Application US/08601132
: GENERAL INFORMATION:
: APPLICANT: Alltalo, Karl
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Receptor Ligand
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/601,132
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28113/33118
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4416 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-601-132-36
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Query Match

Best Local Similarity 100.0%; Score 471; DB 10; Length 4416;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgaccatggaagatctgtctgtactaagcttcaggctggccgagagatgagttcccg 60
Db 3044 CTGACATGGAAGATCTGTCTGTACTACAGCTTCCAGGTGCGCAGAGGATGAGTCTCTG 3103
```

OY	61	gcctccccaagatgcacatccaaagagactgctgcctcgcgaacatctctgctctgcgaagc	120
Db	3104	gctttcccaaaagtcattctccACAGAGACTTGGCTGCGAACTTCTGCTGCGAAAC	3163
OY	121	gaagtgatgaagactctgtagctcttgacctgcgcggagacatcacaaagaacctgaactac	180
Db	3164	GACGTGGTGAAGATCTGTGAATTTGGGCTTGCCCGGACATCTACAAAGACCTTGACTAC	3222
OY	181	gtccgcgaaggcagctccggcctgacccctgaagtgagatggccctgnaagacatctctgac	240
Db	3224	GTCCGCAAGGGCACTGTCCCGGCTGCCCTGAATGGATGGCCCTGAAGCATTTTCAGC	3283
OY	241	aagtgatcacaccagaagatgaaagctgtgagctcttgagggtgctctctcggagaatcttc	300
Db	3284	AAGGTGTACACACCCAGAGTGAAGCTGTGGTCTCTTTGGGGTCTCTTCGGGAGATTTTC	3343
OY	301	tctctggggagcctcccccgtaccctctgggggtgcagatcaatgaagagctctgcagcagcgctg	360
Db	3344	TCTCTGGGGGCTCCCTCGTACCCTGGGGGTGCATATATGAGAGATTTCTGCCAGCGGCTG	3403
OY	361	agaaagcgcacaaagatgatagggcccccggagctgagccatcccgacataacgcgcatacgt	420
Db	3404	AGAAACGGCACAAAGGATGAGAGGCCCGCGAGACTGTGGCACTCCGCATAGCCGCATCATG	3463
OY	421	ctggaactgcgcgtctcgagaaagcccaaggagagaaacctgaaattcttggagctg	471
Db	3464	CTGAACTGCTGTGCTCCGAGACGCCCAAGGGGAGAGCTGCATTTCTGGAGCTTG	3514

```

; LENGTH: 4416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-671-573A-36

```

QY	1	cttagaccctggaaagatctgtctgtctataagctctccaaagtgcgaagaggaatgtaagttcctg	60
Db	3044	CTGACCATTGGAAAGATCTTGTCTCTACAGCTTCACAGTGGCGAGAGGATGTGACATTCTCTG	3103
QY	61	gcttcaccgaagaatgatcatccacagagaacctggtctctcggaaacatctctgtctcggaagac	120
Db	3104	GCTTCCCGAAAGTGCATCCACAGACACTGGCTGCGGAAACATTCTGTCGGAAAGC	3163
QY	121	gaagctgtgaagaatctgtgaacttttgaccttgcgcggagacatctacaaagacctgtactac	180
Db	3164	GACCTGTGTGAAGATCTGTGACTTTTGGCTTTGCCGGGACATCTACAAAGACCCCTGACTAC	3223
QY	181	gtcccgcaaggacagtgcccggtctgccctcgaagatgatggtccctcgaaagacatctctgcac	240
Db	3224	GTCGCGCAAGGGACAGTGTCCCGGCTGCCCTCTGAAGTGAATGACCCCTGAAAGCAATCTTCTCAC	3283
QY	241	aaggtgtacacacacgacagagtgaaegtgtgtctcttcttggtgtctctctctctcggaagcttc	300
Db	3284	AAAGGTGTACACCCACGACAGAGTGAAGCTGTGTGCTCTTTGGGGTCTCTCTGGAGATCTTC	3343
QY	301	tctcttgagggtccctcccccgtacaccttggtgtgacgaatcgaatgtgaatcttctgccaaagcgtctg	360
Db	3344	TCTCTGGGGGCTCTCCCTGTACCTGTGGGGTGAGATCAATGAGAACTTGTGCACGGCTG	3403
QY	361	agagacgtgcacaaagatgaagggtcccggtgactctgtgcacttccgcatacgcgcatactg	420
Db	3404	AGAGACGCGCAACAGAGTGAAGGGCCCGGAGCTGGGCACCTCCCGCATATGCGCGCATATG	3463
QY	421	cttaaatctgtctgtcggagagaccctcaagcgagaaactgcatactctctggagcgtg	471
Db	3464	CTTAACCTGCTGGTCTCGGAGACCCCAAGGCGAATCCTGTGATTCTGTGGACACTTG	3514

APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-671-573b-36

Query Match
Best Local Similarity 100.0%; Score 471; DB 10; Length 4416;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgacatgtgaagatctgtctgtacagcttcacagtgccagagagatgttctc 60
DB 3044 CTGACATGGAAGATCTGTCTGTCTGACAGTTCACAGTCCGACAGCATGATTCCTG 3103
QY 61 gctcccaagaagtcattccacagagagactgtgtctcggaaacttcgtgtcggaaagc 120
DB 3104 GCTTCCGGAAGTGCATTCACAGAGACCTGCTCGGAACATTCCTGCGAAAGC 3163
QY 121 gaagtgtgaagatctgtacttgccttcgcccggagacatctacaagaccctgactac 180
DB 3164 GACCTGTGAAGATCTGTGACTTTGGCCTTGGCCGGAGACATCTCAAGACCTGACTAC 3223
QY 181 gtccgaaggcgaatgcccggctgtgcccctgaagtgtgagtgccctgaagcatcttcgac 240
DB 3224 GTCCGCAAGGCGATGCCCGCTGCCCTGAGTGTGAGTGCCTCGAAGCATCTTCGAC 3283
QY 241 aaggtgtacacacagcagagatgaagtggtgttcttgggtgtgtcttcctggagatcttc 300
DB 3284 AAGGTGTACACACAGCAGATGAGCTGTGCTTTGGGTCTTCTCTGCGAGATCTTC 3343
QY 301 tctctgggggctcccccgtacacctgggggtgcagatcaatgagagttcttcagcgagctg 360
DB 3344 TCTCTGGGGCTCCCGTACCTGGGGTGCAGATCAATGAGAGTTCTGCGAGCGCTG 3403
QY 361 agagacgcaagagatgaagggcccgagctgtgccaactccgcataagcgacatcatg 420
DB 3404 AGAGACGGCAAGATGAGGGCCCGAGCTGCCCATCTCCCGCATACCCCGCATCATG 3463
QY 421 ctgaactgtgtgtcggagagaccccaagcgagacactgcatcttcggagctg 471
DB 3464 CTGAACGTGTGTGCGGAGACCCCAAGCGAGACGTGCAATTCCTGCGAGCTG 3514

RESULT 9
US-09-355-700-1
Sequence 1, Application US/09355700

GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research
Helsinki University Licensing
Aittalo, Kari(U.S. only)
Joukov, Vladimir (U.S. only)
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,700
FILING DATE: 05-Nov-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,430
FILING DATE: 05-FEB-1997
APPLICATION NUMBER: PCT/US96/00427
FILING DATE: 01-AUG-1996
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-355-700-1

Query Match
Best Local Similarity 100.0%; Score 471; DB 17; Length 4416;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgacatgtgaagatctgtctgtacagcttcacagtgccagagagatgttctc 60
DB 3044 CTGACATGGAAGATCTGTCTGTCTGACAGTTCACAGTCCGACAGCATGATTCCTG 3103
QY 61 gctcccaagaagtcattccacagagagactgtgtctcggaaacttcgtgtcggaaagc 120
DB 3104 GCTTCCGGAAGTGCATTCACAGAGACCTGCTCGGAACATTCCTGCGAAAGC 3163
QY 121 gaagtgtgaagatctgtacttgccttcgcccggagacatctacaagaccctgactac 180
DB 3164 GACCTGTGAAGATCTGTGACTTTGGCCTTGGCCGGAGACATCTCAAGACCTGACTAC 3223
QY 181 gtccgaaggcgaatgcccggctgtgcccctgaagtgtgagtgccctgaagcatcttcgac 240
DB 3224 GTCCGCAAGGCGATGCCCGCTGCCCTGAGTGTGAGTGCCTCGAAGCATCTTCGAC 3283
QY 241 aaggtgtacacacagcagagatgaagtggtgttcttgggtgtgtcttcctggagatcttc 300
DB 3284 AAGGTGTACACACAGCAGATGAGCTGTGCTTTGGGTCTTCTCTGCGAGATCTTC 3343
QY 301 tctctgggggctcccccgtacacctgggggtgcagatcaatgagagttcttcgacagcgctg 360

```
Db 3344 TCTCTGGGGCCCTCCCTGACCTGGGCTGCAGATCAATGAGAGTTCTGCAGCGGCTG 3403
Oy 361 agagacgacacagatgagagggcccgagctgagccatcccgacatagcgagctcag 420
Db 3404 AGAGACGGCACAAGATGAGGGCCCCGGAGCTGGCCACTCCGCCCATACGCCGATCATG 3463
Oy 421 ctgaactgctgctcgagagaccccaagcgagacctgcatctcggagctg 471
Db 3464 CTGAACCTGCTCGTCCGAGACCCCAAGCGAGACCTGCATTCGCGAGCTG 3514
```

```
RESULT 10
US-09-440-302A-1035
; Sequence 1035, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey E.
; FILE REFERENCE: CIJON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440.302A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053.375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1035
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-440-302A-1035
```

```
Query Match 100.0%; Score 471; DB 18; Length 4416;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 ctgacacatgagaatctctgtctacagctccagctgacagagagatgagctctg 60
Db 3044 ctgacacatgagaatctctgtctacagctccagctgacagagagatgagctctg 3103
Oy 61 gctcccgaaagtgatccacacagagacctgctcggaacatctgctcggaagc 120
Db 3104 gctcccgaaagtgatccacacagagacctgctcggaacatctgctcggaagc 3163
Oy 121 gacgtgtagaagatctgacattgacctgcccggagacatctacaaagacctgactac 180
Db 3164 gacgtgtagaagatctgacattgacctgcccggagacatctacaaagacctgactac 3223
Oy 181 gtcgcgaagggcagtgccgcgctgcccctgaagtgaatggccccctgaagacatctcgac 240
Db 3224 gtcgcgaagggcagtgccgcgctgcccctgaagtgaatggccccctgaagacatctcgac 3283
Oy 241 aaggtgacacacagagatgagctggtctcttgagggtctctctctgagagatctc 300
Db 3284 aaggtgacacacagagatgagctggtctcttgagggtctctctctgagagatctc 3343
Oy 301 tctctgggggctcccccgtacccctgggtgagatcaatgaagagatctctccggcgctg 360
Db 3344 tctctgggggctcccccgtacccctgggtgagatcaatgaagagatctctccggcgctg 3403
Oy 361 agagacgacacagagatgagggcccgagacctgacacatcccgacatagcgacatag 420
Db 3404 agagacgacacagagatgagggcccgagacctgacacatcccgacatagcgacatag 3463
Oy 421 ctgaactgctgctcgagagaccccaagcgagacctgcatctcggagctg 471
Db 3464 ctgaactgctgctcgagagaccccaagcgagacctgcatctcggagctg 3514
```

```
RESULT 11
US-09-442-384A-447
; Sequence 447, Application US/09442384A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey
; FILE REFERENCE: Hematology/Immunology Array
; CURRENT APPLICATION NUMBER: US/09/442.384A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053.375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-442-384A-447
```

```
Query Match 100.0%; Score 471; DB 18; Length 4416;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 ctgacacatgagaatctctgtctacagctccagctgacagagagatgagctctg 60
Db 3044 ctgacacatgagaatctctgtctacagctccagctgacagagagatgagctctg 3103
Oy 61 gctcccgaaagtgatccacacagagacctgctcggaacatctgctcggaagc 120
Db 3104 gctcccgaaagtgatccacacagagacctgctcggaacatctgctcggaagc 3163
Oy 121 gacgtgtagaagatctgacattgacctgcccggagacatctacaaagacctgactac 180
Db 3164 gacgtgtagaagatctgacattgacctgcccggagacatctacaaagacctgactac 3223
Oy 181 gtcgcgaagggcagtgccgcgctgcccctgaagtgaatggccccctgaagacatctcgac 240
Db 3224 gtcgcgaagggcagtgccgcgctgcccctgaagtgaatggccccctgaagacatctcgac 3283
Oy 241 aaggtgacacacagagatgagctggtctcttgagggtctctctctgagagatctc 300
Db 3284 aaggtgacacacagagatgagctggtctcttgagggtctctctctgagagatctc 3343
Oy 301 tctctgggggctcccccgtacccctgggtgagatcaatgaagagatctctccggcgctg 360
Db 3344 tctctgggggctcccccgtacccctgggtgagatcaatgaagagatctctccggcgctg 3403
Oy 361 agagacgacacagagatgagggcccgagacctgacacatcccgacatagcgacatag 420
Db 3404 agagacgacacagagatgagggcccgagacctgacacatcccgacatagcgacatag 3463
Oy 421 ctgaactgctgctcgagagaccccaagcgagacctgcatctcggagctg 471
Db 3464 ctgaactgctgctcgagagaccccaagcgagacctgcatctcggagctg 3514
```

```
RESULT 12
US-09-442-589B-636
; Sequence 636, Application US/09442589B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey
; FILE REFERENCE: Human Cardiovascular Array
```

RESULT 13
 US-09-534-376A-1
 : Sequence 1, Application US/09534376A
 : GENERAL INFORMATION:
 : APPLICANT: Altalo, Karl
 : APPLICANT: Joukov, Vladimir
 : TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN
 : TITLE OF INVENTION: AND GENE, MUTANTS THEREOF, AND USES THEREOF
 : FILE REFERENCE: 28967/24140A
 : CURRENT APPLICATION NUMBER: US/09/534, 376A
 : CURRENT FILING DATE: 2000-03-24
 : PRIOR APPLICATION NUMBER: 09/355,700

OY	1	ctgaccactggaaagatcttctgtctgtactaacgtctccaaagtctgcagaagagatgaaagtctctcg	60
Db	3044	ctgaccactggaaagatcttctgtctgtactaacgtctccaaagtctgcagaagagatgaaagtctctcg	310
OY	61	gtctcccgaaagtgcattccatacaagaagaccctgctgcctcggagacattctgtcgtctcggaagc	120
Db	3104	gtctcccgaaagtgcattccatacaagaagaccctgctgcctcggagacattctgtcgtctcggaagc	316
OY	121	gacgtggtgaaagatcttgaattcttgacctgtgccggagacattctataaagaaccctgactaac	180
Db	3164	gacgtggtgaaagatcttgaattcttgacctgtgccggagacattctataaagaaccctgactaac	322
OY	181	gtccgcgaagggcagctgcgcgcgcgtgccctctaaattgatactgcgcccttgaaagacattcttcac	240
Db	3224	gtccgcgaagggcagctgcgcgcgcgtgccctctaaattgatactgcgcccttgaaagacattcttcac	328
OY	241	aagctgtataccacacgcacgacgaatgaacgtgtgacctcttgaggctctctctcgtggagattctc	300
Db	3284	aagctgtataccacacgcacgacgaatgaacgtgtgacctcttgaggctctctctcgtggagattctc	334
OY	301	tctctcgggggcctctcccgctacccctctgggtgcgcagatacaatgaagaagtctctgcagaagctgtc	360
Db	3344	tctctcgggggcctctcccgctacccctctgggtgcgcagatacaatgaagaagtctctgcagaagctgtc	340
OY	361	agaagacggcccaagatgatgaaggtcccggaagctgtgcacatcccgccatatagcgcgcatcatgt	420
Db	3404	agaagacggcccaagatgatgaaggtcccggaagctgtgcacatcccgccatatagcgcgcatcatgt	346
OY	421	ctgaactgctgtgcctgcagaccaccaagaagggaaccttgattctctggagctgt	471
Db	3464	ctgaactgctgtgcctgcagaccaccaagaagggaaccttgattctctggagctgt	3514

RESULT 14
US-09-631-092-36
Sequence 36, Application US/09631092
GENERAL INFORMATION:
APPLICANT: Alltalo, Kari
Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/631,092
FILING DATE: 02-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gase, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-631-092-36

Query Match 100.0%; Score 471; DB 24; Length 4416;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacatgtaaatctctgtctctacagcttcaggtgagcagaaggaagttcctg 60
DB 3044 CTGACCATGGAAGATCTTGTCTCTACACCTTCACAGTGGCCAGAGGATGAGTTCTCG 3103

OY 61 gcttccgaagtgatccacagaagcctgctgctcggaacatctgctcgaagaac 120
DB 3104 GCTTCCGGAAGTGATCCACAGACAGCTGCTCGGACACATTCTGCTGCGAAGAC 3163

OY 121 gacgtgtgaagatctgtacttgctgctcccgagacatctacaagaacctgactac 180
DB 3164 GACGTGTGAAGATCTGTACTTTGGCTTGGCCGGACATCTACAAAGACCTGACTAC 3223

OY 181 gtccgaagggcagtgcccgctgctccctgaagtgtatgccccctgaagaagcattctgac 240
DB 3224 GTCCGCAAGGCGAGTCCCGCTGCCCTGAAGTGGATGGCCCTGAAGCATCTTTCAGC 3283

OY 241 aaggtgtacaacagcagatgaagtgatgctccttggtggtgctctctctggaagcgtc 300
DB 3284 AAGGTGTACAACAGCAGATGACGTGCTGCTTGGGGTCTCTCTCGGAGATCTTTC 3343

OY 301 tctctgggggccccccgaaccttggtggtgagatcaatgaggaagttctgcccagcgctg 360
DB 3344 TCTCTGGGGCCCTCCCGTACCCTGGGGTGCGATCAATGAGGAGTTCTCCGACGGCTG 3403

OY 361 agagacgacagaagatgagggcccgagctgagcactcccgacatacgccgacatacg 420
DB 361 AGAGACGACAGAAGATGAGGGCCCGAGCTGAGCCTCCCGCCATFAGCCGCATCATG 3463

DB 3404 AGAGACGACAGAAGATGAGGGCCCGGAGCTGAGCCTCCCGCCATFAGCCGCATCATG 3463

OY 421 ctgaactgtgtccgagagaccacagagcagaccgtgactctcgagctg 471
DB 3464 CTGAACCTGTGTCCGAGAGCCCAAGCGAGACCTGCATTCGTGAGACTG 3514

RESULT 15
US-08-446-648-31
Sequence 31, Application US/08446648
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,648
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ. ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-446-648-31

Query Match 100.0%; Score 471; DB 8; Length 4425;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacatgtaaatctctgtctctacagcttcaggtgagcagaaggaagttcctg 60
DB 3055 CTGACCATGGAAGATCTTGTCTCTACACCTTCACAGTGGCCAGAGGATGAGTTCTCG 3114

OY 61 gcttccgaagtgatccacagaagcctgctgctcggaacatctgctcgaagaac 120
DB 3115 GCTTCCGGAAGTGATCCACAGACAGCTGCTCGGACACATTCTGCTGCGAAGAC 3174

OY 121 gacgtgtgaagatctgtacttgctgctcccgagacatctacaagaacctgactac 180
DB 3175 GACGTGTGAAGATCTGTACTTTGGCTTGGCCGGACATCTACAAAGACCTGACTAC 3234

OY 181 gtccgaagggcagtgcccgctgctccctgaagtgtatgagccccctgaagaagcattctgac 240

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 889:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1150990
US-09-023-655-889

Query Match 100.0%; Score 471; DB 14; Length 4425;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcacgaagagatctgtctgtacagcttccaggtggccgaagagatgtcttcctg 60
DB 3055 CTGACCATGAGAGATCTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGATGAGTCTCTG 3114
OY 61 gctcccgaaagtgatccacagagaccctgctcgcgcgaacattctgtctggaagc 120
DB 3115 GCTTCCCGAAGTGCAATCCACAGACCTGGCTCTCGGACATTCTCTCGGAAAGC 3174
OY 121 gaagtgatgaagatctgtgactttgaccttgccggagacatctaaagaccctgactac 180
DB 3175 GACGTGTGAAGATCTGTGACTTTGGCCCTTCCGCGACATCTCAAAAGACCTGACTAC 3234
OY 181 gtccgaagagcagtgccgcgcctccctgaagtgatgagtgcccttgaaagatcttcgac 240
DB 3235 GTCCGCAAGGCAATGCCCGGCTCCCTGAGTGAAGTGGCCCTGAAAGCATCTTTCGAC 3294
OY 241 aaggtgtaacacacagcagagtgacgtggtgctcttgaggtgctctctcctggaagatcttc 300
DB 3295 AAGGTGTACACACAGCAGAGTGAAGTGTGCTTGGGGGTCTTCTGTGGAATCTTC 3354
OY 301 tctctgggggctccctccgtacccctgggggtgcaagatcaatgagaagctctgcagagcgtg 360
DB 3355 TCTCTGGGGGCTCCCGTACCCCTGGGGGTGCAATGATGAGGATCTCTGACACGGCTG 3414
OY 361 aagagcgcgcacaaagatgaagggcccgagagctgagccactcccgacatcagccgcatcatg 420
DB 3415 AGAGACGGCACAAGATGAGAGGCCCGGAGCTGGCACTCCCGCATACCCGCATCATG 3474
OY 421 ctgaactgctgtgctcggaagaccacaaagcgagaccctgcatctcgaagcgtg 471
DB 3475 CTGAACCTGTGTCTCGGAGACCCCAAGCGAGACCTGATTTCTGGAGCTG 3525

RESULT 18
US-09-982-610-31
Sequence 31, Application US/09982610
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
Bennett, Brian D.
Goeddel, David
Lee, James M.
Matthews, William
Tsai, Siao Ping
Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,648
FILING DATE: 1996-MAY-23
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-982-610-31

Query Match 100.0%; Score 471; DB 36; Length 4425;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctaccatgtaaatctgtctgtctacagcttccaggtggccgaagagatgtcttcctg 60
DB 3055 CTGACCATGAGAGATCTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGATGAGTCTCTG 3114
OY 61 gctcccgaaagtgatccacagagaccctgctcgcgcgaacattctgtctggaagc 120
DB 3115 GCTTCCCGAAGTGCAATCCACAGACCTGGCTCTCGGACATTCTCTCGGAAAGC 3174
OY 121 gaagtgatgaagatctgtgactttgaccttgccggagacatctaaagaccctgactac 180
DB 3175 GACGTGTGAAGATCTGTGACTTTGGCCCTTCCGCGACATCTCAAAAGACCTGACTAC 3234
OY 181 gtccgaagagcagtgccgcgcctccctgaagtgatgagtgcccttgaaagatcttcgac 240
DB 3235 GTCCGCAAGGCAATGCCCGGCTCCCTGAGTGAAGTGGCCCTGAAAGCATCTTTCGAC 3294
OY 241 aaggtgtaacacacagcagagtgacgtggtgctcttgaggtgctctctcctggaagatcttc 300
DB 3295 AAGGTGTACACACAGCAGAGTGAAGTGTGCTTGGGGGTCTTCTGTGGAATCTTC 3354
OY 301 tctctgggggctccctccgtacccctgggggtgcaagatcaatgagaagctctgcagagcgtg 360
DB 3355 TCTCTGGGGGCTCCCGTACCCCTGGGGGTGCAATGATGAGGATCTCTGACACGGCTG 3414
OY 361 aagagcgcgcacaaagatgaagggcccgagagctgagccactcccgacatcagccgcatcatg 420
DB 3415 AGAGACGGCACAAGATGAGAGGCCCGGAGCTGGCACTCCCGCATACCCGCATCATG 3474
OY 421 ctgaactgctgtgctcggaagaccacaaagcgagaccctgcatctcgaagcgtg 471
DB 3475 CTGAACCTGTGTCTCGGAGACCCCAAGCGAGACCTGATTTCTGGAGCTG 3525

RESULT 19
US-60-167-943-103
Sequence 103, Application US/60167943
GENERAL INFORMATION:
APPLICANT: Hodgson, David M.
Lincoln, Stephen E.
Jones, Antissa L.
Yu, Jimmy Y.

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: APPLICANT: Russo, Frank D.
: APPLICANT: Spiro, Peter A.
: APPLICANT: Banville, Steve C.
: APPLICANT: Bratner, Shawn R.
: APPLICANT: Dufour, Gerard E.
: APPLICANT: Cohen, Howard J.
: APPLICANT: Rosen, Bruce
: APPLICANT: Shah, Purvi
: APPLICANT: Chalup, Michael S.
: APPLICANT: Hillman, Jennifer L.
: TITLE OF INVENTION: RECEPTOR MOLECULES
: FILE REFERENCE: PT-0093 P
: CURRENT APPLICATION NUMBER: US/60/167,943
: CURRENT FILING DATE: 1999-11-29
: NUMBER OF SEQ ID NOS: 244
: SOFTWARE: PERL Program
: SEQ ID NO 103
: LENGTH: 4461
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: 902563.1
: NAME/KEY: unsure
: LOCATION: 2402-2421
: OTHER INFORMATION: a, t, c, g, or other
US-60-167-943-103

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Query Match
Best Local Similarity 100.0%; Score 471; DB 55; Length 4461;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgacatgagaagatctgtctgtctacagcttccaggctggcgaagagagatgaggttccg 60
Db 3056 ctgacatgagaagatctgtctgtctacagcttccaggctggcgaagagagatgaggttccg 3115
Oy 61 gcttccgaaagtgcattccacacagagacctgtgtctcgaaacattctgtctcgaaagc 120
Db 3116 gcttccgaaagtgcattccacacagagacctgtgtctcgaaacattctgtctcgaaagc 3175
Oy 121 gacgtgtgaaagatctgtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
Db 3176 gacgtgtgaaagatctgtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3235
Oy 181 gtcgcaaggagcagtgccggctgtcccttgaagtgatgagcccttgaagcattctcgac 240
Db 3236 gtcgcaaggagcagtgccggctgtcccttgaagtgatgagcccttgaagcattctcgac 3295
Oy 241 aaggtgtacacacacacacacacacacacacacacacacacacacacacacacacacacac 300
Db 3296 aaggtgtacacacacacacacacacacacacacacacacacacacacacacacacacacac 3355
Oy 301 tctctgggggctccctccgtacccctgggtgtcagatcaatgaaagatcttgcacagcgctg 360
Db 3356 tctctgggggctccctccgtacccctgggtgtcagatcaatgaaagatcttgcacagcgctg 3415
Oy 361 agagacggcacaagaatgaggggcccggagctgagcactcccgacatacgcgcacatg 420
Db 3416 agagacggcacaagaatgaggggcccggagctgagcactcccgacatacgcgcacatg 3475
Oy 421 ctgaactgtgtctcgagagaccacaaagcgagacatgacatcttcgagactg 471
Db 3476 ctgaactgtgtctcgagagaccacaaagcgagacatgacatcttcgagactg 3526

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RESULT 20
: Sequence 15763, Application US/6017373
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti

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: APPLICANT: Died, Dinh
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: FILE REFERENCE: Polynucleotide Sequence Databases, and Single Nucleotide Poly
: CURRENT APPLICATION NUMBER: US/60/172,373
: CURRENT FILING DATE: 1999-12-16
: NUMBER OF SEQ ID NOS: 25,772
: SOFTWARE: PERL Program
: SEQ ID NO 15763
: LENGTH: 4462
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: 902563.2
: NAME/KEY: unsure
: LOCATION: 2402-2421, 2907, 3602
: OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-15763

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Query Match
Best Local Similarity 100.0%; Score 471; DB 56; Length 4462;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgacatgagaagatctgtctgtctacagcttccaggctggcgaagagagatgaggttccg 60
Db 3058 ctgacatgagaagatctgtctgtctacagcttccaggctggcgaagagagatgaggttccg 3117
Oy 61 gcttccgaaagtgcattccacacagagacctgtgtctcgaaacattctgtctcgaaagc 120
Db 3118 gcttccgaaagtgcattccacacagagacctgtgtctcgaaacattctgtctcgaaagc 3177
Oy 121 gacgtgtgaaagatctgtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
Db 3178 gacgtgtgaaagatctgtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3237
Oy 181 gtcgcaaggagcagtgccggctgtcccttgaagtgatgagcccttgaagcattctcgac 240
Db 3238 gtcgcaaggagcagtgccggctgtcccttgaagtgatgagcccttgaagcattctcgac 3297
Oy 241 aaggtgtacacacacacacacacacacacacacacacacacacacacacacacacacacac 300
Db 3298 aaggtgtacacacacacacacacacacacacacacacacacacacacacacacacacacac 3357
Oy 301 tctctgggggctccctccgtacccctgggtgtcagatcaatgaaagatcttgcacagcgctg 360
Db 3358 tctctgggggctccctccgtacccctgggtgtcagatcaatgaaagatcttgcacagcgctg 3417
Oy 361 agagacggcacaagaatgaggggcccggagctgagcactcccgacatacgcgcacatg 420
Db 3418 agagacggcacaagaatgaggggcccggagctgagcactcccgacatacgcgcacatg 3477
Oy 421 ctgaactgtgtctcgagagaccacaaagcgagacatgacatcttcgagactg 471
Db 3478 ctgaactgtgtctcgagagaccacaaagcgagacatgacatcttcgagactg 3528

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RESULT 21
US-07-959-951A-3
: Sequence 3, Application US/0795951A
: GENERAL INFORMATION:
: APPLICANT: Alltalo, Karl, et al.
: TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/959,951A
APPLICATION DATE: 19921009
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 28113/31104
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-07-959-951A-3

Query Match      100.0%: Score 471: DB 3: Length 4795:
Best Local Similarity 100.0%: Pred. No. 1.2e-239:
Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ctgaccatgtaagatctgtctgtctacagcttcagatgagcagaaggaatgagctc 60
DB 3044 CTCACCATGGAAGATCTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGGAGTCTCTG 3103

QY 61 gctccccaagaatgacacacagagacctgtctctggaacattctgctcggaaagc 120
DB 3104 GCTTCCCAAGATGCTATCCACAGAGACCTGCTCTCGAATCTTCTCGAAGC 3163

QY 121 gaagtgtaagatctgacttgccttgcggagacatctcaaaagacctgactac 180
DB 3164 GACGTGGTGAAGATCTGTGATTTGGCCTTCCGGGACATCTCAAAAGACCTGACTAC 3223

QY 181 gtccgaaggaagatgcccgcctgagatgagatgagccctgaaacatcttcac 240
DB 3224 GTCCGCAAGGGCAGTGCCTCCGCTTCTGAATGATGCCCCCTGAAGCATCTTCGAC 3283

QY 241 aaggtgtaaccacagatgagatgagtgcttcttgggtgcttctcgtggagatctc 300
DB 3284 AAGGTGTACACACGACGAGTGTGCTTGGGCTTGGGCTTCTCTGCGACATCTTC 3343

QY 301 tctctggggcctcccgtaacccttgggtgagatcaatgagatctctcgaagcgtg 360
DB 3344 TCTCTGGGGCCTCCCGTACCTGCGGTGACATCAATGAGAGTCTCTCGACGCGCTG 3403

QY 361 agagagcagaagatgagaagggcccggaagctggcaccctccgcacatgacgcgcatatg 420
DB 3404 AGAGACGCGCAAGAGATGAGAGGCGCCCGAGAGTGGCCACTCCCGCAATACCCCGATCATG 3463

QY 421 ctgaactgctgtccgagagaccacaagcgagacctcattctcgaagctg 471
DB 3464 CTGAACGTGCTGTCCGAGACCCCAAGCGAGACACTTCCTCGGAGCTG 3514

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RESULT 22

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US-08-257-754-3
Sequence 3, Application US/08257754
GENERAL INFORMATION:
APPLICANT: Alltalo, Karl
APPLICANT: Kalpalainen, Arja

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APPLICANT: Korhonen, Jaana
APPLICANT: Mustonen, Tuja
APPLICANT: Pajusola, Karl
APPLICANT: Malikainen, Marja-Terttu
APPLICANT: Karjalainen, Paivi
TITLE OF INVENTION: FLT4 RECEPTOR TYROSINE KINASE AND ITS USE IN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,754
FILING DATE: 09-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28344/32133
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-08-257-754-3

Query Match      100.0%: Score 471: DB 6: Length 4795:
Best Local Similarity 100.0%: Pred. No. 1.2e-239:
Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ctgaccatgtaagatctgtctgtctacagcttcagatgagcagaaggaatgagctc 60
DB 3044 CTCACCATGGAAGATCTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGGAGTCTCTG 3103

QY 61 gctccccaagaatgacacacagagacctgtctctggaacattctgctcggaaagc 120
DB 3104 GCTTCCCAAGATGCTATCCACAGAGACCTGCTCTCGAATCTTCTCGAAGC 3163

QY 121 gaagtgtaagatctgacttgccttgcggagacatctcaaaagacctgactac 180
DB 3164 GACGTGGTGAAGATCTGTGATTTGGCCTTGGGACATCTCAAAAGACCTGACTAC 3223

QY 181 gtccgaaggaagatgcccgcctgagatgagatgagccctgaaacatcttcac 240
DB 3224 GTCCGCAAGGGCAGTGCCTCCGCTTCTGAATGATGCCCCCTGAAGCATCTTCGAC 3283

QY 241 aaggtgtaaccacagatgagatgagtgcttcttgggtgcttctcgtggagatctc 300
DB 3284 AAGGTGTACACACGACGAGTGTGCTTGGGCTTGGGCTTCTCTGCGACATCTTC 3343

QY 301 tctctggggcctcccgtaacccttgggtgagatcaatgagatctctcgaagcgtg 360

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Db 3344 TCTCTGGGGGCTCCCTGTAACCTGGGCTGTCAGATCAATGAGAGATTCTGCCAGCGCTG 3403
OY 361 agagaagcgaagaatgagggcccccgaagctggccaccctccgcaatacgcacatctg 420
Db 3404 AGAGACGGCCACAAGATGAGGGCCCGGAGCTGGCAGCTCCGCCATACGCCCATCATG 3463
OY 421 ctgaactgctggtcgggaagaccccaagcgagactgcatctcggagctg 471
Db 3464 CTGACTGCTGCTCCGAGACCCCAAGCGGAGAGACCTGCATTCGAGCTG 3514

RESULT 23

US-09-169-079-3
Sequence 3, Application US/09169079
GENERAL INFORMATION:
APPLICANT: Alltalo, Karl
APPLICANT: Kaipainen, Arja
APPLICANT: Valtola, Reija
APPLICANT: Jussila, Lotta
TITLE OF INVENTION: Fil4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera
FILE REFERENCE: 28113/34891
CURRENT APPLICATION NUMBER: US/09/169,079
EARLIER FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: 08/901,710
EARLIER FILING DATE: 1997-07-28
EARLIER APPLICATION NUMBER: 08/340,011
EARLIER FILING DATE: 1994-11-14
EARLIER APPLICATION NUMBER: 08/257,754
EARLIER FILING DATE: 1994-07-09
EARLIER APPLICATION NUMBER: 07/959,951
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 4795
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (20)..(4108)
US-09-169-079-3

Query Match 100.0%: Score 471; DB 15; Length 4795;
Best Local Similarity 100.0%: Pred. No. 1.2e-239;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacgaatgaagatctgtctgtctacagcttcacagctggcagagagatgagttctg 60
Db 3044 ctgacgaatgaagatctgtctgtctacagcttcacagctggcagagagatgagttctg 60
OY 61 gctcccgaaagtgatccacagagacctggtctcgaacatctcgtcggaaagc 120
Db 3104 gctcccgaaagtgatccacagagacctggtctcgaacatctcgtcggaaagc 3163
OY 121 gacgtggaagatctgtactctgtccttcgcccggagatctacaaagaccctgactac 180
Db 3164 gacgtggaagatctgtactctgtccttcgcccggagatctacaaagaccctgactac 3223
OY 181 gtcgcgaagagcagtgcccggtcgtccctgaagtgatgagccctgaaagatctcgac 240
Db 3224 gtcgcgaagagcagtgcccggtcgtccctgaagtgatgagccctgaaagatctcgac 3283
OY 241 aaggtgtacacacgacagatgagctgtgtccttcgggtgtccttcctcggagatcttc 300
Db 3284 aaggtgtacacacgacagatgagctgtgtccttcgggtgtccttcctcggagatcttc 3343
OY 301 tctctgggggctcctccgctacccctggggctgacatcaatgagaggtctctgacagctg 360
Db 3344 tctctgggggctcctccgctacccctggggctgacatcaatgagaggtctctgacagctg 3403
OY 361 agagaagcgaagaatgagggcccgagactggtccactcccgcatatgcgcatcatg 420

Db 3404 agagaagcgaagaatgagggcccccgaagctggccaccctccgcaatacgcacatctg 3463
OY 421 ctgaactgctggtcgggaagaccccaagcgagactgcatctcggagctg 471
Db 3464 ctgaactgctggtcgggaagaccccaagcgagactgcatctcggagctg 3514

RESULT 24

US-08-446-648-45
Sequence 45, Application US/08446648
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao ping
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,648
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 9108 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-446-648-45

Query Match 100.0%: Score 471; DB 8; Length 9108;
Best Local Similarity 100.0%: Pred. No. 1.2e-239;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacgaatgaagatctgtctgtctacagcttcacagctggcagagagatgagttctg 60
Db 3987 ctgacgaatgaagatctgtctgtctacagcttcacagctggcagagagatgagttctg 4046
OY 61 gctcccgaaagtgatccacagagacctggtctcgaacatctcgtcggaaagc 120
Db 4047 GCTTCCCGAAAGTCATCCACAGAGACCTGCTCGGAAATTTCTGTCGAAAGC 4106
OY 121 gacgtggaagatctgtactctgtccttcgcccggagatctacaaagaccctgactac 180
Db 4107 GACGTGCTGAAGATCTGTGACTTTGGCTTCCCGGAGACATCTACAAAGACCTGACTAC 4166

44-010 700 60 00

044

Db 645 gacgtgtgaagatctgtacttggccttgcgggacatctacaagaagcccgactac 704
Oy 181 gtccgcaaggagcagtcggcgtctcccttgagatgtgagtcgccctgaaagacatctcgac 240
Db 705 gtccgcaaggagcagtcggcgtctcccttgagatgtgagtcgccctgaaagacatctcgac 764
Oy 241 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtctctctgaggagatcttc 300
Db 765 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtctctctgaggagatcttc 824
Oy 301 tctctggggggtctcccgtaaccttgagggtgacatcaatgagagatctgtccagcgagctg 360
Db 825 tctctggggggtctcccgtaaccttgagggtgacatcaatgagagatctgtccagcgagctg 884
Oy 361 agagacggcacaagaatgagagagcccgagagctggacatcccgcccaatgcgcatcatg 420
Db 885 agagacggcacaagaatgagagagcccgagagctggacatcccgcccaatgcgcatcatg 944
Oy 421 ctgaacgtcgtgtccggagagaccccaaggcgagacctgtcatctcggagctg 471
Db 945 ctgaacgtcgtgtccggagagaccccaaggcgagacctgtcatctcggagctg 995

RESULT 27
US-60-213-360-951
; Sequence 951, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; NUMBER OF SEQ ID NOS: 2000-06-21
; SOFTWARE: PERL Program
; SEQ ID NO 951
; LENGTH: 3277
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: 1084493.6
US-60-213-360-951

Query Match 89.2%; Score 420; DB 60; Length 3277;
Best Local Similarity 99.8%; Pred. No. 1.7e-212;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ctgacatggaagatctgtctgtcaagcttccaggtgagcgaagagatggagttcctg 60
Db 525 ctgacatggaagatctgtctgtcaagcttccaggtgagcgaagagatggagttcctg 584
Oy 61 gtctccgaaagtgcattccacagagacctgtgtctcgagaaccttctgtctcgagaagc 120
Db 585 gtctccgaaagtgcattccacagagacctgtgtctcgagaaccttctgtctcgagaagc 644
Oy 121 gacgtgtgaagatctgtacttggccttgcgggagacatctacaagaagccctgtactc 180
Db 645 gacgtgtgaagatctgtacttggccttgcgggagacatctacaagaagccctgtactc 240
Oy 181 gtccgcaaggcagtcggcgtctcccttgagatgtgagtcgcccttaagaagacatctcgac 240
Db 705 gtccgcaaggcagtcggcgtctcccttgagatgtgagtcgcccttaagaagacatctcgac 764
Oy 241 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtctctctgaggagatcttc 300
Db 765 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtctctctgaggagatcttc 824
Oy 301 tctctggggggtctcccgtaaccttgagggtgacatcaatgagagatctgtccagcgagctg 360

Db 825 tctctggggggtctcccgtaaccttgagggtgacatcaatgagagatctgtccagcgagctg 884
Oy 361 agagacggcacaagaatgagagagcccgagagctggacatcccgcccaatgcgcatcatg 420
Db 885 agagacggcacaagaatgagagagcccgagagctggacatcccgcccaatgcgcatcatg 944
Oy 421 ctgaacgtcgtgtccggagagaccccaaggcgagacctgtcatctcggagctg 471
Db 945 ctgaacgtcgtgtccggagagaccccaaggcgagacctgtcatctcggagctg 995

RESULT 28
US-60-324-185-4300
; Sequence 4300, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; NUMBER OF SEQ ID NOS: 2001-09-21
; SOFTWARE: PERL Program
; SEQ ID NO 4300
; LENGTH: 3277
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: 1084493.6
US-60-324-185-4300

Query Match 89.2%; Score 420; DB 71; Length 3277;
Best Local Similarity 99.8%; Pred. No. 1.7e-212;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ctgacatggaagatctgtctgtcaagcttccaggtgagcgaagagatggagttcctg 60
Db 525 ctgacatggaagatctgtctgtcaagcttccaggtgagcgaagagatggagttcctg 584
Oy 61 gtctccgaaagtgcattccacagagacctgtgtctcgagaaccttctgtctcgagaagc 120
Db 585 gtctccgaaagtgcattccacagagacctgtgtctcgagaaccttctgtctcgagaagc 644
Oy 121 gacgtgtgaagatctgtacttggccttgcgggagacatctacaagaagccctgtactc 180
Db 645 gacgtgtgaagatctgtacttggccttgcgggagacatctacaagaagccctgtactc 240
Oy 181 gtccgcaaggcagtcggcgtctcccttgagatgtgagtcgcccttaagaagacatctcgac 240
Db 705 gtccgcaaggcagtcggcgtctcccttgagatgtgagtcgcccttaagaagacatctcgac 764
Oy 241 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtctctctgaggagatcttc 300
Db 765 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtctctctgaggagatcttc 824
Oy 301 tctctggggggtctcccgtaaccttgagggtgacatcaatgagagatctgtccagcgagctg 360
Db 825 tctctggggggtctcccgtaaccttgagggtgacatcaatgagagatctgtccagcgagctg 884
Oy 361 agagacggcacaagaatgagagagcccgagagctggacatcccgcccaatgcgcatcatg 420
Db 885 agagacggcacaagaatgagagagcccgagagctggacatcccgcccaatgcgcatcatg 944
Oy 421 ctgaacgtcgtgtccggagagaccccaaggcgagacctgtcatctcggagctg 471
Db 945 ctgaacgtcgtgtccggagagaccccaaggcgagacctgtcatctcggagctg 995

```
RESULT 29
US-60-324-185-4274
: Sequence 4274, Application US/60324185
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diop, Dinah
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0019-1 P
: CURRENT APPLICATION NUMBER: US/60/324,185
: NUMBER OF SEQ ID NOS: 35862
: SOFTWARE: PERL Program
: SEQ ID NO 4274
: LENGTH: 4459
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 1082992.1
: NAME/KEY: unsure
: LOCATION: 2402-2421
: OTHER INFORMATION: a, t, c, g, or other
US-60-324-185-4274

Query Match          89.2%  Score 420: DB 71: Length 4459:
Best Local Similarity 99.8%  Pred. No. 1.8e-212:
Matches 470: Conservative 0; Mismatches 1; Indels 0; Gaps 0:

OY 1 ctgacctggaagaatcttctctctcctcagctccaggtgagcagaaggaatgagttctctg 60
Db 3055 ctgacctggaagaatcttctctctcctcagctccaggtgagcagaaggaatgagttctctg 60
OY 61 gctctccgaagaatgcatccacagaagacccgctgctcgcgaagaatctctctcgcgaagc 120
Db 3115 gctctccgaagaatgcatccacagaagacccgctgctcgcgaagaatctctctcgcgaagc 120
OY 121 gaagtggtgaagaatctctgtaacttgacctgcccggagacatctacaaagacctgaactac 180
Db 3175 gaagtggtgaagaatctctgtaacttgacctgcccggagacatctacaaagacctgaactac 180
OY 181 gtcgcgaagggcagtgcccggctgcccctgaagtgaatgagccctggaagcatctctgcac 240
Db 3235 gtcgcgaagggcagtgcccggctgcccctgaagtgaatgagccctggaagcatctctgcac 240
OY 241 aaggtgtacacacagcagaatgacgtgtgtctctctgtggtgtctctctgtggaagatcttc 300
Db 3295 aaggtgtacacacagcagaatgacgtgtgtctctctgtggtgtctctctgtggaagatcttc 300
OY 301 tctctgggggctctcccgtaacctggtgtgagatcaatgaagatctctcgaacgagctg 360
Db 3355 tctctgggggctctcccgtaacctggtgtgagatcaatgaagatctctcgaacgagctg 360
OY 361 agagacgcagacaagaatgagggcccgagagctgagcactccgcgcacatagcgcgcatcatg 420
Db 3415 agagacgcagacaagaatgagggcccgagagctgagcactccgcgcacatagcgcgcatcatg 420
OY 421 ctgaactgctgtctcggagagaccccaagagagacatgcatctcggagctg 471
Db 3475 ctgaactgctgtctcggagagaccccaagagagacatgcatctcggagctg 471

RESULT 30
US-08-256-769B-19/c
: Sequence 19, Application US/08256769B
: GENERAL INFORMATION:
: APPLICANT: Avraham, Hava
: APPLICANT: Groopman, Jerome
: APPLICANT: Cowley, Sally
```

```
APPLICANT: Scadden, David
APPLICANT: Mon Lee, James
APPLICANT: Bennett, Brian D.
APPLICANT: Wood, William I.
APPLICANT: Goeddel, David
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASES
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,769B
FILING DATE: 22-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: NEDH91-11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 6826 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (1880..2923)
US-08-256-769B-19

Query Match          89.2%  Score 420: DB 6: Length 6826:
Best Local Similarity 99.8%  Pred. No. 1.8e-212:
Matches 470: Conservative 0; Mismatches 1; Indels 0; Gaps 0:

OY 1 ctgacctggaagaatcttctctcctcagctccaggtgagcagaaggaatgagttctctg 60
Db 2749 ctgacctggaagaatcttctctcctcagctccaggtgagcagaaggaatgagttctctg 60
OY 61 gctctccgaagaatgcatccacagaagacccgctgctcgcgaagaatctctctcgcgaagc 120
Db 2689 gctctccgaagaatgcatccacagaagacccgctgctcgcgaagaatctctctcgcgaagc 120
OY 121 gaagtggtgaagaatctctgtaacttgacctgcccggagacatctacaaagacctgaactac 180
Db 2629 gaagtggtgaagaatctctgtaacttgacctgcccggagacatctacaaagacctgaactac 180
OY 181 gtcgcgaagggcagtgcccggctgcccctgaagtgaatgagccctggaagcatctctgcac 240
Db 2569 gtcgcgaagggcagtgcccggctgcccctgaagtgaatgagccctggaagcatctctgcac 240
OY 241 aaggtgtacacacagcagaatgacgtgtgtctctctgtggtgtctctctgtggaagatcttc 300
Db 2509 aaggtgtacacacagcagaatgacgtgtgtctctctgtggtgtctctctgtggaagatcttc 300
OY 301 tctctgggggctctcccgtaacctggtgtgagatcaatgaagatctctcgaacgagctg 360
Db 2449 tctctgggggctctcccgtaacctggtgtgagatcaatgaagatctctcgaacgagctg 360
```


Oy 361 agagacgacacagatgatgagagcccgagctggtccactcccccacacgcatcatg 420
|||||
Db 2389 AGAGACGGCACACAGATGAGCGCCCGGAGCTGGCCACTCCCGCATACGCCCATCATG 2330
Oy 421 ctgaactgctgctcgagagaccccaaggcgagactgcatctcgagctg 471
|||||
Db 2329 CTGAACCTGCTGCTCCGGAGACCCCAAGCGAGACTCATTTCTCGAGCTG 2279

RESULT 31

US-08-446-648-17/C
: Sequence 17, Application US/08446648
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Bennett, Brian D.
: APPLICANT: Goeddel, David
: APPLICANT: Lee, James M.
: APPLICANT: Matthews, William
: APPLICANT: Tsai, Siao Ping
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/446,648
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/222616
: FILING DATE: 04-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0821P3PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9861
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6827 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: US-08-446-648-17

Query Match 89.2%; Score 420; DB 8; Length 6827;
Best Local Similarity 99.8%; Pred. No. 1.8e-212;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ctgaacatgaaagatctgtctgtctacagcttcacagtgagccagaagagatctccg 60
|||||
Db 2749 CTGACCATGGAAGATCTTGTCTCTACAGCTTCAGGCGGAGATGAGTTCTCG 2690
Oy 61 gctccccaagatgcatccacagagaccggtgctgctcggaacatctgctcggaagc 120
|||||
Db 2689 GCTTCCGGAAGTGCATCCACAGACGTGGCTGCTCGGAACTTCTCTCGGAAAGC 2630
Oy 121 gacgtggtgaagatctgtgacttgcttgcgcggagacatctacaagaccctgactac 180
|||||

Db 2629 GACGTGTGGAAGATCTGTACTTTTGCTTGCCCGGAGCATCTACAAAGACCCGACTAC 2570
Oy 181 gtcgcgaaggaagtgcccgctgcccctgaatgagatgcccctgaagaatctcgac 240
|||||
Db 2569 CTCGCCAAGGCGAGTGCCTCCGCTGCTGCTGAAGTGGTGGCCCTGAAGCATCTTCGAC 2510
Oy 241 aagtgtaacacacagagatgacgltggtccttgagggtctctctcggaagatcttc 300
|||||
Db 2509 AAGGTACACACGACGACAGTGTGCTGCTTTGGGTGCTTCTCTGGAGATCTTC 2450
Oy 301 tctctgggggctccctccgttaacctgagggtgcaataaaggagatctgccaagctg 360
Db 2449 TCTCTGGGGGCTCCCTCCGTACCTCGGGTGCAGATCAATGAGAGTTCTCCGACGGCTG 2390
Oy 361 agagacgacacagatgatgagagcccgagctggtccactccgcacataagcgcatcctg 420
Db 2389 AGAGACGGCACAAAGATGAGGCGCCCGGAGCTGACCTCCCGCATACGCCCATCATG 2330
Oy 421 ctgaactgctgctcgagagaccccaaggcgagactgcatctcgagctg 471
Db 2329 CTGAACCTGCTGCTCCGGAGACCCCAAGCGAGACTCATTTCTCGAGCTG 2279

RESULT 32

US-08-770-449-17/C
: Sequence 17, Application US/08770449
: GENERAL INFORMATION:
: APPLICANT: Bennett, Brian D.
: APPLICANT: Goeddel, David
: APPLICANT: Lee, James M.
: APPLICANT: Matthews, William
: APPLICANT: Tsai, Siao Ping
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/770,449
: FILING DATE: 20-Dec-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/00586
: FILING DATE: 22-JAN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/826935
: FILING DATE: 22-JAN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/222616
: FILING DATE: 04-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0821P2D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9861
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6827 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single

TOPOLOGY: Linear
US-08-770-449-17

Query Match 89.2% Score 420; DB 11; Length 6827;
Best Local Similarity 99.8%; Pred. No. 1,8e-212;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgaccatggaagatctgtctgtctacagcttccaggtgagcagaaggaatgagttcttg 60
DB 2749 ctgaccatggaagatctgtctgtctacagcttccaggtgagcagaaggaatgagttcttg 2690
QY 6 gtctccgaaagtgatcctacacagagaccltggtctggaacatctgtctgagaaagc 120
DB 2689 gcttccgaaagtgatcctacacagagaccltggtctggaacatctgtctgagaaagc 2630
QY 121 gacgtggaagatctgtgacttggccttgcgggacatctgacaaagacccctgactac 180
DB 2629 gacgtggaagatctgtgacttggccttgcgggacatctgacaaagacccctgactac 2570
QY 181 gtccgaaagtgatcctgacagctggtccctgagatgagtgccctgaaagacatctcgac 240
DB 2569 gtccgaaagtgatcctgacagctggtccctgagatgagtgccctgaaagacatctcgac 2510
QY 241 aaggtgacacacagagatgagatgtgtcttgggtgtctctctgagagatcttc 300
DB 2509 aaggtgacacacagagatgagatgtgtcttgggtgtctctctgagagatcttc 300
QY 301 tctctgagagcttccctgacagctggtgtgagatcaatgagagatctctgagagcttg 360
DB 2449 tctctgagagcttccctgacagctggtgtgagatcaatgagagatctctgagagcttg 2290
QY 361 agagagagcacaagatgagagagcccgagagctgagcaccctccacatacgagcatatg 420
DB 2389 agagagagcacaagatgagagagcccgagagctgagcaccctccacatacgagcatatg 2330
QY 421 ctgagctgtgtctgagagagcccgagagctgagcaccctccacatacgagcatatg 471
DB 2329 ctgagctgtgtctgagagagcccgagagctgagcaccctccacatacgagcatatg 2279

RESULT 33

US-09-982-610-17/c

Sequence 17, Application US/09982610

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

Bennett, Brian D.

Goeddel, David

Lee, James M.

Matthews, William

Tsai, Siao Ping

Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpasta (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/982,610

FILING DATE: 17-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/446,648

FILING DATE: 1996-MAY-23

APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 6827 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

US-09-982-610-17
SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Query Match 89.2% Score 420; DB 36; Length 6827;
Best Local Similarity 99.8%; Pred. No. 1,8e-212;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgaccatggaagatctgtctgtctacagcttccaggtgagcagaaggaatgagttcttg 60
DB 2749 ctgaccatggaagatctgtctgtctacagcttccaggtgagcagaaggaatgagttcttg 2690
QY 61 gtctccgaaagtgatcctacacagagaccltggtctggaacatctgtctgagaaagc 120
DB 2689 gcttccgaaagtgatcctacacagagaccltggtctggaacatctgtctgagaaagc 2630
QY 121 gacgtggaagatctgtgacttggccttgcgggacatctgacaaagacccctgactac 180
DB 2629 gacgtggaagatctgtgacttggccttgcgggacatctgacaaagacccctgactac 2570
QY 181 gtccgaaagtgatcctgacagctggtccctgagatgagtgccctgaaagacatctcgac 240
DB 2569 gtccgaaagtgatcctgacagctggtccctgagatgagtgccctgaaagacatctcgac 2510
QY 241 aaggtgacacacagagatgagatgtgtcttgggtgtctctctgagagatcttc 300
DB 2509 aaggtgacacacagagatgagatgtgtcttgggtgtctctctgagagatcttc 300
QY 301 tctctgagagcttccctgacagctggtgtgagatcaatgagagatctctgagagcttg 360
DB 2449 tctctgagagcttccctgacagctggtgtgagatcaatgagagatctctgagagcttg 2290
QY 361 agagagagcacaagatgagagagcccgagagctgagcaccctccacatacgagcatatg 420
DB 2389 agagagagcacaagatgagagagcccgagagctgagcaccctccacatacgagcatatg 2330
QY 421 ctgagctgtgtctgagagagcccgagagctgagcaccctccacatacgagcatatg 471
DB 2329 ctgagctgtgtctgagagagcccgagagctgagcaccctccacatacgagcatatg 2279

RESULT 34

US-60-213-178-1247

Sequence 1247, Application US/60213178

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: C1000689

CURRENT APPLICATION NUMBER: US/60/213,178

NUMBER OF SEQ ID NOS: 1425

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1247

LENGTH: 415

TYPE: DNA


```
FILE REFERENCE: 20093-001000US
CURRENT APPLICATION NUMBER: US/10/012,214
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: PCT/US99/08079
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (22)...(3915)
US-10-012-214-1
```

```
Query Match          64.8% Score 305; DB 37; Length 4450;
Best Local Similarity 99.7% Pred. NO. 3.4e-151;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 ctgaccaggaagatctgtctgtctacagctccaggtgacagagagatgagctctg 60
Db 3046 ctgaccatggaagatctgtctgtctacagctccaggtgacagagagatgagctctg 3105
OY 61 gctccgaaagctgacacagagagctgtctgtctgtggaacatctgtctgtggaagc 120
Db 3106 gctccgaaagctgacacagagagctgtctgtctgtggaacatctgtctgtggaagc 3165
OY 121 gacgtgtggaagatctgtgtgtctgtccctgtccggagacatctacaagaacctgtac 180
Db 3166 gacgtgtggaagatctgtgtgtctgtccctgtccggagacatctacaagaacctgtac 3225
OY 181 gtcgcaaggagcagtgccggctgcccctgtgaatgagatgagccctgtgaacatcttcgac 240
Db 3226 gtcgcaaggagcagtgccggctgcccctgtgaatgagatgagccctgtgaacatcttcgac 3285
OY 241 aaggtgtacacacagcagagtgacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
Db 3286 aaggtgtacacacagcagagtgacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3345
OY 301 tctctgggggctccctccgtacccctgggggtgcaagatcaatgagagtgctgtccagcg 356
Db 3346 tctctgggggctccctccgtacccctgggggtgcaagatcaatgagagtgctgtccagcg 3401
```

```
RESULT 38
US-09-710-286-674
; Sequence 674, Application US/09710286
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2005-001
; CURRENT APPLICATION NUMBER: US/09/710,286
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164,255
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 674
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-710-286-674
```

```
Query Match          40.1% Score 189; DB 28; Length 443;
Best Local Similarity 100.0% Pred. NO. 2e-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 219 gcccctgaaagcatcttcgacaaggtgtacaccacgacagatgacgtgtgtctcttg 278
Db 25 gcccctgaaagcatcttcgacaaggtgtacaccacgacagatgacgtgtgtctcttg 84
OY 279 ggtctctctcggagatctctctctctgtggggtccctccgtacctgtgggtgcaatcaa 338
Db 85 ggtctctctcggagatctctctctctgtggggtccctccgtacctgtgggtgcaatcaa 144
OY 339 tgaagagttctgcacagcgctgagagacgcacaaagatgtagggcccgagcttgccac 398
Db 145 tgaagagttctgcacagcgctgagagacgcacaaagatgtagggcccgagcttgccac 204
OY 399 tcccgccat 407
Db 205 tcccgccat 213
```

```
RESULT 39
US-09-710-286-2884
; Sequence 2884, Application US/09710286
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2005-001
; CURRENT APPLICATION NUMBER: US/09/710,286
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164,255
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2884
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(1046)
; OTHER INFORMATION: n = A,T,C or G
US-09-710-286-2884
```

```
Query Match          40.1% Score 189; DB 28; Length 1046;
Best Local Similarity 100.0% Pred. NO. 2.1e-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 219 gcccctgaaagcatcttcgacaaggtgtacaccacgacagatgacgtgtgtctcttg 278
Db 1 gcccctgaaagcatcttcgacaaggtgtacaccacgacagatgacgtgtgtctcttg 60
OY 279 ggtctctctcggagatctctctctctgtggggtccctccgtacctgtgggtgcaatcaa 338
Db 61 ggtctctctcggagatctctctctctgtggggtccctccgtacctgtgggtgcaatcaa 120
OY 339 tgaagagttctgcacagcgctgagagacgcacaaagatgtagggcccgagcttgccac 398
Db 121 tgaagagttctgcacagcgctgagagacgcacaaagatgtagggcccgagcttgccac 180
OY 399 tcccgccat 407
Db 181 tcccgccat 189
```

```
RESULT 40
US-09-716-953-1245
; Sequence 1245, Application US/09716953
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
```

FILE OF INVENTION: THEREFOR
FILE REFERENCE: 1600,2044-001
CURRENT APPLICATION NUMBER: US/09/716,953
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/167,413
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 2620
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1245
LENGTH: 535
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(535)
OTHER INFORMATION: n = A,T,C or G
US-09-716-953-1245

Query Match 38.9%; Score 183; DB 28; Length 535;
Best Local Similarity 99.6%; Pred. No. 3.2e-86;
Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 238 gacaaagtgatcacacacagacagatgagctgtgtcccttgagggtctctctcctcggagatc 297
Db 15 gacaaagtgatcacacacagacagatgagctgtgtcccttgagggtctctctcctcggagatc 74
Qy 298 ttctctctggggggtccctccgtacccctggggtgcagatcaatggaggtctcgcacgg 357
Db 75 ttctctctggggggtccctccgtacccctggggtgcagatcaatggaggtctcgcacgg 134
Qy 358 ctgagagacggcacaaagatgagggcccgagctggccacatccgcacatcgcgcac 417
Db 135 ctgagagacggcacaaagatgagggcccgagctggccacatccgcacatcgcgcacatc 194
Qy 418 atgctgacgcgtgtgtcgcgagaccaccaaggagacctcatctctcggagctg 471
Db 195 atgctgacgcgtgtgtcgcgagaccaccaaggagacctcatctcggagctg 248
RESULT 41
US-60-170-374-1824/C
Sequence 1824, Application US/60170374
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
FILE REFERENCE: CL000146
CURRENT APPLICATION NUMBER: US/60/170,374
CURRENT FILING DATE: 1999-12-13
NUMBER OF SEQ ID NOS: 3666
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1824
LENGTH: 610
TYPE: DNA
ORGANISM: Human
US-60-170-374-1824

Query Match 26.8%; Score 126; DB 56; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.7e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 agtgcatacaagacacgtgtgtcgtgaaacatctcgtctcgtcgaagcgaagcgtgtga 130
Db 568 AGTGATCTGACACAGACAGACGTGCTCGGAACTCTGCTGCGAAGCAAGCACTGTGTA 509
Qy 131 agatctgtgacttggccttgcgcggagacatctacaagaacccctgactcgtccgaagg 190
Db 508 AGATCTGTGACTTTGGCTTGGCCGGGACATCTACAAAGACCCTGACTACGTCCGCAAGC 449
Qy 191 gcagtg 196

Db 448 GCAGTG 443

RESULT 42
US-60-213-178-4/C
Sequence 4, Application US/60213178
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL000689
CURRENT APPLICATION NUMBER: US/60/213,178
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 1425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1077
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1077)
OTHER INFORMATION: n = A,T,C or G
US-60-213-178-4

Query Match 26.8%; Score 126; DB 60; Length 1077;
Best Local Similarity 100.0%; Pred. No. 7.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 agtgcatacaagacacgtgtgtcgtgaaacatctcgtctcgtcgaagcgaagcgtgtga 130
Db 1007 AGTGATCTGACACAGACAGACGTGCTCGGAACTTCTGCTGCGAAGCAAGCACTGTGTA 948
Qy 131 agatctgtgacttggccttgcgcggagacatctacaagaacccctgactcgtccgaagg 190
Db 947 AGATCTGTGACTTTGGCTTGGCCGGGACATCTACAAAGACCCTGACTACGTCCGCAAGC 888
Qy 191 gcagtg 196
Db 887 GCAGTG 882

RESULT 43
US-60-213-178-297/C
Sequence 297, Application US/60213178
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL000689
CURRENT APPLICATION NUMBER: US/60/213,178
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 1425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 297
LENGTH: 32768
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(32768)
OTHER INFORMATION: n = A,T,C or G
US-60-213-178-297

Query Match 26.8%; Score 126; DB 60; Length 32768;
Best Local Similarity 100.0%; Pred. No. 8.9e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 agtgcacacagagacgtgctgctcggaacattcgtctcggaagcgagctgtga 130
|||||
Db 29337 AGTGCATCCACAGACGCTGCTCGACATTCCTGTCGGAAGCAGCGTGTA 29478
OY 131 agatcgtgacttgcccttgcccggaacatctacaagaccctgactacgtcgcaag 190
|||||
Db 29477 AGATCTGTACTTTGGCTTGCCCGGACATCTACAAAGCCTGACTACGTCGCCAAG 29418
OY 191 gcaagt 196
|||||
Db 29417 GCAGTC 29412

RESULT 44
US-60-213-178-954

; Sequence 954, Application US/60213178
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000689
; CURRENT APPLICATION NUMBER: US/60/213,178
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 1425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 954
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Human
US-60-213-178-954

Query Match 26.5%; Score 125; DB 60; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.6e-55;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 tgcacacacagagacgtgctgctcggaacattcgtctcggaagcgagctgtgaag 132
|||||
Db 2 tgcacacacagagacgtgctgctcggaacattcgtctcggaagcgagctgtgaag 61
OY 133 atcgtgacttgcccttgcccggaacatctacaagaccctgactacgtcgcaagggc 192
|||||
Db 62 atcgtgacttgcccttgcccggaacatctacaagaccctgactacgtcgcaagggc 121
OY 193 agtgc 197
|||||
Db 122 agtgc 126

RESULT 45

US-60-178-305-229/C
; Sequence 229, Application US/60178305
; GENERAL INFORMATION:

; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000207
; CURRENT APPLICATION NUMBER: US/60/178,305
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 229
; LENGTH: 516
; TYPE: DNA
; ORGANISM: HUMAN
US-60-178-305-229

Query Match 24.0%; Score 113; DB 56; Length 516;
Best Local Similarity 100.0%; Pred. No. 6.5e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 gcccgctgcccctgaagtgagtgagcccccgaagacatctcgacaagggtgacaccag 255
|||||
Db 473 GCCCGCTGCCCTGAAGTGAATGGCCCCGAAAGCATCTTCACAAAGTGTACACACG 414
OY 256 caagtgagtgatggtctcttggtggtgctctctcggaagacatctctctggg 308
|||||
Db 413 CAGAGTACGTGTGTCCTTGGGGTGTCTCTCGAGATCTTCTCTCGG 361

Search completed: July 16, 2002, 02:50:25
Job time: 31278 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:17 : Search time 223.79 seconds

(without alignments)
516.973 Million cell updates/sec

Title: US-09-375-248-1_COPY_3044_3514

Perfect score: 471

Sequence: 1 ctgaccatggaagatctgt.....gacctgcatctcgagctg 471

Scoring table:

OLIGO.NUC

Gapop 60.0 , Capext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/pdata/2/1na/5A.COMB.seq:*
- 2: /cgn2_6/pdata/2/1na/5B.COMB.seq:*
- 3: /cgn2_6/pdata/2/1na/6A.COMB.seq:*
- 4: /cgn2_6/pdata/2/1na/6B.COMB.seq:*
- 5: /cgn2_6/pdata/2/1na/PCRTUS.COMB.seq:*
- 6: /cgn2_6/pdata/2/1na/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	100.0	4195	1 US-08-340-011-1	Sequence 1, Appl1
2	471	100.0	4195	3 US-08-901-710-1	Sequence 1, Appl1
3	471	100.0	4416	1 US-08-795-430-1	Sequence 1, Appl1
4	471	100.0	4425	1 US-08-223-616-31	Sequence 31, Appl1
5	471	100.0	4425	5 PCT-US95-04228-31	Sequence 31, Appl1
6	471	100.0	4795	1 US-08-340-011-3	Sequence 31, Appl1
7	471	100.0	4795	3 US-08-901-710-3	Sequence 3, Appl1
8	471	100.0	9108	5 PCT-US95-04228-45	Sequence 45, Appl1
9	420	89.2	6827	1 US-08-222-616-17	Sequence 17, Appl1
C 10	420	89.2	6827	5 PCT-US95-04228-17	Sequence 17, Appl1
11	76	16.1	160	1 US-08-223-616-5	Sequence 5, Appl1
12	76	16.1	160	5 PCT-US95-04228-5	Sequence 5, Appl1
13	26	5.5	1467	1 US-08-176-630A-3	Sequence 3, Appl1
14	26	5.5	1467	1 US-08-463-862-3	Sequence 3, Appl1
15	26	5.5	1467	2 US-08-463-862-3	Sequence 3, Appl1
16	26	5.5	1467	2 US-08-461-985-3	Sequence 3, Appl1
17	26	5.5	1467	2 US-08-458-887-3	Sequence 3, Appl1
18	26	5.5	1467	4 US-08-933-787B-3	Sequence 3, Appl1
19	26	5.5	1467	4 US-08-933-012C-3	Sequence 3, Appl1
20	23	4.9	159	2 US-08-888-818C-3	Sequence 3, Appl1
21	23	4.9	1894	2 US-08-469-537A-19	Sequence 19, Appl1
22	23	4.9	1894	5 PCT-US93-06404-3	Sequence 3, Appl1
23	23	4.9	3453	1 US-07-813-593-1	Sequence 3, Appl1
24	23	4.9	3453	1 US-07-977-451-1	Sequence 1, Appl1
25	23	4.9	3453	1 US-07-946-507-1	Sequence 1, Appl1
26	23	4.9	3453	1 US-08-252-517-1	Sequence 1, Appl1
27	23	4.9	3453	1 US-07-906-397A-1	Sequence 1, Appl1

28	23	4.9	3453	1 US-08-601-891-1	Sequence 1, Appl1
29	23	4.9	3453	2 US-09-021-324-1	Sequence 1, Appl1
30	23	4.9	3453	5 PCT-US92-02750-1	Sequence 1, Appl1
31	23	4.9	3453	5 PCT-US92-05401-1	Sequence 1, Appl1
32	23	4.9	3453	5 PCT-US92-09893-1	Sequence 1, Appl1
33	23	4.9	3521	1 US-08-232-299-1	Sequence 11, Appl1
34	23	4.9	3521	2 US-08-434-878-1	Sequence 1, Appl1
35	23	4.9	3521	5 PCT-US95-03718-1	Sequence 1, Appl1
36	23	4.9	4054	1 US-08-180-195-35	Sequence 35, Appl1
37	23	4.9	4054	1 US-08-477-329-35	Sequence 35, Appl1
38	23	4.9	4054	2 US-08-475-458-35	Sequence 35, Appl1
39	23	4.9	4054	3 US-08-980-400-35	Sequence 35, Appl1
40	23	4.9	4054	4 US-08-583-459A-35	Sequence 35, Appl1
41	23	4.9	4054	4 US-09-583-210-35	Sequence 35, Appl1
42	23	4.9	4054	4 US-09-583-449A-35	Sequence 35, Appl1
43	23	4.9	4100	1 US-08-168-917-3	Sequence 3, Appl1
44	23	4.9	4100	2 US-08-460-510-3	Sequence 3, Appl1
45	23	4.9	4100	2 US-08-460-490-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-340-011-1
Sequence 1, Application US/08340011
Patent No. 576755
GENERAL INFORMATION:
APPLICANT: Alltalo, et al.
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
NUMBER OF SEQUENCES: 20
CORRESPONDING ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,011
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 32267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..3916
US-08-340-011-1

Query Match 100.0%; Score 471; DB 1; Length 4195;
Best Local Similarity 100.0%; Pred. No. 1.8e-223;

Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ctgacatgaaagatctgtctgtacagctccagctgagagagatgagcttg 60
DB 3044 CTGACCATGAAAGATCTGTCTGTACACCTCCAGGTGCGAGAGATGAGTTCCTG 3103

QY 61 gcttccgaaagagatccacagagagactgtgctgctggaacatctgtctggaagac 120
DB 3104 GCTTCCGAAAGATGCTGACAGAGACCTGCTCGGAAACATCTGCTGTGGAAAGC 3163

QY 121 gacgtgtgaaagatctgtacattgtgacctgcccggagacatctaaagaccctgactac 180
DB 3164 GACGTGTGAACATGTGTACTTTGGCTTGGCCGGACATCTTCAAGACCTGACACAC 3223

QY 181 gtccgaagagcagtgcccgagctgcccctgaagtgagtgagccctgaagacatcttgac 240
DB 3224 GTCCGAAAGCAGTGCCGCTGCTGCTGCTCGGAAACATCTGCTGTGGAAAGC 3233

QY 241 aaggtgtacacagcagagatgagtggtgtcccttggtgtgtctgtctggaagatcttc 300
DB 3284 AAGGTGTACACCAACCAAGATGACGTGTGTCTTGTGGGTCTTCTGTGGAGATCTTC 3343

QY 301 tctctgggggcttcccgctgacctgaggtgagatcaatgagagatctgtccagagctg 360
DB 3344 TCTCTGGGGGCTTCCCGCTACCTGTGGCTGAGATGAGAGATCTGTCCAGCGCTG 3403

QY 361 agagagcagcagagatgagtgagggcccgagctgtgagcactccgcacatgcgcagcatg 420
DB 3404 AGAGAGCAGCAAGATGAGGCGCCCGGACCTGCGACCTCCCGCATACCGCCGATCATG 3463

QY 421 ctgaactgtgtctgagagaccccaagagagactgtcatcttgagagctg 471
DB 3464 CTGAACCTGTGTGTCGGAGACCCCAAGCGGAGACCTGTCTGTGGAGCTG 3514

RESULT 2
US-08-901-710-1
: Sequence 1, Application US/08901710
: Patent No. 6107046
: GENERAL INFORMATION:
: APPLICANT: Alltalo, Karl
: APPLICANT: Aprelikova, Olga
: APPLICANT: Pajusola, Katri
: APPLICANT: Armstrong, Elina
: APPLICANT: Korhonen, Jaana
: APPLICANT: Kaipainen, Arja
: APPLICANT: Matikainen, Marja-Terttu
: TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: City: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/901,710
: FILING DATE:
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/340,011
: FILING DATE: 14-NOV-1994
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/257,754
: FILING DATE: 09-JUL-1994
: PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/33824
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..3916
US-08-901-710-1

Query Match 100.0% Score 471: DB 3: Length 4195:
Best Local Similarity 100.0% Pred. No. 1.8e-223:
Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ctgacatgaaagatctgtctgtacagctccagctgagagagatgagcttg 60
DB 3044 CTGACCATGAAAGATCTGTCTGTACACCTCCAGGTGCGAGAGATGAGTTCCTG 3103

QY 61 gcttccgaaagagatccacagagagactgtgctgctggaacatctgtctggaagac 120
DB 3104 GCTTCCGAAAGATGCTGACAGAGACCTGCTCGGAAACATCTGCTGTGGAAAGC 3163

QY 121 gacgtgtgaaagatctgtacattgtgacctgcccggagacatctaaagaccctgactac 180
DB 3164 GACGTGTGAACATGTGTACTTTGGCTTGGCCGGACATCTTCAAGACCTGACACAC 3223

QY 181 gtccgaagagcagtgcccgagctgcccctgaagtgagtgagccctgaagacatcttgac 240
DB 3224 GTCCGAAAGCAGTGCCGCTGCTGCTGCTCGGAAACATCTGCTGTGGAAAGC 3233

QY 241 aaggtgtacacagcagagatgagtggtgtcccttggtgtgtctgtctggaagatcttc 300
DB 3284 AAGGTGTACACCAACCAAGATGACGTGTGTCTTGTGGGTCTTCTGTGGAGATCTTC 3343

QY 301 tctctgggggcttcccgctgacctgaggtgagatcaatgagagatctgtccagagctg 360
DB 3344 TCTCTGGGGGCTTCCCGCTACCTGTGGCTGAGATGAGAGATCTGTCCAGCGCTG 3403

QY 361 agagagcagcagagatgagtgagggcccgagctgtgagcactccgcacatgcgcagcatg 420
DB 3404 AGAGAGCAGCAAGATGAGGCGCCCGGACCTGCGACCTCCCGCATACCGCCGATCATG 3463

QY 421 ctgaactgtgtctgagagaccccaagagagactgtcatcttgagagctg 471
DB 3464 CTGAACCTGTGTGTCGGAGACCCCAAGCGGAGACCTGTCTGTGGAGCTG 3514

RESULT 3
US-08-795-430-1
: Sequence 1, Application US/08795430
: Patent No. 6130071
: GENERAL INFORMATION:
: APPLICANT: Alltalo, Karl
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
: TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
: STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-795-430-1

Query Match 100.0% Score 471: DB 3: Length 4416:
Best Local Similarity 100.0% Pred. No. 1.8e-223:

Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 ctgacacatgaaagatcttctgctacagcttcccaagtgagccagaggaatgagttccctg 60
DB 3044 CTGACCATGGAAGATCTTGTCTGCTACAGCTTCACAGTGGCCAGAGCATGAGTTCTCTG 3103
OY 61 gcttccgaagtgatcctcagagagcctgctgctcgaagaattcgtctgctggaagc 120
DB 3104 GCTTCCCGAAGGATCCACAGAGACTGGCTGCTCGAACAATCTGCTGTCGCAAGC 3163
OY 121 gacgtgtagaagatctgtaatttgacctgcccggagacatctacaaaacctgactac 180
DB 3164 GACGTGTGAAGATCTGTACTTTGGCTTGGCCGGACATCTACAAAGACCTTGACTAC 3223
OY 181 gtccgaagggcagtgctccggctgcccctgaagtgagtgagcccttaagaacatcttcgac 240
DB 3224 GTCCGCAAGGGCGAGTCCCGGCTCGAGTGATGGCCCTGAAGCATCTTTCGAC 3283
OY 241 aaggtgtacacacagcagagtgagctgtggtcccttgagggtgctctctcgtggagatctc 300
DB 3284 AAGGTGTACACACAGCAGAGTGAAGTGTGCTTGGGCTCTTCTGAGGAGATCTTTC 3343

OY 301 tctctgggggctcccccgtacccctgggggtgagatcacaatgaagaattctgcccagcgctg 360
DB 3344 TCTCTGGGGGCTCCCGGCTGAGCTGGGTGCGAGATCAATGAGAGATTCTGCGACGGCTG 3403
OY 361 agagacggcacaaagatgagggcccgagctggccactcccgcatagcgccgcatcag 420
DB 3404 AGAGAGGCGCACAAAGATGAGGGCCCGGAGCTGGCCACTCCCGCATACGCCGATCATG 3463
OY 421 ctgaactgtgtgtccggagagaccccaaggcgagacctgcatcttggaagctg 471
DB 3464 CTGAAGTGTGTGTCGGAGACCCCAAGCGAGACCTGATCTCGAGCTG 3514

RESULT 4

US-08-222-616-31

; Sequence 31: Application US/08222616

; Patent No. 5635177

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST

; TITLE OF INVENTION: ANTIBODIES

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,616

; FILING DATE: 4-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/00586

; FILING DATE: 22-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/826935

; FILING DATE: 22-JAN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER: 821P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4425 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-222-616-31

Query Match 100.0% Score 471: DB 1: Length 4425:
Best Local Similarity 100.0% Pred. No. 1.8e-223:

Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 ctgacacatgaaagatcttctgctacagcttcccaagtgagccagaggaatgagttccctg 60
DB 3055 CTGACCATGGAAGATCTTGTCTGCTACAGCTTCACAGTGGCCAGAGGAGTGAAGTTCTCTG 3114

REFERENCE/DOCKET NUMBER: 32267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-08-340-011-3

Query Match 100.0%; Score 471; DB 1; Length 4795;
Best Local Similarity 100.0%; Pred. No. 1.8e-223;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgacacatggaagatctgtctgtacacgttccaggctgaggaagatgagctctg 60
DB 3044 CTGACCATGGAAGATCTGTCTGTCTACAGCTTCAGGTGGCCAGAGGATGGAATTCCTG 3103
QY 61 gcttccgaaagtgacatccacagagaccctgctgctggaacatctgtctggaagc 120
DB 3104 GCTTCCGAAAGTGACATCCACAGAGACCTGGCTCGGAACATTCGTCTCGGAAGC 3163
QY 121 gacgtgtgaaagatctgtctgtacacgttccaggctgaggaagatgagctctg 180
DB 3164 GACGTGTGAAGATCTGTCTGTCTACAGCTTCAGGTGGCCAGAGGATGGAATTCCTG 3223
QY 181 gtccgaagagcagctgcccgcctgagctgagctgagctgagctgagctgagc 240
DB 3224 GTCCGAGAGGAGCTGCCGCTGCCCTGAGTGATGAGCTGCCCTGAAACATCTTGAC 3283
QY 241 aaggtgtacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
DB 3284 AAGGTGTACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3343
QY 301 lctctgggggctcccccgtacacctggtggtgacatcaatgaagatcttccagcagc 360
DB 3344 TCTCTGGGGGCTCCCGCTACCTGGGGTGCATCATAGAGATTCTCCAGGGCTG 3403
QY 361 aggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
DB 3404 AGAGAGGCGCACAGAGATGAGGGCCCGGAGCTGGCCACTCCGCCCATACGCCCATCATG 3463
QY 421 ctgaactgtcgtcgcggaagccccaagcagcagcagcagcagcagcagcagc 471
DB 3464 CTGAACCTGCTGCTCCGAGACCCCAAGGCGAGACCTGCATTCGAGAGCTG 3514

RESULT 7
US-08-901-710-3
Sequence 3, Application US/08901710
Patent No. 6107046
GENERAL INFORMATION:
APPLICANT: Aittalo, Karl
APPLICANT: Aprelikova, Olga
APPLICANT: Pajusola, Katri
APPLICANT: Armstrong, Elna
APPLICANT: Korhonen, Jaana
APPLICANT: Malikainen, Arja
APPLICANT: Malikainen, Marja-Terttu
TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
SYNTH: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,710
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,754
FILING DATE: 09-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/33824
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-08-901-710-3
Query Match 100.0%; Score 471; DB 3; Length 4795;
Best Local Similarity 100.0%; Pred. No. 1.8e-223;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgacacatggaagatctgtctgtacacgttccaggctgaggaagatgagctctg 60
DB 3044 CTGACCATGGAAGATCTGTCTGTCTACAGCTTCAGGTGGCCAGAGGATGGAATTCCTG 3103
QY 61 gcttccgaaagtgacatccacagagaccctgctgctggaacatctgtctggaagc 120
DB 3104 GCTTCCGAAAGTGACATCCACAGAGACCTGGCTCGGAACATTCGTCTCGGAAGC 3163
QY 121 gacgtgtgaaagatctgtctgtacacgttccaggctgaggaagatgagctctg 180
DB 3164 GACGTGTGAAGATCTGTCTGTCTACAGCTTCAGGTGGCCAGAGGATGGAATTCCTG 3223
QY 181 gtccgaagagcagctgcccgcctgagctgagctgagctgagctgagctgagc 240
DB 3224 GTCCGAGAGGAGCTGCCGCTGCCCTGAGTGATGAGCTGCCCTGAAACATCTTGAC 3283
QY 241 aaggtgtacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
DB 3284 AAGGTGTACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3343
QY 301 lctctgggggctcccccgtacacctggtggtgacatcaatgaagatcttccagcagc 360
DB 3344 TCTCTGGGGGCTCCCGCTACCTGGGGTGCATCATAGAGATTCTCCAGGGCTG 3403
QY 361 aggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420

Db 3404 AGAGACGACACAGATGAGGGCCCCGAGAGTGGCCACTCCCGCATACGCCGATCATG 3463
Oy 421 ctgaactgtgttccggagaccacgaagcgagactgattctcggagctg 471
|||||
Db 3464 CTGAACTGCTGTGTCGGAGACCCCAAGCGAGACTGCTGATTCGGAGCTG 3514

RESULT 8
PCT-US95-04228-45

/ Sequence 45, Application PC/TUS9504228
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Bennett, Brian D.
/ APPLICANT: Goeddel, David
/ APPLICANT: Lee, James M.
/ APPLICANT: Matthews, William
/ APPLICANT: Tsai, Shao Ping
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/04228
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/222616
/ FILING DATE: 04-APR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wendy M. Lee
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 821P3PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ. ID NO.: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9108 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ PCT-US95-04228-45

Query Match 100.0%; Score 471; DB 5; Length 9108;
Best Local Similarity 100.0%; Pred. No. 1.7e-223;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgacatggaagatcttctgtcaagattccaggtggccagaggaatgagttcctg 60
|||||
Db 3987 CTGACATGGAAGATCTTCTGTCTACAGCTTCCAGTGGCCAGAGGATGAGTCTCTG 4046
Oy 61 gcttccgaagtgatcacacagagaccctggctgtcgaaacattctgtcggaaagc 120
|||||
Db 4047 GCTTCCGAAAGTGCATCCAGAGACTGCTCGGAACATTCTGCTCGAAAGC 4106
Oy 121 gacgtgggaagatctgtgacttggccttgcgggagacatctaaagaacctgactac 180
|||||
Db 4107 GACGTGGTGAAGATCTGTGACTTTGGCTTGCCTGCGGACATCTCAAAAGACCTGACTAC 4166
Oy 181 gtccgcaagggcagtgcccgctgcacctgaagtgaatgagccctgaagaacatcttcgac 240

Db 4167 GTCCGCAAGGGCAGTCCCGCGGTGCCCTGAAGTGATGGCCCTGAAAGCATCTTCAC 4226
Oy 241 aaagtgtacaccacgaaggtgacgtgtgttcttgggggtctctcggagacatctc 300
|||||
Db 4227 AAGGTGTACACACGACGAGTACGTGTGCTCTTGGGTCTCTCTCGGACATCTTC 4286
Oy 301 tctctggggccttcccgtaaccttgggtgtcagatcaatgaagattctgcacgcgctg 360
|||||
Db 4287 TCTCTGGGGCTCCCGGTACCTGGGTGCAGATCAATGAGACTTCTGCACGCGCTG 4346
Oy 361 aagagcgcacaaagatgagggcccggaagctgtgcaactccgcacatacgcgacatg 420
|||||
Db 4347 AGAGACGACACAGATGAGGGCCCCGAGACTGGCCACTCCCGCATACGCCGATCATG 4406
Oy 421 ctgaactgtgttccggagaccacgaagcgagactgattctcggagctg 471
|||||
Db 4407 CTGAACTGCTGTGTCGGAGACCCCAAGCGAGACTGCTGATTCGGAGCTG 4457

RESULT 9

US-08-222-616-17/c

/ Sequence 17, Application US/08222616
/ Patent No. 5635177

/ GENERAL INFORMATION:

/ APPLICANT: Bennett, Brian D.
/ APPLICANT: Goeddel, David
/ APPLICANT: Lee, James M.
/ APPLICANT: Matthews, William
/ APPLICANT: Tsai, Shao Ping
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/222,616
/ FILING DATE: 4-APR-1994

/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/00586
/ FILING DATE: 22-JAN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/826935
/ FILING DATE: 22-JAN-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER:
/ REFERENCE/DOCKET NUMBER: 821P2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168

/ INFORMATION FOR SEQ ID NO.: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6827 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-222-616-17

Query Match 89.2%; Score 420; DB 1; Length 6827;
Best Local Similarity 99.8%; Pred. No. 2,6e-198;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgacccaaggaagatctgtctgtctacagctccagagggcgaagagatgagttcctg 60
|||||
DB 2749 CTGACCATGGAAGATCTGTCTGTCTACAGCTTCCAGCGTGGCCAGAGGATGAGATTCTTG 2690

QY 61 gctccccaagatgacatccacagagaccctgctcctcgaacattctcctcgaagc 120
|||||
DB 2689 GCTTCCCGAAGATGATCCACAGAGACTGGCTCTCGGAACATTCTCTCTCGGAAGC 2630

QY 121 gacgtgtgaagatcctgtgactttgacctgacctggagacatctacaagaccctgactac 180
|||||
DB 2629 GACGTGTGAAGATCTGTGACTTTGGCCTTCCCGGACATCTCAAGACCCCGACTAC 2570

QY 181 gtccgaagggcagtgctcccgctgccccctgaagtgaatgagtccttgaagatcttgac 240
|||||
DB 2569 GTCCGCAAGGCAAGTCCCGGCTGCTGTAAGTGATGGCCCTCGAAGCATCTTTCGAC 2510

QY 241 aaggtgtaacacacagagatgacgtgtgtcctcttgaggtgtctctcctcgaagcctc 300
|||||
DB 2509 AAGGTGTACACACAGAGAGAGTGTGTCTTTGGGCTCTTCTGTGGAATCTTC 2450

QY 301 tctctgggggctcccccgtacccctgggggtgcagatcaatgaagagttctcgaagcgtg 360
|||||
DB 2449 TCTCTGGGGCTCCCGGTACCTGGGGTGAGATCAATGAGAGATTCTGCGACGCGCTG 2390

QY 361 agagaagggcacaagatgagagggcccgagctgagccatcccgacatacgccgacatg 420
|||||
DB 2389 AGAAGCGGCAAGAGATGAGGGCCCCGAGCTGGCCACTCCCGCATACGCCCGCATCATG 2330

QY 421 ctgaactgtcgtcgcgagaccccaagggcgaagcctgcatctcgaagcgtg 471
|||||
DB 2329 CTGAAGTGTGTGTCGGAGACCCCAAGGCGAGACTGTGATTTCTGGAGCTG 2279

RESULT 10
PCT-US95-04228-17/C
Sequence 17, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 6827 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-17

Query Match 89.2%; Score 420; DB 5; Length 6827;
Best Local Similarity 99.8%; Pred. No. 2,6e-198;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgacccaaggaagatctgtctgtctacagctccagagggcgaagagatgagttcctg 60
|||||
DB 2749 CTGACCATGGAAGATCTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGATGAGATTCTTG 2690

QY 61 gctccccaagatgacatccacagagaccctgctcctcgaacattctcctcgaagc 120
|||||
DB 2689 GCTTCCCGAAGATGATCCACAGAGACTGGCTCTCGGAACATTCTCTCTCGGAAGC 2630

QY 121 gacgtgtgaagatcctgtgactttgacctgacctggagacatctacaagaccctgactac 180
|||||
DB 2629 GACGTGTGAAGATCTGTGACTTTGGCCTTCCCGGACATCTCAAGACCCCGACTAC 2570

QY 181 gtccgaagggcagtgctcccgctgccccctgaagtgaatgagtccttgaagatcttgac 240
|||||
DB 2569 GTCCGCAAGGCAAGTCCCGGCTGCTGTAAGTGATGGCCCTCGAAGCATCTTTCGAC 2510

QY 241 aaggtgtaacacacagagatgacgtgtgtcctcttgaggtgtctctcctcgaagcctc 300
|||||
DB 2509 AAGGTGTACACACAGAGAGTGTGTCTTTGGGCTCTTCTGTGGAATCTTC 2450

QY 301 tctctgggggctcccccgtacccctgggggtgcagatcaatgaagagttctcgaagcgtg 360
|||||
DB 2449 TCTCTGGGGCTCCCGGTACCTGGGGTGAGATCAATGAGAGATTCTTGGCGGCTG 2390

QY 361 agagaagggcacaagatgagagggcccgagcctgagccatcccgacatacgccgacatg 420
|||||
DB 2389 AGAAGCGGCAAGAGATGAGGGCCCCGAGCTGGCCACTCCCGCATACGCCCGCATCATG 2330

QY 421 ctgaactgtcgtcgcgagaccccaagggcgaagcctgcatctcgaagcgtg 471
|||||
DB 2329 CTGAAGTGTGTGTCGGAGACCCCAAGGCGAGACTGTGATTTCTGGAGCTG 2279

RESULT 11
US-08-222-616-5
Sequence 5, Application US/08222616
Patent No. 5635177
GENERAL INFORMATION:
APPLICANT: Genentech, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-616-5

Query Match 16.1%; Score 76; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 1,7e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 ggaacatctctgtcggaagcgagctgtggaagatctgtgacttggccttgcggg 157
Db 30 ggaacatctctgtcggaagcgagctgtggaagatctgtgacttggccttgcggg 89
Qy 158 acatctacaagacc 173
Db 90 ACATCTACAAAGACC 105

RESULT 12
PCT-US95-04228-5
Sequence 5, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-5

Query Match 16.1%; Score 76; DB 5; Length 160;
Best Local Similarity 100.0%; Pred. No. 1,7e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 ggaacatctctgtcggaagcgagctgtggaagatctgtgacttggccttgcggg 157
Db 30 ggaacatctctgtcggaagcgagctgtggaagatctgtgacttggccttgcggg 89
Qy 158 acatctacaagacc 173
Db 90 ACATCTACAAAGACC 105

RESULT 13
US-08-176-620A-3
Sequence 3, Application US/08176620A
Patent No. 5595904
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-176-620A-3

Query Match 5.5%: Score 26; DB 1; Length 1467;
Best Local Similarity 100.0%: Pred. No. 0.00075;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aa:aatcgtgacttgagccttcgccg 155
|||||
Db 655 AAGATCTGTGACTTGGCGCTTGCCCG 680

RESULT 14
US-08-463-862-3
Sequence 3, Application US/08463862
Patent No. 576751
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G. et al.
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,862
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-463-862-3

Query Match 5.5%: Score 26; DB 1; Length 1467;
Best Local Similarity 100.0%: Pred. No. 0.00075;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatcgtgacttgagccttcgccg 155
|||||
Db 655 AAGATCTGTGACTTGGCGCTTGCCCG 680

RESULT 15
US-08-461-985-3
Sequence 3, Application US/08461985
Patent No. 587206
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayiotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,620
FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-461-985-3

Query Match 5.5%: Score 26; DB 2; Length 1467;
Best Local Similarity 100.0%: Pred. No. 0.00075;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatcgtgacttgagccttcgccg 155
|||||
Db 655 AAGATCTGTGACTTGGCGCTTGCCCG 680

RESULT 16
US-08-458-887-3
Sequence 3, Application US/08458887
Patent No. 5914261
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G. et al.
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas


```

: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/458,887
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/701,544
: FILING DATE: 16-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Mirock, S. Leslie
: REGISTRATION NUMBER: 18,872
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1467 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1245
:
: US-08-458-887-3
:
Query Match          5.5%; Score 26; DB 2; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatcgtgacttgctgctgcgcg 155
   |||||||
Db 655 AAGATCTGTGACTTTGGCGCTGCCGC 680

RESULT 17
US-08-932-787B-3
: Sequence 3, Application US/08932787B
: Patent No. 6277963
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED
: FILE REFERENCE: REG 430-A-1
: CURRENT APPLICATION NUMBER: US/08/932,787B
: CURRENT FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 08/469,547
: PRIOR FILING DATE: 1995-06-06
: PRIOR APPLICATION NUMBER: 08/178,488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701,544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532,004
: PRIOR FILING DATE: 1990-06-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1467
: TYPE: DNA
: ORGANISM: RAT
: FEATURE:
: NAME/KEY: CDS
:
: US-08-932-787B-3
:

```

```

: LOCATION: (1)...(1245)
: OTHER INFORMATION: ERK2 CDNA
:
: US-08-932-787B-3
:

```

```

Query Match          5.5%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 130 aagatcgtgacttgctgctgcgcg 155
   |||||||
Db 655 aagatcgtgacttgctgctgcgcg 680

```

```

RESULT 18
US-08-932-012C-3
: Sequence 3, Application US/08932012C
: Patent No. 6297035
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
: FILE REFERENCE: REG 430-Y-1
: CURRENT APPLICATION NUMBER: US/08/932,012C
: CURRENT FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 08/462,874
: PRIOR FILING DATE: 1995-06-05
: PRIOR APPLICATION NUMBER: 08/178,488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701,544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532,004
: PRIOR FILING DATE: 1990-06-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1467
: TYPE: DNA
: ORGANISM: RAT
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1245)
: OTHER INFORMATION: ERK2 CDNA
:
: US-08-932-012C-3
:
Query Match          5.5%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatcgtgacttgctgctgcgcg 155
   |||||||
Db 655 aagatcgtgacttgctgctgcgcg 680

RESULT 19
US-08-888-818C-3
: Sequence 3, Application US/08888818C
: Patent No. 6303358
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
: FILE REFERENCE: REG 430-Y-1
: CURRENT APPLICATION NUMBER: US/08/888,818C
: CURRENT FILING DATE: 1997-07-07
: PRIOR APPLICATION NUMBER: 08/478,985
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 08/178,488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701,544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532,004
: PRIOR FILING DATE: 1990-06-01
: NUMBER OF SEQ ID NOS: 21
:
: US-08-888-818C-3
:

```

```

: SOFTWARE: FastSeq for Windows Version 3.0.
: SEQ ID NO 3
:
: LENGTH: 1467
:
: TYPE: DNA
:
: ORGANISM: RAT
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (1)...(1245)
:
: OTHER INFORMATION: ERK2 CDNA
US-08-888-818C-3

```

```

Query Match      5.5%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. NO. 0.00075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

```

1      RESULT 20
2      US-08-469-537A-19
3      : Sequence 19, Application US/08469537A
4      : Patent No. 5843748
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Maisonnierre, et al.
9      : TITLE OF INVENTION: EHK AND ROH TYROSINE
10     : TITLE OF INVENTION: KINASES
11     : NUMBER OF SEQUENCES: 107
12     : CORRESPONDENCE ADDRESS:
13     : ADDRESSEE: Regeneron Pharmaceuticals, Inc
14     : STREET: 777 Old Saw Mill River Road
15     : CITY: Tarrytown
16     : STATE: NY
17     :
18     : COUNTRY: U.S.A.
19     : ZIP: 10591
20     :
21     : COMPUTER READABLE FORM:
22     : MEDIUM TYPE: Diskette
23     : COMPUTER: IBM Compatible
24     : OPERATING SYSTEM: DOS
25     : SOFTWARE: FASTSEQ Version 2.0
26     :
27     : CURRENT APPLICATION DATA:
28     : APPLICATION NUMBER: US/08/469,537A
29     : FILING DATE: 06-JUN-1995
30     : CLASSIFICATION: 435
31     :
32     : PRIOR APPLICATION DATA:
33     : APPLICATION NUMBER: USSN 08/406,247
34     : FILING DATE: 17-MAR-1995
35     : APPLICATION NUMBER: USSN 08/144,992
36     : FILING DATE: 28-OCT-1993
37     : APPLICATION NUMBER: USSN 07/736,559
38     : FILING DATE: 26-JUL-1991
39     : ATTORNEY/AGENT INFORMATION:
40     : NAME: Kempier, Ph.D., Gall M
41     : REGISTRATION NUMBER: 32,143
42     : REFERENCE/DOCKET NUMBER: REG 070C
43     : TELECOMMUNICATION INFORMATION:
44     : TELEPHONE: 914-345-7400
45     : TELEFAX: 914-345-7721
46     :
47     : TELEX:
48     :
49     : INFORMATION FOR SEQ ID NO: 19:
50     :
51     : SEQUENCE CHARACTERISTICS:
52     : LENGTH: 159 base pairs
53     : TYPE: nucleic acid
54     : STRANDEDNESS: double
55     : TOPOLOGY: unknown
56     : MOLECULE TYPE: cDNA
57     :
58     : FEATURE:
59     :
60     : NAME/KEY: CDS
61     : LOCATION: 1..159
62     :
63     : US-08-469-537A-19

```

Query Match	4.98;	Score 23;	DB 2;	Length 159;
Best Local Similarity	100.08;	Pred. No. 0.025;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```

1      RESULT 21
2      US-07-912-122-3
3      Sequence 3, Application US/07912122
4      Patent No. 6228609
5      GENERAL INFORMATION:
6      APPLICANT: YANG, Zh1
7      TITLE OF INVENTION: NOVEL FLK-2 AND ANALOGS
8      NUMBER OF SEQUENCES: 6
9      CORRESPONDENCE ADDRESS:
10     ADDRESSED: Berttram I. Rowland
11     STREET: 4 Embarcadero Center, Suite 3400
12     CITY: San Francisco
13     STATE: California
14     COUNTRY: USA
15     ZIP: 94111
16     COMPUTER READABLE FORM:
17     MEDIUM TYPE: Floppy disk
18     COMPUTER: IBM PC compatible
19     OPERATING SYSTEM: PC-DOS/MS-DOS
20     SOFTWARE: PatentIn Release #1.0, Version #1.25
21     CURRENT APPLICATION DATA:
22     APPLICATION NUMBER: US/07/912,122
23     FILING DATE: 19920709
24     CLASSIFICATION: 435
25     ATTORNEY/AGENT INFORMATION:
26     NAME: Rowland, Berttram I.
27     REGISTRATION NUMBER: 20,015
28     REFERENCE/DOCKET NUMBER: A-55931/BIR
29     TELECOMMUNICATION INFORMATION:
30     TELEPHONE: (415)789-1989
31     TELEFAX: (415) 398-3249
32     INFORMATION FOR SEQ. ID NO.: 3:
33     SEQUENCE CHARACTERISTICS:
34     LENGTH: 1894 base pairs
35     TYPE: NUCLEIC ACID
36     STRANDEDNESS: single
37     TOPOLOGY: linear
38     MOLECULE TYPE: cDNA
39     FEATURE:
40     NAME/KEY: CDS
41     LOCATION: 31..1473
42     US-07-912-122-3

```

Query Match 4.9%; Score 23; DB 4; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

RESULT 2
PCT-US93-06404-3
Sequence 3, Application PC/TUS9306404
GENERAL INFORMATION:
APPLICANT: YANG, Zhi
TITLE OF INVENTION: NOVEL FLK-2 AND ANALOSES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bertram I. Rowland
STREET: 4 Embacadero Center, Suite 3400

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06404
FILING DATE: 19930707
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: FP-55931/BIR
TELEPHONE: (415) 789-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1473
PCT-US93-06404-3

Query Match 4.9%; Score 23; DB 5; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 124 gtggggaagatctgacttg 146
|||||
Db 976 GTGGTGAAGATCTGTGACTTTGG 998

RESULT 23
US-07-813-593-1
Sequence 1, Application US/07813593
Patent No. 5185438
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/813,593
FILING DATE: 19920415
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
NAME/KEY: mat-peptide
LOCATION: 31..3006
US-07-813-593-1

Query Match 4.9%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 124 gtggggaagatctgacttg 146
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 24
US-07-977-451-1
Sequence 1, Application US/07977451
Patent No. 5270458
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,451
FILING DATE: 19921119
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNASSIGNED
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TM 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:

```

: APPLICATION NUMBER: US PCT/US92/02750
: FILING DATE: 02-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/813,593
: FILING DATE: 24-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/793,065
: FILING DATE: 15-NOV-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/728,913
: FILING DATE: 28-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/679,666
: FILING DATE: 02-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Felt, Irving N.
: REGISTRATION NUMBER: 28,601
: REFERENCE/DOCKET NUMBER: LEM-3-7P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3453 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 112..3006
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: 31..111
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 31..3009
: US-07-977-451-1

Query Match 4.9%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gtggtaagatctgtgacttgg 146
      |||||||||||||||||||
DB 2509 gtgctgaagatctgtgacttgg 2531

RESULT 25
: US-07-946-507-1
: Sequence 1, Application US/07946507
: Patent No. 5283354
: GENERAL INFORMATION:
: APPLICANT: Lemischka, Ihor R.
: TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
: STREET: 180 VARICK STREET
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: U.S.A.
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PC-DOS/MS-DOS
: APPLICATION NUMBER: US/07/252,517
: FILING DATE: 31-OCT-1994
: CLASSIFICATION: 530
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/946,507
: FILING DATE: 19920917
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/813,593
: FILING DATE: 24-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/793,065
: FILING DATE: 15-NOV-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/728,913
: FILING DATE: 28-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/679,666
: FILING DATE: 02-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Felt, Irving N.
: REGISTRATION NUMBER: 28,601
: REFERENCE/DOCKET NUMBER: LEM-3-PPP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3453 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 31..3009
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 31..3006
: US-07-946-507-1

Query Match 4.9%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gtggtaagatctgtgacttgg 146
      |||||||||||||||||||
DB 2509 gtgctgaagatctgtgacttgg 2531

RESULT 26
: US-08-252-517-1
: Sequence 1, Application US/08252517
: Patent No. 5548065
: GENERAL INFORMATION:
: APPLICANT: Lemischka, Ihor R.
: TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: APPLICATION NUMBER: US/08/252,517
: FILING DATE: 31-OCT-1994
: CLASSIFICATION: 530
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? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/977,451
? FILING DATE: 19-NOV-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/906,397
? FILING DATE: 26-JUN-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US PCT/US92/05401
? FILING DATE: 26-JUN-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: TM 81102961
? FILING DATE: 15-APR-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US PCT/US92/02750
? FILING DATE: 02-APR-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/813,593
? FILING DATE: 24-DEC-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/793,065
? FILING DATE: 15-NOV-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/728,913
? FILING DATE: 28-JUN-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/679,666
? FILING DATE: 02-APR-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Felt, Irving N.
? REGISTRATION NUMBER: 28,601
? REFERENCE/DOCKET NUMBER: LEM-3-7P
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-645-1405
? TELEFAX: 212-645-2054
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3453 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 112..3006
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 31..111
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 31..3009
? US-08-252-517-1

Query Match 4.9%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gttgtgaagatctgtgactttg 146
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 27
US-07-906-397A-1
; Sequence 1, Application US/07906397A
; Patent No. 5621090
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TORIOPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
```

```

? NUMBER OF SEQUENCES: 6
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: IMCONE SYSTEMS INCORPORATED
? STREET: 180 VARICK STREET
? CITY: NEW YORK
? STATE: NEW YORK
? COUNTRY: U.S.A.
? ZIP: 10014
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC Compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/906,397A
? FILING DATE: 19920626
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/813,593
? FILING DATE: 24-DEC-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/793,065
? FILING DATE: 15-NOV-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/728,913
? FILING DATE: 28-JUN-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/679,666
? FILING DATE: 02-APR-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Felt, Irving N.
? REGISTRATION NUMBER: 28,601
? REFERENCE/DOCKET NUMBER: LEM-3-PPPPP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-645-1405
? TELEFAX: 212-645-2054
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3453 base pairs
? TYPE: NUCLEIC ACID
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 31..3009
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 31..3006
? US-07-906-397A-1

Query Match 4.9%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gttgtgaagatctgtgactttg 146
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 28
US-08-601-891-1
; Sequence 1, Application US/08601891
; Patent No. 5747651
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TORIOPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
```

CORRESPONDENCE ADDRESS:

ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,891
FILING DATE: 15-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 112..3006
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 31..111
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
US-08-601-891-1

Query Match 4.9%; Score 23; DB 1; Length 3453;

Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 124 gtgtgaagatctgtgacttgg 146
|||||
Db 2509 gtgtgaagatctgtgacttgg 2531

RESULT 29

US-09-021-324-1
Sequence 1, Application US/09021324
Patent No. 5912133

GENERAL INFORMATION:

APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 112..3006
FEATURE:
NAME/KEY: s19_peptide
LOCATION: 31..111
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
US-09-021-324-1

Query Match 4.9%: Score 23; DB 2; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 124 gtggtgaagatctgtgacttgg 146
|||||
Db 2509 gtggtgaagatctgtgacttgg 2531

RESULT 30
PCT-US92-02750-1
Sequence 1, Application PC/TUS9202750
GENERAL INFORMATION:
APPLICANT: LEMISCHKA, ITHOR R.
TITLE OF INVENTION: Totipotent Hematopoietic Stem Cell
TITLE OF INVENTION: Receptors And Their Ligands
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: US
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02750
FILING DATE: 19920402
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FELT, IRVING N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPPT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 31..3006
PCT-US92-02750-1

Query Match 4.9%: Score 23; DB 5; Length 3453;

Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 124 gtggtgaagatctgtgacttgg 146
|||||
Db 2509 gtggtgaagatctgtgacttgg 2531

RESULT 31
PCT-US92-05401-1
Sequence 1, Application PC/TUS9205401
GENERAL INFORMATION:
APPLICANT: Lemischka, Ithor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05401
FILING DATE: 19920626
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPPT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 31..3006
PCT-US92-05401-1

Query Match 4.9%: Score 23; DB 5; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 gtggtgaagatctgtgacttgg 146
|||||
Db 2509 gtggtgaagatctgtgacttgg 2531

RESULT 32
PCT-US92-09893-1
Sequence 1, Application PC/TUS9209893
GENERAL INFORMATION:
APPLICANT: Lemischka, Ithor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:

```

ADDRESSER: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09893
FILING DATE: 19921116
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7PT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: mal-peptide
LOCATION: 112..3006
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 31..111
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
PCT-US92-09893-1

Query Match          4.9%; Score 23; DB 5; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gtgtgaagatctgtgacttgg 146
|||||
Db 2509 GTGTGAAGATCTGTGACTTTGG 2531

RESULT 33
US-08-222-299-1
Sequence 11, Application US/08122795B
Patent No. 5635385
GENERAL INFORMATION:
APPLICANT: Lance H. Leopold
APPLICANT: Scott K. Shore
APPLICANT: Moolle V. R. Reddy
APPLICANT: E. Premkumar Reddy
TITLE OF INVENTION: MULTI-UNIT RIBOZYME
TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Seidel, Conda, Lavorgna
ADDRESSER: 6 Monaco, P.C.
STREET: Two Penn Center Plaza, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,795B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122,795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
Sequence 1, Application US/08222299
Patent No. 5635388
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William
APPLICANT: Zeligler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,299
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3521 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-299-1

Query Match          4.9%; Score 23; DB 1; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


OY 124 gtggtgaagatctgtgactttg 146
|||||
DB 2560 GTGCTGAAGATCTGTGACTTTGG 2582

RESULT 34

US-08-434-878-1
Sequence 1, Application US/08434878
Patent No. 5997865
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,878
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3521 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-434-878-1

Query Match 4.9%; Score 23; DB 2; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 23: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgtgactttg 146
|||||
DB 2560 GTGCTGAAGATCTGTGACTTTGG 2582

RESULT 35

PCT-US95-03718-1
Sequence 1, Application PC/TUS9503718
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: palin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03718

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 879PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 3521 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
PCT-US95-03718-1

Query Match 4.9%; Score 23; DB 5; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 23: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgtgactttg 146
|||||
DB 2560 GTGCTGAAGATCTGTGACTTTGG 2582

RESULT 36

US-08-180-195-35
Sequence 35, Application US/08180195
Patent No. 5567584
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,195
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,510
FILING DATE:
APPLICATION NUMBER: US 07/146,877

FILING DATE: 22-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: MAKI J.D., David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:
US-08-180-195-35

Query Match 4.9%; Score 23; DB 1; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtgacttgacct 149
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 37
US-08-477-329-35
Sequence 35, Application US/08477329
Patent No. 5750375
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,329
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900

TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:
US-08-477-329-35

Query Match 4.9%; Score 23; DB 1; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtgacttgacct 149
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 38
US-08-475-458-35
Sequence 35, Application US/08475458
Patent No. 5843725
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGIC
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,458
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N

ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:
US-08-475-458-35

Query Match 4.9%; Score 23; DB 2; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 gtgaagatctgtgacttgacct 149
|||||
Db 2698 CTGAAGATCTGTGACTTTGGCCT 2720

RESULT 39
US-08-980-400-35
Sequence 35, Application US/08980400
Patent No. 6018026
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,400
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,329
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS

LOCATION: 205..3471
OTHER INFORMATION:
US-08-980-400-35

Query Match 4.9%; Score 23; DB 3; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 gtgaagatctgtgacttgacct 149
|||||
Db 2698 CTGAAGATCTGTGACTTTGGCCT 2720

RESULT 40
US-09-583-459A-35
Sequence 35, Application US/09583459A
Patent No. 6291212
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,459A
FILING DATE: 30-MAY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,510
FILING DATE: 27-DEC-1990
APPLICATION NUMBER: US 07/146,877
FILING DATE: 22-JAN-1988
APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Maki J.D., David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471

OTHER INFORMATION:
US-09-583-459A-35

Query Match 4.9%; Score 23; DB 4; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 gtgaagatctgtgacttgccct 149
|||||
Db 2698 GTGAAGATCTGTGACTTGCCCT 2720

RESULT 41
US-09-583-210-35

; Sequence 35, Application US/09583210
; Patent No. 6291646

; GENERAL INFORMATION:

; APPLICANT: Sledziewski Ph.D., Andrzej Z

; APPLICANT: Bell, Lillian A.

; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS

; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry

; STREET: 6300 Columbia Center

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/583,210

; FILING DATE: 30-MAY-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/634,510

; FILING DATE: 27-DEC-1990

; APPLICATION NUMBER: US 07/146,877

; FILING DATE: 22-JAN-1988

; APPLICATION NUMBER: US 07/347,291

; FILING DATE: 02-MAY-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki J.D., David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 990008.446C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-622-4900

; TELEFAX: 206-682-6031

; TELEX: 3723836

; INFORMATION FOR SEQ ID NO: 35:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4054 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: N

; ANTI-SENSE: N

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:

; CLONE: p-alpha-17B

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 205..3471

; OTHER INFORMATION:

US-09-583-210-35

Query Match 4.9%; Score 23; DB 4; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 gtgaagatctgtgacttgccct 149
|||||
Db 2698 GTGAAGATCTGTGACTTGCCCT 2720

RESULT 42
US-09-583-449A-35

; Sequence 35, Application US/09583449A
; Patent No. 6300099

; GENERAL INFORMATION:

; APPLICANT: Sledziewski Ph.D., Andrzej Z

; APPLICANT: Bell, Lillian A.

; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS

; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry

; STREET: 6300 Columbia Center

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/583,449A

; FILING DATE: 30-MAY-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/634,510

; FILING DATE: 27-DEC-1990

; APPLICATION NUMBER: US 07/146,877

; FILING DATE: 22-JAN-1988

; APPLICATION NUMBER: US 07/347,291

; FILING DATE: 02-MAY-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki J.D., David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 990008.446C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-622-4900

; TELEFAX: 206-682-6031

; TELEX: 3723836

; INFORMATION FOR SEQ ID NO: 35:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4054 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: N

; ANTI-SENSE: N

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:

; CLONE: p-alpha-17B

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 205..3471

; OTHER INFORMATION:

US-09-583-449A-35

Query Match 4.9%; Score 23; DB 4; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtacttggcct 149
|||||
DB 2698 GTGAAGATCTGTACTTGGCCT 2720

RESULT 43

US-08-168-917-3
; Sequence 3, Application US/08168917
; Patent No. 5686572

GENERAL INFORMATION:

APPLICANT: Wolf, David
APPLICANT: Tomlinson, James E.
APPLICANT: Fretto, Larry J.
APPLICANT: Giese, Neil A.
APPLICANT: Escobedo, Jaime A.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND
STREET: Stewart Street Tower, 20th Floor \ One Market
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,917
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/650,793
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 12418-14

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 4100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Homo Sapiens
STRAIN: lambda gt10
FEATURE:

NAME/KEY: CDS
LOCATION: 129..3395
US-08-168-917-3

Query Match 4.9%; Score 23; DB 1; Length 4100;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtacttggcct 149
|||||
DB 2622 GTGAAGATCTGTACTTGGCCT 2644

RESULT 44

US-08-460-510-3
; Sequence 3, Application US/08460510
; Patent No. 5872218

GENERAL INFORMATION:

APPLICANT: Wolf, David
APPLICANT: Tomlinson, James E.
APPLICANT: Fretto, Larry J.
APPLICANT: Giese, Neil A.
APPLICANT: Escobedo, Jaime A.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW
STREET: One Market Plaza, Stewart Street Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,510
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 012418-001430

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 4100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Homo Sapiens
STRAIN: lambda gt10
FEATURE:

NAME/KEY: CDS
LOCATION: 129..3395
US-08-460-510-3

Query Match 4.9%; Score 23; DB 2; Length 4100;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtacttggcct 149
|||||
DB 2622 GTGAAGATCTGTACTTGGCCT 2644

RESULT 45

US-08-460-490-3
; Sequence 3, Application US/08460490

Patent No. 5891652
GENERAL INFORMATION:
APPLICANT: Wolf, David
APPLICANT: Tomlinson, James E.
APPLICANT: Fretto, Larry J.
APPLICANT: Giese, Neill A.
APPLICANT: Escobedo, Jaime A.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: One Market Plaza, Stewart Street Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,490
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 012418-001420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
STRAIN: lambda gt10
FEATURE:
NAME/KEY: CDS
LOCATION: 129..3395
US-08-460-490-3

Query Match 4.9%; Score 23; DB 2; Length 4100;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 127 gtcgaagatctgtacttgacct 149
|||||
Db 2622 GTGAGACTCTGTGACTTGTGGCCT 2644

Search completed: July 15, 2002, 23:07:38
Job time: 22991 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:09:50 ; Search time 932.4 Seconds

(without alignments)
867.296 Million cell updates/sec

Title: US-09-375-248-1_COPY_3044_3514

Sequence: 471 ctgaccatcggaagatcctgtc.....gacctgcattcgcgagctcy 471

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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2: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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21: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	100.0	4111	21	Human Flt4/VEGFR-3
2	471	100.0	4111	22	Human Flt4/VEGFR-3
3	471	100.0	4195	17	Human Flt4/VEGFR-3
4	471	100.0	4195	21	Human Flt4/VEGFR-3
5	471	100.0	4195	21	Human Flt4/VEGFR-3
6	471	100.0	4425	16	Human Flt4/VEGFR-3
7	471	100.0	4795	21	Human Flt4/VEGFR-3
8	471	100.0	4795	21	Human Flt4/VEGFR-3
9	471	100.0	9108	16	Human Flt4/VEGFR-3

C	10	420	89.2	6827	14	AA049753
C	11	420	89.2	6827	16	AA0703101
C	12	305	64.8	4450	21	AA062210
C	13	76	16.1	160	14	AA049747
C	14	76	16.1	160	16	AA0703089
C	15	26	5.5	1047	20	AA069501
C	16	26	5.5	1467	13	AA020261
C	17	26	5.5	1815	19	AA071031
C	18	26	5.5	1818	19	AA071023
C	19	26	5.5	1818	19	AA071023
C	20	26	5.5	1818	19	AA071023
C	21	23	4.9	159	13	AA030721
C	22	23	4.9	159	13	AA070215
C	23	23	4.9	1894	15	AA054036
C	24	23	4.9	3453	13	AA029954
C	25	23	4.9	3453	14	AA035502
C	26	23	4.9	3453	14	AA035549
C	27	23	4.9	3453	14	AA040914
C	28	23	4.9	3453	16	AA081012
C	29	23	4.9	3453	16	AA079068
C	30	23	4.9	3453	17	AA038733
C	31	23	4.9	3453	18	AA072118
C	32	23	4.9	3521	20	AA077514
C	33	23	4.9	4054	16	AA008801
C	34	23	4.9	6412	11	AA006869
C	35	22	4.7	4479	24	AA005989
C	36	21	4.5	2574	18	AA079406
C	37	20	4.2	20	21	AA073125
C	38	20	4.2	20	21	AA062208
C	39	20	4.2	1611	19	AA062479
C	40	20	4.2	1611	19	AA062479
C	41	20	4.2	4544	10	AA089336
C	42	20	4.2	4544	17	AA090355
C	43	20	4.2	4544	17	AA073452
C	44	20	4.2	5427	13	AA059189
C	45	20	4.2	5602	23	AA027447
C						AA084940

ALIGNMENTS

RESULT 1	AA062405	standard; cDNA; 4111 BP.
ID	AA062405	standard; cDNA; 4111 BP.
AC	AA062405	
XX		
DT	31-JAN-2001	(first entry)
XX		
DE	Human Flt4/VEGFR-3 coding sequence.	
XX		
KW	Human: Flt4; fms-like tyrosine kinase 4; lymphoedema;	
KW	vascular endothelial growth factor receptor 3; VEGFR-3;	
KW	Milroy-Nonne syndrome; lymphoedema praecox; ss.	
OS	Homo sapiens.	
XX		
PN	WO200058511-A1.	
XX		
PD	05-OCT-2000.	
XX		
PF	26-MAR-1999;	99WO-US06133.
XX		
PR	26-MAR-1999;	99WO-US06133.
XX		
PA	(LUDW-) LUDWIG INST CANCER RES.	
PA	(UYRE-) UNIV HELSINKI LICENSING LTD OY.	
PA	(UYPI-) UNIV PITTSBURGH.	
XX		
PI	Ferrell RE, Allitalo K, Finegold DN, Karkkainen M;	
XX		
DR	WPI: 2000-679298/66.	
DR	P-PSDB: AAB29047.	

PTK gene SAL-S1.
Protein tyrosine-k
Nucleotide sequenc
PTK gene SAL-S1 pa
Protein tyrosine-k
Human extracellular
ERK2. Rat ratius.
Erk2-green flouresc
Green flourescent
Rat type I insulin
Tyrosine kinase c1
Rat orphan tyrosin
Flk-2as gene. Mus
Murine flk-2 cDNA.
Murine flk-2 cDNA.
Murine flk-2 cDNA.
Murine flk-2 recep
Murine flk-2 recep
Human foetal liver
Human flk-2 recep
Flk2/flt3 tyrosine
Sequence encodes P
TR4 cDNA clone rel
Mouse ischaemic co
Mouse Tec tyrosine
PCR primer used to
Human MAP kinase.
Human MAP kinase.
Platelet-derived g
cDNA encoding plat
Platelet-derived g
Human secreted pro
Type B human plate
DNA encoding novel

XX Screening a human subject for increased risk of developing a lymphatic
PT disorder, comprises assaying a nucleic acid to determine a mutation
PT altering the sequence of a vascular endothelial growth factor
PT receptor-3.

XX Claim 14: Page 46-52; 76pp; English.

XX The present sequence is the coding sequence for the human vascular
CC endothelial growth factor receptor 3 (VEGFR-3), also known as Flt4 or
CC fms-like tyrosine kinase 4). It was used in the methods of the invention,
CC which involve the screening of individuals to determine which VEGFR-3
CC alleles they possess and thus their likelihood of developing hereditary
CC lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne
CC syndrome, which is early onset lymphoedema and lymphoedema praecox, which
CC is late onset.

XX Sequence 4111 BP; 846 A; 1273 C; 1298 G; 694 T; 0 other;

Query Match 100.0%; Score 471; DB 21; Length 4111;
Best Local Similarity 100.0%; Pred. No. 1e-225;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacacatggaagatctgtctgtctacagcttccaggtgagcagaagagatgagttcctg 60
DB 3044 ctgacacatggaagatctgtctgtctacagcttccaggtgagcagaagagatgagttcctg 3103
OY 61 gcttccggaagatgcatccacagaagacgtgctgtcgtggaacatctcgtcgtggaagc 120
DB 3104 gcttccggaagatgcatccacagaagacgtgctgtcgtggaacatctcgtcgtggaagc 3163
OY 121 gaagtgatgaagatctgacttgccttgccctgagacatctacaagaccctgagctac 180
DB 3164 gaagtgatgaagatctgacttgccttgccctgagacatctacaagaccctgagctac 3223
OY 181 gtcgcaagagcagctgcctgctgcccctgaaagtgaatgagtgccctgaaagcatcttcgac 240
DB 3224 gtcgcaagagcagctgcctgctgcccctgaaagtgaatgagtgccctgaaagcatcttcgac 3283
OY 241 aaggtgacacacagcagaatgagctgagtgcttcttgagggtgcttctcttgaggagatcttc 300
DB 3284 aaggtgacacacagcagaatgagctgagtgcttcttgagggtgcttctcttgaggagatcttc 3343
OY 301 tctctgggggctccctgac 360
DB 3344 tctctgggggctccctgac 3403
OY 361 aaggaagcagcagaagatgagtgagggcccgagagctgagccacacacacacacacacacac 420
DB 3404 aaggaagcagcagaagatgagtgagggcccgagagctgagccacacacacacacacacacac 3463
OY 421 ctgaacatgctgctcggagagaccccaagcgagacatcttcctcgagagctg 471
DB 3464 ctgaacatgctgctcggagagaccccaagcgagacatcttcctcgagagctg 3514

RESULT 2

AAC68952 AAC68952 standard; cDNA; 4111 BP.

AC AAC68952:

XX 27-FEB-2001 (first entry)

XX Human Flt4/VEGFR-3 coding sequence.

XX Human: gene therapy; lymphatic disorder; hereditary lymphoedema; Flt4;
KW vascular endothelial growth factor receptor-3; VEGFR-3; VEGF-C; VEGF-D;
XX fms-like tyrosine kinase 4; ss.

OS Homo sapiens.

PH Key Location/Qualifiers
FT CDS 20..4111
FT /*tag= a
FT /product= "Human Flt4/VEGFR-3"

PN CA283470-A1.

XX 26-SEP-2000.

XX 29-SEP-1999; 99CA-2283470.

XX 26-MAR-1999; 99NO-US06133.

XX 16-AUG-1999; 99US-0375248.

XX (UYPI-) UNIV PITTSBURGH.

XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Altalo K, Ferrell RE, Finegold DN, Karkkainen M;

XX WPI, 2001-007762/02.

XX P-PSDB: AAB37604.

XX Claim 15: Pages 48-54; 99pp; English.

CC The present invention relates to a method for screening a human subject
CC for an increased risk of developing a lymphatic disorder e.g. hereditary
CC lymphoedema. The method comprises assaying nucleic acid of a human
CC subject to determine a presence or an absence of a mutation altering the
CC sequence or expression of vascular endothelial growth factor receptor-3
CC (VEGFR-3)/fms-like tyrosine kinase 4 (Flt4) allele and determining an
CC increased risk of developing lymphatic disorder from presence or absence
CC of the mutation. The present sequence is the coding sequence for human
CC VEGFR-3/Flt4. The presence of a mutation altering the encoded amino acid
CC sequence or expression of at least 1 VEGFR-3 allele in the nucleic acid
CC correlates with an increased risk of developing a lymphatic disorder.
CC Treatment for hereditary lymphoedema can be provided through the
CC administration of VEGF-C and VEGF-D genes (via gene therapy) and
CC proteins.

SO Sequence 4111 BP; 846 A; 1272 C; 1299 G; 694 T; 0 other;

Query Match 100.0%; Score 471; DB 22; Length 4111;
Best Local Similarity 100.0%; Pred. No. 1e-225;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacacatggaagatctgtctgtctacagcttccaggtgagcagaagagatgagttcctg 60
DB 3044 ctgacacatggaagatctgtctgtctacagcttccaggtgagcagaagagatgagttcctg 3103
OY 61 gcttccggaagatgcatccacagaagacgtgctgtcgtggaacatctcgtcgtggaagc 120
DB 3104 gcttccggaagatgcatccacagaagacgtgctgtcgtggaacatctcgtcgtggaagc 3163
OY 121 gaagtgatgaagatctgacttgccttgccctgagacatctacaagaccctgagctac 180
DB 3164 gaagtgatgaagatctgacttgccttgccctgagacatctacaagaccctgagctac 3223
OY 181 gtcgcaagagcagtgccgctgcccctgaaagtgaatgagtgccctgaaagcatcttcgac 240
DB 3224 gtcgcaagagcagtgccgctgcccctgaaagtgaatgagtgccctgaaagcatcttcgac 3283
OY 241 aaggtgacacacagcagaatgagctgagtgcttcttgagggtgcttctcttgaggagatcttc 300
DB 3284 aaggtgacacacagcagaatgagctgagtgcttcttgagggtgcttctcttgaggagatcttc 3343
OY 301 tctctgggggctccctgac 360
|||||

PT Antibody to extracellular domain of or to an epitope unique to a
PT vertebrate Flt4 receptor tyrosine kinase protein useful for diagnosing
PT lymphoma and imaging lymphatic vessels or high endothelial venules in
PT tissue
XX
XX
PS Disclosure: Column 41-50; 66pp; English.
CC This sequence encodes the human Flt4 receptor tyrosine kinase short
CC form protein. The invention relates to an antibody (I) specific to the
CC extracellular domain of or to an epitope unique to a vertebrate Flt4
CC receptor tyrosine kinase protein (II). A composition comprising (I) is
CC useful for detecting lymphatic vessels, lymphatic tissue comprising lymph
CC node tissue or high endothelial venules in an organism preferably mammal
CC especially human. The method comprises administering the composition and
CC detecting (I) bound to lymphatic vessels, lymphatic tissue or high
CC endothelial venules. (I) is also useful for screening a biological sample
CC for the presence of (II) or diagnosing a disease state. The diagnosing
CC method of the disease state preferably lymphoma comprises obtaining a
CC tissue sample on a vertebrate organism suspected of being in a diseased
CC state characterised by in Flt4 expression in lymphatic cells or high
CC endothelial venules and screening the diseased state utilising (I).
CC (I) is also useful for imaging lymphatic vessels or high endothelial
CC venules in a tissue by contacting the tissue with (I) and imaging the
CC vessels by detecting (I) bound to the tissues.
XX
S0 Sequence 4195 BP; 889 A; 1279 C; 1305 G; 722 T; 0 other:

Query Match 100.0%; Score 471; DB 21; Length 4195;
Best Local Similarity 100.0%; Pred. No. 1e-225;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgaccatggaagatctgtctgctacagcttccaggtgagcagagagatgagttctc 60
DB 3044 ctgaccatggaagatctgtctgctacagcttccaggtgagcagagagatgagttctc 3103
OY 61 gcttccgaaagtgcattccacagagacctggtctcgcggaacattctgctcgaagc 120
DB 3104 gcttccgaaagtgcattccacagagacctggtctcgcggaacattctgctcgaagc 3163
OY 121 gaagtggtgaagatcgtgacttgccttgcctgcggaacattctcgaagc 180
DB 3164 gaagtggtgaagatcgtgacttgccttgcctgcggaacattctcgaagc 3223
OY 181 gtcgcaagggcagctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgc 240
DB 3224 gtcgcaagggcagctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgc 3283
OY 241 aaggtgtacacacagcagagtgagctgtgcttgcctgcctgcctgcctgcctgcctgc 300
DB 3284 aaggtgtacacacagcagagtgagctgtgcttgcctgcctgcctgcctgcctgcctgc 3343
OY 301 tctctgggggctccctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgc 360
DB 3344 tctctgggggctccctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgc 3403
OY 361 agagagcagcacaagatgagtgagcctgcctgcctgcctgcctgcctgcctgcctgcctgc 420
DB 3404 agagagcagcacaagatgagtgagcctgcctgcctgcctgcctgcctgcctgcctgcctgc 3463
OY 421 ctgaactgctggttccggaagaccgaagcgaagcgtcattctcgaagct 471
DB 3464 ctgaactgctggttccggaagaccgaagcgaagcgtcattctcgaagct 3514

RESULT 5
AA52333
ID AA52333 standard; cDNA; 4195 BP.
XX
AC AA52333;
XX
DT 17-AUG-2000 (first entry)
XX

DE Human tyrosine kinase receptor Flt4-short form cDNA.
XX
XX Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4;
KW VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
KW cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
KW neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
KW sarcoma; malignancy; ss.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 20..3916
FT /tag= a
FT /product= "Flt4 receptor-short form"
FT /note= "The start codon is surrounded by typical
FT consensus kozak sequence"
FT sig_peptide 20..79
FT /tag= b
FT /note= "Directs protein to endoplasmic reticulum"
FT mat_peptide 80..3913
FT /tag= C
FT /product= "Mature Flt4 receptor-short form"
XX
XX WO200021560-A1.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-US23525.
XX
XX 09-OCT-1998; 98US-0169079.
XX
XX (LUDWIG) LUDWIG INST CANCER RES.
XX (UYNE-) UNIV HELSINKI LICENSING LTD OY.
XX
XX Alltalo K, Kaipainen A, Valtola R, Jussila L;
XX
XX WPI: 2000-317850/27.
XX P-PSDB: AAV70746.
XX
XX Treating neoplastic diseases such as lymphoma, carcinomas, melanomas
PT and sarcomas, involves administering a compound capable of inhibiting
PT binding of ligand proteins to fms-like tyrosine kinase-4 receptor
XX
XX Example 14; Page 109-115; 148pp; English.
XX
XX The patent discloses a method to treat neoplastic disease characterised
CC by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also
CC referred as vascular endothelial growth factor receptor-3, VEGFR-3) in
CC endothelial cells of blood vessels adjacent to malignant neoplasm. The
CC method involves administering a compound that inhibits binding of a
CC ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
CC endothelial cells. The compound is useful for treating neoplastic disease
CC such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
CC and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used
CC for manufacturing medicament useful for diagnostic screening, imaging and
CC treatment of malignancies characterised by Flt4-expressing blood cells.
CC The present sequence is a cDNA encoding the short form of Flt4 receptor
CC from an oligo-dT primed human erythroleukaemia cell line (HEL) cDNA
CC library in bacteriophage lambda gt11. The Flt4 gene maps to chromosomal
CC region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in
CC their 3' sequences and are differentially expressed in HEL and DMI cell
CC lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases
CC (RTKs). It is used as a target for tumour imaging and anti-tumour
CC therapy.
XX
XX
S0 Sequence 4195 BP; 889 A; 1279 C; 1305 G; 722 T; 0 other:

Query Match 100.0%; Score 471; DB 21; Length 4195;
Best Local Similarity 100.0%; Pred. No. 1e-225;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgaccatggaagatctgtctgctacagcttccaggtgagcagagagatgagttctc 60

```
|||||
Db 3044 ctgacacatggaagatctctgctctacagcttcacaggtgagcagaggaagatcttcctg 3103
Oy 61 gcttcccgaaagatgcatcccaagagacctgagctgctcggaaacatctgctgctcgaaagc 120
Db 3104 gcttcccgaaagatgcatcccaagagacctgagctgctcggaaacatctgctgctcgaaagc 3163
Oy 121 gacgtgctgaagatctctgacatcttgcgcttgcgagacatcttacaagaagccttgactac 180
Db 3164 gacgtgctgaagatctctgacatcttgcgcttgcgagacatcttacaagaagccttgactac 3223
Oy 181 gtcgcgaagagcagctgagctgagccttgcgcttgcgagacatcttgcgagacatcttgcgac 240
Db 3224 gtcgcgaagagcagctgagccttgcgcttgcgagacatcttgcgagacatcttgcgac 3283
Oy 241 aaggtgctgaagatctctgacatcttgcgcttgcgagacatcttgcgagacatcttgcgac 300
Db 3284 aaggtgctgaagatctctgacatcttgcgcttgcgagacatcttgcgagacatcttgcgac 3343
Oy 301 tctctgggggctcctccgctcctgagctgagacatcttgcgagacatcttgcgagacatcttgcgac 360
Db 3344 tctctgggggctcctccgctcctgagctgagacatcttgcgagacatcttgcgagacatcttgcgac 3403
Oy 361 agagacgagcacaagatgagagcctcgagagctgagacatcttgcgagacatcttgcgagacatcttgcgac 420
Db 3404 agagacgagcacaagatgagagcctcgagagctgagacatcttgcgagacatcttgcgagacatcttgcgac 3463
Oy 421 ctgaactgctgctcggagagaccccaagagcagacatcttgcgagacatcttgcgagacatcttgcgac 471
Db 3464 ctgaactgctgctcggagagaccccaagagcagacatcttgcgagacatcttgcgagacatcttgcgac 3514

RESULT 6
AA03090
ID AA03090 standard; DNA: 4425 BP.
XX
AC AA03090:
DT 14-FEB-1996 (first entry)
XX
DE Protein tyrosine-kinase SAL-S1 gene.
XX
KM Protein tyrosine-kinase; PTK; SAL-S1; agonist; cell growth;
XX
OS differentiation; ss.
XX
XX Homo sapiens.
XX
OS
XX
FH Key 30..3927
FT CDS
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c
XX
PN WO9527061-A1.
XX
XX 12-OCT-1995.
XX
PD 04-APR-1995; 95WO-US04228.
XX
PF 04-APR-1994; 94US-0222616.
XX
PR (GETH ) GENENTECH INC.
XX
PA Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP:
XX
PI Wood WI.
XX
DR WPI: 1995-366160/47.
XX
DR P-PSDB: AAR85937.
XX
PT Agonist antibodies which activate specific protein tyrosine
kinase(s) - also activate chimeric proteins of kinase extracellular
```

```
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
XX
XX PS Disclosure: Fig 15A-F, 125pp; English.
XX
XX CC DNA probes based on protein tyrosine-kinase (PTK) sequences were used
XX to screen cDNA libraries to identify novel PTK genes. The SAL-S1
XX CC gene (see also AA03090) was isolated from several megakaryocytic cell
XX CC libraries. The gene can be used to produce recombinant SAL-S1 or its
XX CC fragments, to detect related genes, and to design drugs, peptides
XX CC or antisense nucleotides that modulate PTK activity.
XX
SQ Sequence 4425 BP: 939 A; 1348 C; 1361 G; 777 T; 0 other:

Query Match 100.0%; Score 471; DB 16; Length 4425;
Best Local Similarity 100.0%; Pred. No. 1e-225;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgacacatggaagatctctgacatcttgcgcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 60
Db 3055 ctgacacatggaagatctctgacatcttgcgcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 3114
Oy 61 gcttcccgaaagatgcatcccaagagacctgagctgctcggaaacatctgctgctcgaaagc 120
Db 3115 gcttcccgaaagatgcatcccaagagacctgagctgctcggaaacatctgctgctcgaaagc 3174
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Oy 181 gtcgcgaagagcagctgagccttgcgcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 240
Db 3235 gtcgcgaagagcagctgagccttgcgcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 3294
Oy 241 aaggtgctgaagatctctgacatcttgcgcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 300
Db 3295 aaggtgctgaagatctctgacatcttgcgcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 3354
Oy 301 tctctgggggctcctccgctcctgagctgagacatcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 360
Db 3355 tctctgggggctcctccgctcctgagctgagacatcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 3414
Oy 361 agagacgagcacaagatgagagcctcgagagctgagacatcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 420
Db 3415 agagacgagcacaagatgagagcctcgagagctgagacatcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 3474
Oy 421 ctgaactgctgctcggagagaccccaagagcagacatcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 471
Db 3475 ctgaactgctgctcggagagaccccaagagcagacatcttgcgagacatcttgcgagacatcttgcgagacatcttgcgac 3525

RESULT 7
AAA37816
ID AAA37816 standard; cDNA: 4795 BP.
XX
AC AAA37816:
XX
DT 15-JAN-2001 (first entry)
XX
DE Human FLT4 receptor tyrosine kinase long form coding sequence.
XX
XX Human FLT4 receptor tyrosine kinase; antibody; extracellular domain;
XX KM lymphatic vessel detection; lymphatic tissue; lymph node tissue;
XX KM endothelial venule; diagnosis; lymphoma; long form; ss.
XX
XX Homo sapiens.
XX
OS
XX
FH Key 20..4111
FT CDS
FT /*tag= a
FT /product= FLT4 receptor tyrosine kinase long form
XX
```

Query Match	100.0%	Score 471:	DB 21:	Length 4795:
Best Local Similarity	100.0%	Pred. No. 1e-225:		
Matches 471:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0
QY 1	ctgacccatggaatactctgtgtacagcttcacagtgccgaagagatggaattcttcg	60		
Db 3044	ctgacccatggaatactctgtgtacagcttcacagtgccgaagagatggaattcttcg	3103		
QY 61	gctctccgaagaatgcatccacagagaccggtgtctcggaaattctgtctggaagc	120		
Db 3104	gctctccgaagaatgcatccacagagaccggtgtctcggaaattctgtctggaagc	3163		
QY 121	gaacgtggtgaagaatctgtgactcttgaccttcgccggagacatacaagaagccgtgac	180		
Db 3164	gaacgtggtgaagaatctgtgactcttgaccttcgccggagacatacaagaagccgtgac	3223		
QY 181	gtccgcgaagggcagtgccgcgtgcgccctgaaatgtagatgagccctgaaagcatcttcgac	240		
Db 3224	gtccgcgaagggcagtgccgcgtgcgccctgaaatgtagatgagccctgaaagcatcttcgac	3283		
QY 241	aaggtgtacacacagcagagatgagatgtagtgcctcttggtgggtgctctctcgtgagaatcttc	300		
Db 3284	aaggtgtgtacacacagcagagatgagatgtagtgcctcttggtgggtgctctctcgtgagaatcttc	3343		
QY 301	tctcttggtggacctccgcgtacacctgtgagatgtagatgtagatcttcgcaggcggtg	360		

RESULT	8
AAZ52334	
ID	AAZ52334 standard; cDNA; 4795 BP.
XX	
AC	AAZ52334:
XX	
DT	17-AUG-2000 (first entry)

PT Treating neoplastic diseases such as lymphoma, carcinomas, melanomas
PT and sarcomas, involves administering a compound capable of inhibiting
PT binding of ligand proteins to fms-like tyrosine kinase-4 receptor -
XX
XS Disclosure; Page 120-127; 148pp; English.

The patent discloses a method to treat neoplastic disease characterised by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also referred as vascular endothelial growth factor receptor-3, VEGFR-3) in endothelial cells of blood vessels adjacent to malignant neoplasm. The method involves administering a compound that inhibits binding of a ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular endothelial cells. The compound is useful for treating neoplastic diseases such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used for manufacturing medicament useful for diagnostic screening, imaging and treatment of malignancies characterised by Flt4-expressing blood cells. The present sequence is a cDNA encoding the long form of Flt4 receptor from an oligo-dT primed human erythroleukaemia cell line (HEL) cDNA library in bacteriophage lambda g11. The Flt4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in their 3' sequences and are differentially expressed in HEL and DAPI cell lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases

CC (RTKs). It is used as a target for tumour imaging and anti-tumour
CC therapy.

Sequence 4795 BP: 977 A; 1490 C; 1494 G; 834 T; 0 other:

Query Match 100.0%; Score 471; DB 21; Length 4795;
Best Local Similarity 100.0%; Pred. No. 1e-225;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgacacatggaagatctgtctgtctacacgtctccaggtgagcagagatgagttccg 60
DB |||||||
DB 3044 ctgacacatggaagatctgtctgtctacacgtctccaggtgagcagagatgagttccg 3103
OY 61 gcttcccgaaagtgcacacacagagacctgtgctcggaaacatctgtctgcgaaagc 120
DB |||||||
DB 3104 gcttcccgaaagtgcacacacagagacctgtgctcggaaacatctgtctgcgaaagc 3163
OY 121 gacgtgtgtaagaatctgtgacttggccttgcgcggagacatctacaagaacctgactac 180
DB |||||||
DB 3164 gacgtgtgtaagaatctgtgacttggccttgcgcggagacatctacaagaacctgactac 3223
OY 181 gtcgcgaaggagcagtgcccggtctgccttgaaagtgaatgagccctgaaagcactctgcac 240
DB |||||||
DB 3224 gtcgcgaaggagcagtgcccggtctgccttgaaagtgaatgagccctgaaagcactctgcac 3283
OY 241 aaggtgtacacacagcagagtgacgtgtgtctcttgggggtgctctctgcgaaagccttc 300
DB |||||||
DB 3284 aaggtgtacacacagcagagtgacgtgtgtctcttgggggtgctctctgcgaaagccttc 3343
OY 301 tctctggggggtcctccgtacacctgggggtgcagatcaatgaggaattctgcgaagcgtcg 360
DB |||||||
DB 3344 tctctggggggtcctccgtacacctgggggtgcagatcaatgaggaattctgcgaagcgtcg 3403
OY 361 agagacgagcacaagatgagggccccggagctgtgacctccgcacatagcgcgacatcg 420
DB |||||||
DB 3404 agagacgagcacaagatgagggccccggagctgtgacctccgcacatagcgcgacatcg 3463
OY 421 ctgaactgtcgttcgcgagaccccaaggcgaagctgacatctctcgagctg 471
DB |||||||
DB 3464 ctgaactgtcgttcgcgagaccccaaggcgaagctgacatctctcgagctg 3514
```

RESULT 9
AAT03104
ID AAT03104 standard; DNA: 9108 BP.
XX
AC AAT03104:
XX
DT 14-FEB-1996 (first entry)
XX
DE Plasmid pRK5.tk1-1.1 encoding Sal S-1.
XX
KW Protein tyrosine-kinase; PTK; SAL-S1; agonist; cell growth;
KM differentiation; pRK5.tk1-1.1; ss.
XX
OS Chimeric synthetic;
OS Chimeric Homo sapiens.
XX
PN M09527061-A1.
XX
PD 12-OCT-1995.
XX
PF 04-APR-1995; 95MO-US044228.
XX
PR 04-APR-1994; 94US-0222616.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP.
XX
PI Wood WI;
XX
DR MPI; 1995-366160/47.

XX Agonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation

XX Example 7; Page 102-111; 125pp; English.

XX PCR primers given in AAT03102-03 were used to amplify plasmid
CC PRK5.tk1-1.1 (AAT03104) incorporating SAL-S1 (see AAT03090) DNA.
CC The product was used to construct a fusion of the SAL-S1
CC extracellular domain and human IgG1 Fc domain, which was expressed
CC in 293 and COS7 cells and used to raise antibodies having
CC protein tyrosine-kinase agonist activity.
XX

Sequence 9108 BP: 2086 A; 2554 C; 2491 G; 1977 T; 0 other:

Query Match 100.0%; Score 471; DB 16; Length 9108;
Best Local Similarity 100.0%; Pred. No. 9.9e-226;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgacacatggaagatctgtctgtctacacgtctccaggtgagcagagatgagttccg 60
DB |||||||
DB 3987 ctgacacatggaagatctgtctgtctacacgtctccaggtgagcagagatgagttccg 4046
OY 61 gcttcccgaaagtgcacacacagagacctgtgctcggaaacatctgtctgcgaaagc 120
DB |||||||
DB 4047 gcttcccgaaagtgcacacacagagacctgtgctcggaaacatctgtctgcgaaagc 4106
OY 121 gacgtgtgtaagaatctgtgacttggccttgcgcggagacatctacaagaacctgactac 180
DB |||||||
DB 4107 gacgtgtgtaagaatctgtgacttggccttgcgcggagacatctacaagaacctgactac 4166
OY 181 gtcgcgaaggagcagtgcccggtctgccttgaaagtgaatgagccctgaaagcactctgcac 240
DB |||||||
DB 4167 gtcgcgaaggagcagtgcccggtctgccttgaaagtgaatgagccctgaaagcactctgcac 4226
OY 241 aaggtgtacacacagcagagtgacgtgtgtctcttgggggtgctctctgcgaaagccttc 300
DB |||||||
DB 4227 aaggtgtacacacagcagagtgacgtgtgtctcttgggggtgctctctgcgaaagccttc 4286
OY 301 tctctggggggtcctccgtacacctgggggtgcagatcaatgaggaattctgcgaagcgtcg 360
DB |||||||
DB 4287 tctctggggggtcctccgtacacctgggggtgcagatcaatgaggaattctgcgaagcgtcg 4346
OY 361 agagacgagcacaagatgagggccccggagctgtgacctccgcacatagcgcgacatcg 420
DB |||||||
DB 4347 agagacgagcacaagatgagggccccggagctgtgacctccgcacatagcgcgacatcg 4406
OY 421 ctgaactgtcgttcgcgagaccccaaggcgaagctgacatctctcgagctg 471
DB |||||||
DB 4407 ctgaactgtcgttcgcgagaccccaaggcgaagctgacatctctcgagctg 4457
```

RESULT 10
AAQ49753/C
ID AAQ49753 standard; DNA: 6827 BP.
XX
AC AAQ49753:
XX
DT 10-MAR-1994 (first entry)
XX
DE PTK gene SAL-S1.
XX
DE PTK: protein tyrosine kinase; catalytic domain; c-kit; FLT/FLK;
XX fetal liver kinase; megakaryocyte; amplification; primer;
KW polymerase chain reaction; PCR; ds.
XX
OS Homo sapiens.
XX
OS
FH Key Location/Qualifiers
FH CDS complement (1877..2923)

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FT      /*tag- a
FT      misc-difference 3026
FT      /*tag- b
FT      /note- "base labelled as X in the specification"
FT      misc-difference 5000
FT      /*tag- c
FT      /note- "base illegible in the specification"
FT      misc-difference 5699..5700
FT      /*tag- d
FT      /note- "bases illegible in the specification"
XX
XX      WO9315201-A.
XX      05-AUG-1993.
XX
XX      22-JAN-1993: 93WO-0500586.
XX
XX      22-JAN-1992: 92US-0826935.
XX
XX      (NMEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX
XX      Avraham H, Cowley S, Groopman J, Scadden D;
XX
XX      WPI: 1993-320330/40.
XX      P-PSDB: AAR41940.
XX
XX      New protein tyrosine kinase genes and proteins encoded by genes -
XX      are of human mega-karyocytic origin
XX
XX      Claim 2: Fig 4: 60pp: English.
XX
XX      PTK genes were identified using two sets of degenerative
XX      oligonucleotide primers: a first set which amplifies all PTK DNA
XX      segments (AA049743-44), and a second set which amplifies highly
XX      conserved sequences present in the catalytic domain of the c-kit
XX      subgroup of PTKs (AA049745-46). The PTK genes identified are described
XX      in AA049747-57 and AAR41997-02.
XX      SAL-S1 is expressed in several megakaryocytic cell lines, but not
XX      in erythroid cell lines. The SAL-S1 expression prod. exhibited
XX      significant sequence homology with known protein tyrosine kinases
XX      of the FLT/FLK family. The partial and full-length SAL-S1 gene
XX      sequences are given in AA049747 and AA049753 respectively.
XX
XX      Sequence 6827 BP; 1555 A; 1868 C; 1740 G; 1660 T; 4 other:
SQ
Query Match      89.2%; Score 420; DB 14; Length 6827;
Best Local Similarity 99.8%; Pred. No. 3.2e-200;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 ctgaccatggaagatctgtctgtacagcttcaggtgagcagaagatgagtcctg 60
DB      2749 CTGACCATGGAAGATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 2690
OY      61 gcttccgaaagtgcattcctcagacagagacctgctgctcgaacattctgtctcgaaagc 120
DB      2689 GCTTCCCGAAAGTGCATCCACAGACACTGCTGCTCGAATCTGTCTGTCTGTCTGTCTG 2630
OY      121 gaagtggtgaagatctgtgacttctgaccttgcccgagacatcacaagaacctgactac 180
DB      2629 GAGCTGCTGAAGATCTGTGACTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 2570
OY      181 gtcgcaagagcagctgcccgcctgcccctgaagtgatggccctgaaagacatcttcgac 240
DB      2569 GTCCCGCAAGGCGACATGCCCGCTGCCCTGAGTGAATGATGAGCCCTGAACCATCTTTCGAC 2510
OY      241 aaagtgtgacacacagcagaagatgacggtggttcttcttgagggtgtctctctcgaggatcttc 300
DB      2509 AAGGTGTACACCAAGCAGACGATGACGTGTGCTTGTGGGTGCTTGTCTGTCTGTCTGTCTGTCT 2450
OY      301 tctctgaggagctctcccgatcccttgagggtgacatcaatgaagatctcgacagcgagctg 360
DB      2449 TCTCTGGGGGCTCTCCCGTACCTTGGGGGTGCACATCATGAGAGTTCTTCCAGCGGCTG 2390
```

```
OY      361 agagacgycacaagatgaggcccgagagcttggccactcccgcatcagcgcacatcatg 420
DB      2389 AGAGACGCGACAAAGATGAGAGCGCCCGAGACTGACCTGCCCATACGCCGATCATCATG 2330
OY      421 ctgaactgtctgtctcgagagaccccaaggcagagaccctgcatctcggagctg 471
DB      2329 CTGAAGTGTGTCGTCGAGACCCCAAGCGAGACATTCATTCGAGCTG 2279
RESULT 11
AA03101/C
ID      AA03101 standard; DNA: 6827 BP.
XX
XX      AA03101;
AC      XX
XX      14-FEB-1996 (first entry)
DT      XX
XX      Protein tyrosine-kinase SAL-S1 gene.
DE      XX
XX      Protein tyrosine-kinase; PTK; SAL-S1; agonist; cell growth;
KW      differentialiation; ss.
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
FH      misc-difference 3026
FT      /*tag- a
FT      /note- "base n at position 3026 is not identified
FT      in the specification"
XX
XX      WO9527061-A1.
XX      12-OCT-1995.
XX
XX      04-APR-1995: 95WO-US04228.
XX
XX      04-APR-1994: 94US-0222616.
XX
XX      (GENE) GENENTECH INC.
XX
XX      Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
XX      Wood WI;
XX      WPI: 1995-366160/47.
XX      P-PSDB: AAR85938.
XX
XX      Agonist antibodies which activate specific protein tyrosine
XX      kinase(s) - also activate chimeric proteins of kinase extracellular
XX      domain and Ig constant domain, useful for studying, and therapeutic
XX      modulation of, cell growth and differentiation
XX
XX      Disclosure: Page 39-46; 125pp: English.
XX
XX      DNA probes based on protein tyrosine-kinase (PTK) sequences were used
XX      to screen cDNA libraries to identify novel PTK genes. The SAL-S1
XX      gene (see also AA03090) was isolated from several megakaryocytic cell
XX      libraries. The gene can be used to produce recombinant SAL-S1 or its
XX      fragments, to detect related genes, and to design drugs, peptides
XX      or antisense nucleotides that modulate PTK activity.
XX
XX      Sequence 6827 BP; 1558 A; 1870 C; 1738 G; 1660 T; 1 other:
SQ
Query Match      89.2%; Score 420; DB 16; Length 6827;
Best Local Similarity 99.8%; Pred. No. 3.2e-200;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 ctgaccatggaagatctgtctgtacagcttcaggtgagcagaagatgagtcctg 60
DB      2749 CTGACCATGGAAGATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 2690
OY      61 gcttccgaaagtgcattcctcagacagagacctgctgctcgaacattctgtctcgaaagc 120
```

```
Db 2689 GCTTCCCAAGTGCATTCACAGACCTGCTCTCGAACATTCCTGCGAAAGC 2630
Oy 121 gaagtgatgaagatctgtgacttggcttgcgggagacatacaagaccctgactac 180
Db 2629 GACGTGCTGAAGATCTGTGACTTTGGCTTCCCGGAGATCTACAAAGACCCGACTAC 2570
Oy 181 gtcgcaaggagcagtgcccgagctgcctcgaagtgtgagtgagccctgaagatcttcgac 240
Db 2569 CTCCGCAAGCGCAGTGCCTCCGCTCGAAGTGAATGGCCCTCGAAAGCATCTTCAC 2510
Oy 241 aaggtgtacacacagcagatgtgactgtgtccttggggtgtctctctggaagatcttc 300
Db 2509 AAGCTGTACACGACGACAGTGTGCTGTGCTTTGGGCTCTTCTGTGGAATCTTC 2450
Oy 301 tctctgggggctcccccgtacccttgagggtgcagatcaatgagagatcttcgacagcgctg 360
Db 2449 TCTCTGGGGGCTCTCCCTTACCCTTGCGGTGAGATCAATGAGACTTCTGCGACGCTG 2390
Oy 361 agagacggacaaagatgagggcccgagactgtggccactccgcacatacgccgacatg 420
Db 2389 AGACACGCGCACAGCATGAGGCGCCCGACGCTGGCCACTCCGCCATACGCCCATCATG 2330
Oy 421 ctgaactgtgtctcgagagaccgagacgagactgtgacttctctgagagctg 471
Db 2329 CTGAATCTCTGCTCGGAGACCCCAAGCGCAGACCTGCAATTCTCGAGCTG 2279

RESULT 12
AAC62210
ID AAC62210 standard; DNA: 4450 BP.
XX
AC AAC62210;
XX
DT 06-MAR-2001 (first entry)
XX
DE Nucleotide sequence of the human flt-4 gene.
XX
KW Antisense oligonucleotide; flt-4; receptor type tyrosine kinase;
KM lymphangiogenesis; prostate cancer; prostate cell; ss.
XX
OS Homo sapiens.
XX
FH key Location/Qualifiers
FT CDS 22..3918
FT /product= "flt-4"
FT /transl_except= (pos: 55..57, aa: Trp)
FT /transl_except= (pos: 58..60, aa: Leu)
FT /transl_except= (pos: 61..63, aa: Cys)
FT /transl_except= (pos: 64..66, aa: Leu)
FT /transl_except= (pos: 67..69, aa: Gly)
FT /transl_except= (pos: 70..72, aa: Leu)
FT /transl_except= (pos: 73..75, aa: Leu)
FT /transl_except= (pos: 76..78, aa: Asp)
FT /transl_except= (pos: 79..81, aa: Gly)
FT /transl_except= (pos: 82..84, aa: Leu)
FT /transl_except= (pos: 85..87, aa: Val)
FT /transl_except= (pos: 88..90, aa: Ser)
FT /transl_except= (pos: 91..93, aa: Asp)
FT /transl_except= (pos: 94..96, aa: Tyr)
FT /transl_except= (pos: 97..99, aa: Ser)
FT /transl_except= (pos: 1639..1641, aa: Lys)
FT /transl_except= (pos: 2236..2238, aa: Arg)
FT /transl_except= (pos: 3508..3510, aa: Ser)
FT /transl_except= (pos: 3598..3600, aa: Ser)
FT /transl_except= (pos: 3796..3798, aa: Phe)
XX
PN W0200062063-A1.
XX
PD 19-OCT-2000.
XX
PF 13-APR-1999; 99MO-US08079.
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```
XX
PR 13-APR-1999; 99MO-US08079.
XX
PA (MMBL-) NORTHWEST BIOTHEAPUTICS INC.
XX
PI Su SL:
DR WPI: 2000-687067/67.
DR P-PSDB: AAB30542.
XX
PT Detecting metastatic potential, diagnosing metastatic prostate cancer
PT or determining the prognosis of a subject with prostate cancer
PT comprises detecting the expression of flt-4 in a prostate cell
XX
PS Claim 6; Fig 1A-F; 78pp; English.
XX
CC The present sequence encodes human flt-4. Flt-4 is a receptor type
CC tyrosine kinase with 7 Ig-like domains similar to other VEGF receptors.
CC Flt-4 may play a role in lymphangiogenesis. Antisense oligonucleotides
CC can be used for detecting the metastatic potential, diagnosing
CC metastatic prostate cancer or determining the prognosis of a subject
CC with prostate cancer. The method comprises identifying the prostate
CC cell in a body fluid sample and detecting the expression of flt-4 in
CC the cell. Expression of flt-4 in a prostate cell indicates that the
CC cell is a cancerous prostate cell that has metastatic potential or is
CC a secondary tumour metastasis of a primary prostate tumour.
XX
SQ Sequence 4450 BP; 968 A; 1352 C; 1349 G; 781 T; 0 other:

Query Match 64.8%; Score 305; DB 21; Length 4450;
Best Local Similarity 99.7%; Pred. No. 1..1e-142;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ctgaccatggaagatctgtctgtctacagcttccagtgccagagagatgttctc 60
Db 3046 ctgaccatggaagatctgtctgtctacagcttccagtgccagagagatgttctc 3105
Oy 61 gcttccggaagatgcatccacagagacgtgctgtctggaacatctcgtctcgaaagc 120
Db 3106 gcttccggaagatgcatccacagagacgtgctgtctggaacatctcgtctcgaaagc 3165
Oy 121 gaagtgatgaagatctgtgacttggccttgcgggacatctacaagacctgactac 180
Db 3166 gaagtgatgaagatctgtgacttggccttgcgggacatctacaagacctgactac 3225
Oy 181 gtcgcaaggagcagtgcccgagctgcctcgaagtgtgagtgccctgaaacatcttcgac 240
Db 3226 gtcgcaaggagcagtgcccgagctgcctcgaagtgtgagtgccctgaaacatcttcgac 3285
Oy 241 aaggtgtacacacagcagatgtgactgtgtccttggggtgtctctctggagatcttc 300
Db 3286 aaggtgtacacacagcagatgtgactgtgtccttggggtgtctctctggagatcttc 3345
Oy 301 tctctgggggctcccccgtacccttgagggtgcagatcaatgagagatcttcgacg 356
Db 3346 tctctgggggctcccccgtacccttgagggtgcagatcaatgagagatcttcgacg 3401

RESULT 13
AA049747
ID AA049747 standard; DNA: 160 BP.
XX
AC AA049747;
XX
DT 10-MAR-1994 (first entry)
XX
DE PTK gene SAL-S1 partial sequence.
XX
KW PTK; protein tyrosine kinase; catalytic domain; c-Kit; FLT/FLK;
KM fetal liver kinase; megakaryocyte; amplification; primer;
KM polymerase chain reaction; PCR; ss.
```

OS	Homo sapiens.	Location/Qualifiers
XX	Key	2..160
FH	CDS	/*tag- a
FT		1..21
FT	misc_feature	/*tag- b
FT		/note- "PTK1/3 primers"
FT	misc_feature	136..160
FT		/*tag- C
FT		/note- "PTKRW primer"
XX		
PN	W09315201-A.	
XX		
PD	05-AUG-1993.	
XX		
PF	22-JAN-1993:	93WO-US00586.
XX		
PR	22-JAN-1992:	92US-0826935.
XX		
PA	(NEW-) NEW ENGLAND DEACONESS HOSPITAL.	
XX		
PI	Avraham H, Cowley S, Groopman J, Scadden D:	
XX		
DR	WPI: 1993-320330/40.	
XX	P-PSDB: AAR41894.	
PT	New protein tyrosine kinase genes and proteins encoded by genes -	
PT	are of human mega-karyocytic origin	
XX		
PS	Claim 2: Fig 1: 60pp: English.	
XX		
CC	PTK genes were identified using two sets of degenerative	
CC	oligonucleotide primers: a first set which amplifies all PTK DNA	
CC	segments (AAQ49743-44), and a second set which amplifies highly	
CC	conserved sequences present in the catalytic domain of the c-kit	
CC	subgroup of PTKs (AAQ49745-46). The PTK genes identified are described	
CC	in AAQ49747-57 and AAR41897-02.	
CC	SAL-S1 is expressed in several megakaryocytic cell lines, but not	
CC	in erythroid cell lines. The SAL-S1 expression prod. exhibited	
CC	significant sequence homology with known protein tyrosine kinases	
CC	of the FLT/FLK family. The partial and full-length SAL-S1 gene	
CC	sequences are given in AAQ49747 and AAQ49753 respectively.	
XX		
SO	Sequence 160 BP: 35 A: 44 C: 47 G: 34 T: 0 other:	
Query Match 16.1%; Score 76; DB 14: Length 160;		
Best Local Similarity 100.0%; Pred. No. 4,2e-28;		
Matches	76: Conservative	0: Mismatches
	0: Indels	0: Gaps
OY	98 ggaacattctgtctgcgaaagcgacgtgltgaagatctgtgacttgccctgcggg	157
DB	30 ggaacattctgtctgcgaaagcgacgtgltgaagatctgtgacttgccctgcggg	89
OY	158 acatctacaagaacc	173
DB	90 acatctacaagaacc	105
RESULT 14		
AA703089		
ID	AA703089 standard: DNA: 160 BP.	
XX		
AC	AA703089:	
XX		
DT	14-FEB-1996 (first entry)	
XX		
DE	Protein tyrosine-kinase SAL-S1 DNA fragment.	
XX		
KW	Protein tyrosine-kinase; PTK; SAL-S1; agonist; cell growth;	
KW	differentiation; ss.	
XX		

OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 20..160
FT	/tag= a
PN	
XX	
PD	W09527061-A1.
XX	
PD	12-OCT-1995.
XX	
XX	
PF	04-APR-1995; 95WO-US04228.
XX	
PR	04-APR-1994; 94US-0222616.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP,
PI	Wood WI;
XX	
DR	WPI: 1995-366160/47.
XX	P-PSDB: AAR85922.
PT	Agonist antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic modulation of, cell growth and differentiation
XX	
PS	Disclosure; Page 35; 125pp; English.
CC	DNA probes based on protein tyrosine-kinase (PTK) sequences were used to screen cDNA libraries to identify novel PTK genes. A SAL-SI gene fragment (AAT0308) was isolated from several megakaryocytic cell lines (see AAT03090 for the full-length sequence).
CC	
CC	
SQ	Sequence 160 BP; 35 A; 44 C; 47 G; 34 T; 0 other;
Query Match	16.1%; Score 76; DB 16; Length 160;
Best Local Similarity	100.0%; Pred. No. 4.2e-28;
Matches 76; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	98 ggaacatctgctgcggaagcgacgctgtgaagatcgtgacttggccctgccggg 157 Db 30 ggaacatctgctgcggaagcgacgctgtgaagatcgtgacttggccctgccggg 89 OY 158 acatctacaagaacc 173 Db 90 acatctacaagaacc 105
RESULT 15	
ID	ABA96501 standard; CDNA: 1047 BP.
XX	
AC	ABA96501;
XX	
DT	12-MAR-2002 (first entry)
XX	
DE	Human extracellular signal-regulated protein kinase-2 (erk-2) cDNA.
XX	
KX	Human; extracellular signal-regulated protein kinase-2; erk-2;
KM	recombinant production; Escherichia coli; HeLa cell; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1047
FT	/tag= a
FT	/product= "Human erk-2"
XX	
PN	KR98022142-A.
XX	
DD	25-JUN-1998.


```

XX PF 20-SEP-1996: 96KR-0041219.
XX PR 20-SEP-1996: 96KR-0041219.
XX PA (GLDS ) LG CHEM LTD.
XX PI Kim CH, Cho JM, Chung HH, Lee JH;
XX DR WPI: 1999-300710/25.
XX P-PSDB: AAM52700.
XX PS Process for preparing extracellular signal-regulated protein kinase-2
XX PT from E. coli .
XX PS Example 2; Flg 1a-c; 9pp: Korean.
XX CC The invention relates to a process for the recombinant production
XX CC of human extracellular signal-regulated protein kinase-2 (erk-2) in
XX CC Escherichia coli. The present sequence represents cDNA encoding human
XX CC erk-2 initially isolated from HeLa cells.
XX SO Sequence 1047 BP; 303 A; 255 C; 225 G; 264 T; 0 other;

```

```

Query Match 5.5%; Score 26; DB 20; Length 1047;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 130 aagatctgacttgagctgcccgcg 155
    |||||||
Db 454 aagatctgacttgagctgcccgcg 479

```

RESULT 16

```

ID AAO20261
XX AAO20261 standard; DNA: 1467 BP.
AC AAO20261:
XX
DT 31-MAR-1992 (first entry)
XX
DE ERK2.
XX
KW Microtubule-associated protein 2; central nervous system;
KW extracellular signal-regulated kinase; ERK; CNS; MAP2; ss
XX
OS Rat rattus.
XX
FH Key Location/Qualifiers
FT CDS 1..1248
FT FT /*tag= a
FT FT /label= ERK2
FT FT 172..174
FT FT /*tag= b
FT FT /label= initiation_codon
FT FT 202..204
FT FT /*tag= c
FT FT /label= initiation_codon
FT FT 1246..1248
FT FT /*tag= d
XX
PN MO9119008-A.
XX
PD 12-DEC-1991.
XX
PF 03-JUN-1991: 91MO-US03894.
XX
PR 16-MAY-1991: 91US-0701544.
PR 01-JUN-1990: 90US-0532004.
XX
PA (REGC-) REGENERON PHARM INC.
PA (TEXA ) UNIV OF TEXAS SYSTEM.
XX

```

```

XX PI Boulton TG, Cobb MH, Yancopoulos GD, Nye S, Panayotatos N;
XX DR WPI: 1992-007489/01.
XX P-PSDB: AAR20104.
XX PT DNA encoding MAP2 kinase enzyme and vectors or host cells - are
XX PT for assaying cellular factor (e.g. NGF), and drug screening
XX PS Disclosure; Fig 3A; 9pp; English.
XX
XX CC The identification of a family of protein serine/threonine kinases
XX CC which phosphorylate microtubule-associated protein 2 (MAP2) is
XX CC based, in part, on the cloning and characterisation of MAP2 kinases
XX CC designated extracellular signal-regulated kinase 1, 2 and 3 (ERK1,
XX CC ERK2 and ERK3) which are expressed in the central nervous system,
XX CC and on the identification of another ERK family member, ERK4, with
XX CC anlisera.
XX CC ERK1-3 are represented in AAO20260-62.
XX SO Sequence 1467 BP; 365 A; 382 C; 355 G; 365 T; 0 other;

```

```

Query Match 5.5%; Score 26; DB 13; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 130 aagatctgacttgagctgcccgcg 155
    |||||||
Db 655 aagatctgacttgagctgcccgcg 680

```

RESULT 17

```

ID AAV71031
XX AAV71031 standard; cDNA: 1815 BP.
AC AAV71031:
XX
DT 08-FEB-1999 (first entry)
XX
DE Erk2-green fluorescent protein fusion product.
XX
KW Rat; Erk2 gene; fusion protein; green fluorescent protein; GFP;
KW Intracellular signalling; Chimera; ss.
XX
OS Chimeric - Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..1815
FT FT /*tag= a
XX
PN MO9845704-A2.
XX
PD 15-OCT-1998.
XX
PF 07-APR-1998: 98MO-DK00145.
XX
PR 07-APR-1997: 97DK-0000392.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Kasper A, Petersen Bjorn S, Scudder K, Thastrup O;
XX PI Tullin S;
XX DR WPI: 1998-594491/50.
XX P-PSDB: AAM85016.
XX
XX PT Determining effect on signalling pathways in live cells from
XX PT redistribution of luminophores - specifically fusions of green
XX PT fluorescent protein with a signalling component, and new apparatus,
XX PT particularly for identifying toxins and potential therapeutic agents
XX

```

PS Claim 63: Pages 122-125; 326pp: English.

XX The present sequence encodes a rat Erk2-green fluorescent

CC protein fusion product. The fusion protein is used in an assay

CC that exemplifies the invention. The specification describes how

CC quantitative information about the influence of a molecule on a cellular

CC response is obtained by recording the variation, caused by the molecule,

CC on mechanically intact living cells, in the spatially distributed light

CC emitted from a lumiphore present in the cells. The variation in light

CC emission is processed to provide information that correlates spatial

CC distribution to the degree of the molecule. The method is used to

CC identify agents that (in)directly affect intracellular signalling,

CC especially to screen for potential therapeutic agents or toxins, and

CC to identify new drug targets.

XX

SQ Sequence 1815 BP; 480 A; 506 C; 451 G; 378 T; 0 other;

Query Match 5.5%; Score 26; DB 19; Length 1815;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgagcttgcccg 155
 Db 484 aagatctgacttgagcttgcccg 509

RESULT 18
 AAV71023
 ID AAV71023 standard; cDNA; 1818 BP.

XX AAV71023;

XX 08-FEB-1999 (first entry)

DE Green fluorescent protein-Erk2 fusion product.

KW Rat; Erk2 gene; fusion protein; green fluorescent protein; GFP;
 intracellular signalling; chimera; ss.

XX Chimeric - Rattus sp.

OS Chimeric - Rattus sp.

XX Key Location/Qualifiers
 FT CDS 1..1818
 FT /*tag= a

XX MO9845704-A2.

XX 15-OCT-1998.

XX 07-APR-1998; 98WO-DK00145.

XX 07-APR-1997; 97DK-0000392.

PA (NOVO) NOVO-NORDISK AS.

XX Kasper A. Petersen Bjorn S. Scudder K. Thastrup O;
 PI Tullin S;

XX WPI: 1998-594491/50.
 DR P-PSDB: AAW85007.

XX Determining effect on signalling pathways in live cells from
 PT redistribution of lumiphores - specifically fusions of green
 PT fluorescent protein with a signalling component, and new apparatus,
 PT particularly for identifying toxins and potential therapeutic agents

XX Claim 63: Pages 71-74; 326pp: English.

XX The present sequence encodes a green fluorescent protein (GFP)-rat
 CC Erk2 fusion product. The fusion protein is used in an assay
 CC that exemplifies the invention. The specification describes how

CC quantitative information about the influence of a molecule on a cellular

CC response is obtained by recording the variation, caused by the molecule,

CC on mechanically intact living cells, in the spatially distributed light

CC emitted from a lumiphore present in the cells. The variation in light

CC emission is processed to provide information that correlates spatial

CC distribution to the degree of the molecule. The method is used to

CC identify agents that (in)directly affect intracellular signalling,

CC especially to screen for potential therapeutic agents or toxins, and

CC to identify new drug targets.

XX

SQ Sequence 1818 BP; 482 A; 505 C; 451 G; 380 T; 0 other;

Query Match 5.5%; Score 26; DB 19; Length 1818;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgagcttgcccg 155
 Db 1225 aagatctgacttgagcttgcccg 1250

RESULT 19
 AAT13330
 ID AAT13330 standard; cDNA to mRNA; 4696 BP.

XX AAT13330;

XX 09-JUL-1996 (first entry)

DE Rat type I insulin-like growth factor receptor cDNA.

XX Insulin-like growth factor I receptor; IGF 1R; somatomedin C;
 KW smooth muscle; cell growth; cell proliferation; healing;
 KW nerve regeneration; angiogenesis; antisense RNA; atherosclerosis;
 KW tumour; restenosis; ds.

XX Rattus norvegicus strain Sprague-Dawley.

OS Rattus norvegicus strain Sprague-Dawley.

XX Key Location/Qualifiers
 FT CDS 46..4158
 FT /*tag= a
 FT sig-peptide 46..135
 FT /*tag= b
 FT mat-peptide 136..4155
 FT /*tag= C

XX MO9610401-A1.

XX 11-APR-1996.

XX 27-SEP-1995; 95MO-US12563.

XX 04-OCT-1994; 94US-0317898.

PA (UYEM-) UNIV EMORY.

XX Delafontaine P;

XX WPI: 1996-209180/21.
 DR P-PSDB: AAR91430.

XX Insulin-like growth factor I receptor anti-sense RNA and
 PT ATG-directed sense oligo:nucleotide(s) - useful for regulating
 PT growth factor receptor gene expression for e.g. wound healing and
 PT atherosclerosis

XX Claim 18: Page 36-42; 73pp: English.

XX A cDNA clone (AAT13330) codes for rat insulin-like growth factor
 CC I receptor (IGF 1R) (AAR91430). It was obtd. from a rat brain cell
 CC cDNA library by PCR amplification (see AAT13332-33). IGF 1R plays
 CC a crucial role in vascular smooth muscle cell (VSMC) proliferative

CC responses. The gene provides the basis for antisense methods
CC (see AAT13325 and AAT13328) to down-regulate IGF 1R gene expression and
CC retard VSMC growth, e.g. to treat restenosis and atherosclerosis,
CC and also for ATP-directed sense oligonucleotide (see AAT13326)
CC methods to stimulate VSMC growth e.g. for healing wounds and burns.
XX
SO Sequence 4696 BP; 1151 A; 1268 C; 1241 G; 1036 T; 0 other;

Query Match 5.5%; Score 26; DB 17; Length 4696;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 77 tccacagagacctgctgcgcggaac 102
|||||
Db 3443 tccacagagacctgctgcgcggaac 3468

RESULT 20

AAO30721
ID AAO30721 standard; DNA; 159 BP.

XX AAO30721;

XX 22-MAR-1993 (first entry)

XX Tyrosine kinase clone RTK-6.

XX Tyrosine kinase receptor; ss.

XX Rattus rattus.

XX Key Location/Qualifiers
FT CDS 1..159
/*tag= a

XX MO9218149-A.

XX 29-OCT-1992.

XX 23-APR-1992; 92MO-US03376.

XX 23-APR-1991; 91US-0690199.

XX 26-JUL-1991; 91US-0736559.

XX (REG-) REGENERON PHARM INC.

XX Aldrich TH, DiStefano P, Furth ME, Glass D, Masiakowski;
PI P, Maison-Pierre PC, Squinto SP, Stilt T, Yancopoulos GD;

XX WPI: 1992-381778/46.

XX P-PSDB; AAR28603.

XX Assaying neurotrophin activity using cells that express trkB - also
PT for identifying agonists and antagonists, and new recombinant cells
PT and nucleic acid producing trkB, for diagnosis and treatment of
PT neurological disease

XX Disclosure: Fig 12C; 156pp; English.

XX The sequence is that of tyrosine kinase clone RTK-6, isolated
CC from adult or embryonic (E13) rat brain cDNA, which shows
CC homology to the known tyrosine kinase molecules h kit, h csf1r,
CC hpdcd1phar and mcsf1r. It may be of use in the treatment of
CC neurodegenerative disease/neurotrauma including motor neuron
CC disorders such as amyotrophic lateral sclerosis, Merd19-Hoffman
CC disease, chronic proximal spinal muscular atrophy and Guillain-Barre
CC syndrome. It may also be of use in the treatment of neurological
CC disorders associated with diabetes, Parkinson's disease,
CC Alzheimer's disease and Huntington's chorea.

CC Sequence 159 BP; 38 A; 36 C; 50 G; 35 T; 0 other;

Query Match 4.9%; Score 23; DB 13; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtgtgaagatctgacttg 146
|||||
Db 22 gtgtgaagatctgacttg 44

RESULT 21

AAV70215
ID AAV70215 standard; DNA; 159 BP.

XX AAV70215;

XX 11-FEB-1999 (first entry)

XX Rat orphan tyrosine kinase receptor peptide clone RTK-6 encoding DNA.

XX Receptor tyrosine kinase: Ror-1; Ror-2; Ehk-1; Ehk-2; detection;

XX neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
XX binding protein; BDNF; NT-3; diagnosis; ss.

XX Synthetic.

XX Rattus sp.

XX US5843749-A.

XX 01-DEC-1998.

XX 06-JUN-1995; 95US-0469537.

XX 17-MAR-1995; 95US-0406247.

XX 26-JUL-1991; 91US-0736559.

XX 28-OCT-1993; 93US-0144992.

XX 06-JUN-1995; 95US-0469537.

XX (REG-) REGENERON PHARM INC.

XX Maisonnier PC, Masiakowski P, Yancopoulos GD;

XX WPI: 1999-044584/04.

XX P-PSDB; AAW83155.

XX DNA encoding receptor tyrosine kinase proteins - and corresponding
PT proteins

XX Example: Fig 12C; 194pp; English.

XX The present invention describes nucleic acid molecules for ror-1,
CC ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins:
CC Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor
CC tyrosine kinases. The present sequence encodes a rat orphan tyrosine
CC kinase receptors peptide clone from the present invention.

XX Sequence 159 BP; 38 A; 36 C; 51 G; 34 T; 0 other;

Query Match 4.9%; Score 23; DB 20; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtgtgaagatctgacttg 146
|||||
Db 22 gtgtgaagatctgacttg 44

RESULT 22

AAO54036
ID AAO54036 standard; CDNA; 1894 BP.

XX


```

KM proliferation; stromal cell; ds.
XX
OS Mus musculus.
XX
PH Key location/Qualifiers
FT CDS 31..3009 /*tag= a
FT sig_peptide 31..111
FT mat_peptide 112..3006 /*tag= b
FT /*tag= c
XX
PN US5270458-A.
XX
PD 14-DEC-1993.
XX
PF 02-APR-1991; 91US-0679666.
XX
PR 02-APR-1991; 91US-0679666.
PR 28-JUN-1991; 91US-0728913.
PR 15-NOV-1991; 91US-0793065.
PR 24-DEC-1991; 91US-0813593.
PR 26-JUN-1992; 92US-0906397.
PR 12-NOV-1992; 92US-0975049.
PR 19-NOV-1992; 92US-0977451.
XX
PA (UYPR-) UNIV PRINCETON.
XX
PI Lemischka IR;
XX
DR WPI: 1993-405021/50.
XX
DR P-PSDB: AAR44994.
XX
PS isolated nucleic acid molecules of hematopoietic stem cell
PT receptor flk-2 - encoding mammalian receptor protein tyrosine
XX kinases expressed in primitive haematopoietic cells
XX
PS Claim 2: Fig 1a: 60pp: English.
XX
CC Nucleic acid sequences coding for murine flk-2 and specified
CC subfragments of it are claimed. The flk-2 polypeptide is a protein
CC tyrosine kinase expressed only in primitive haematopoietic cells.
CC The CDNA can be used to recombinantly produce flk-2 for stimulating
CC self-renewal of totipotent stem cells and development of all
CC haematopoietic cells.
XX
SO Sequence 3453 BP; 947 A; 821 C; 876 G; 809 T; 0 other;
XX

```

Query Match 4.9%; Score 23; DB 14; Length 3453;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgtgacttgg 146
 |||
 DB 2509 gtggtgaagatctgtgacttgg 2531

```

RESULT 25
AAO35249
ID AAO35249 standard; cDNA: 3453 BP.
XX
AC AAO35249;
XX
DT 25-JUN-1993 (first entry)
XX
DE Murine flk-2 coding sequence.
XX
KM Murine; receptor; protein; tyrosine kinase; PTK; primitive; mammalian;
KM hematopoietic cell; PBC; mature; mHC; fetal; liver kinase 2; flk-2;
KM liver; spleen; thymus; adult; brain; marrow; thymocyte; subset;
KM multipotential; T-lymphoid; lineage; ss.
XX

```

```

OS Mus musculus.
XX
PH Key location/Qualifiers
FT CDS 31..3009 /*tag= a
FT misc_RNA 31..111
FT /*tag= b
FT /*note= "hydrophobic leader"
XX
PN W09300349-A.
XX
PD 07-JAN-1993.
XX
PF 26-JUN-1992; 92WO-US05401.
XX
PR 28-JUN-1991; 91US-0728913.
PR 15-NOV-1991; 91US-0793065.
PR 24-DEC-1991; 91US-0813593.
PR 02-APR-1992; 92WO-US02750.
XX
PA (UYPR-) UNIV PRINCETON.
XX
PI Lemischka IR;
XX
DR WPI: 1993-036323/04.
XX
DR P-PSDB: AAR31375.
XX
PS Nucleic acid encoding receptor protein tyrosine kinase - allows
PT development of ligands to stimulate proliferation and/or
PT differentiation of mammalian haematopoietic stem cells
XX
PS Claim 5; Fig 1a: 78pp: English.
XX
CC This sequence encodes a murine receptor protein tyrosine kinase which
CC belongs to a new functional class of protein tyrosine kinases (PTKs).
CC PTKs in this class are expressed in primitive mammalian hematopoietic
CC (PBC) cells but not in mature hematopoietic cells (mHC). The protein
CC encoded by this sequence is an example of a receptor PTK and is called
CC fetal liver kinase 2 (flk-2). flk-2 is expressed in fetal liver,
CC spleen and thymus, and adult brain and marrow. Expression of flk-2
CC mRNA occurs in the most primitive thymocyte subset, which is believed
CC to be uncommitted. Therefore, thymocytes expressing flk-2 may be
CC multipotential. flk-2 is the first receptor tyrosine kinase known to
CC be expressed in the T-lymphoid lineage.
XX
SO Sequence 3453 BP; 947 A; 821 C; 876 G; 809 T; 0 other;
XX

```

Query Match 4.9%; Score 23; DB 14; Length 3453;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgtgacttgg 146
 |||
 DB 2509 gtggtgaagatctgtgacttgg 2531

```

RESULT 26
AAO40914
ID AAO40914 standard; cDNA: 3453 BP.
XX
AC AAO40914;
XX
DT 19-OCT-1993 (first entry)
XX
DE Murine flk-2 cDNA.
XX
KM Murine; receptor; protein; tyrosine kinase; PTK; flk-2; primitive;
KM hematopoietic cell; mature; family; conserved; region;
KM catalytic domain; c-kit; fetal liver kinase; flk; fetal; spleen;
KM thymus; adult; brain; bone marrow; multipotential; CFU-blast colony;
KM hierarchy; transduction; T-lymphoid; lineage; ss.
XX

```

```

OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 31..3009
FT sig_peptide /tag= a
FT /product= Flk2 receptor protein-tyrosine-kinase
FT /tag= b
FT /note= "Hydrophobic leader sequence"
FT mat_peptide 112..3006
FT /tag= c
XX
XX WO9310136-A.
XX
XX 27-MAY-1993.
XX
XX
XX 16-NOV-1992: 92WO-US09893.
XX
XX
XX 15-NOV-1991: 91US-0793065.
XX
XX (UYP- ) UNIV PRINCETON.
XX
XX
XX Lemischka IR:
XX
XX WPI: 1993-182479/22.
XX
XX P-PSDB: AAR37502.
XX
XX
XX TOLLIPOTENT haematopoietic stem cell receptors, their ligands and
XX DNA sequences - for treating anaemia(s) and bone marrow damage
XX due to e.g. cancer chemotherapy or radiotherapy
XX
XX Claim 6: Fig 1a: 127pp: English.
XX
XX This sequence encodes the murine receptor protein tyrosine kinase
XX (PTK), flk-2. This nucleic acid is expressed in primitive hema-
XX topoietic cells and not in mature hematopoietic cells. Members of
XX this family of PTK's can be recognised by the conserved amino acid
XX regions in the catalytic domain. This family of PTK's also contains
XX c-Kit. These new receptors are termed fetal liver kinases (flk's)
XX after the tissue in which they were discovered. flk-2 is also
XX expressed in fetal spleen, fetal thymus, adult brain and adult
XX bone marrow. flk-2 is expressed in individual multipotential CFU-
XX blast colonies capable of generating numerous multilineage colonies
XX upon replating. It is likely therefore, that flk-2 is expressed in
XX the entire primitive portion of the hematopoietic hierarchy. This is
XX consistent with flk-2 being important in transducing putative self-
XX renewal signals from the environment. flk-2 is the first receptor
XX PTK known to be expressed in the T-lymphoid lineage.
XX
XX Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:
XX
XX
XX Query Match 4.9%; Score 23; DB 14; Length 3453;
XX Best Local Similarity 100.0%; Pred. No. 0.13;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 124 gtggtgaagatctgtgacttgg 146
XX |||||||||||||||||||
XX DB 2509 gtggtgaagatctgtgacttgg 2531
XX
XX
XX RESULT 27
XX ID AA081012 standard; cDNA: 3453 BP.
XX
XX AC AA081012;
XX
XX
XX 16-AUG-1995 (first entry)
XX
XX
XX Flk2 receptor protein-tyrosine-kinase cDNA.
XX
XX Mouse flk2; receptor protein-tyrosine-kinase; primitive
XX hematopoietic cell; fetal liver kinase; ds.
XX
XX

```

```

OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 31..3009
FT sig_peptide /tag= a
FT /product= Flk2 receptor protein-tyrosine-kinase
FT /tag= b
FT mat_peptide 112..3006
FT /tag= c
XX
XX WO9500554-A.
XX
XX
XX 05-JAN-1995.
XX
XX
XX 17-JUN-1994: 94WO-US06944.
XX
XX
XX 18-JUN-1993: 93US-0080244.
XX
XX 21-JUN-1993: 93US-0081508.
XX
XX 23-NOV-1993: 93US-0157490.
XX
XX (UYP- ) UNIV PRINCETON.
XX
XX
XX Lemischka IR:
XX
XX WPI: 1995-052014/07.
XX
XX P-PSDB: AAR67815.
XX
XX
XX Ligand for receptor protein tyrosine kinase - useful for the
XX stimulation of primitive haematopoietic stem cells causing
XX proliferation and/or differentiation
XX
XX Disclosure: Fig 1a: 131pp: English.
XX
XX The sequence corresponds to a cDNA encoding a mouse flk2 (fetal
XX liver kinase) receptor protein-tyrosine-kinase. Flk2 is expressed
XX in primitive hematopoietic cells but not in mature hematopoietic
XX cells. The gene product is useful in isolation of receptor ligands,
XX which have applications in diagnosis of bone marrow disorders and in
XX stimulating proliferation and/or differentiation of primitive
XX hematopoietic stem cells.
XX
XX Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:
XX
XX
XX Query Match 4.9%; Score 23; DB 16; Length 3453;
XX Best Local Similarity 100.0%; Pred. No. 0.13;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 124 gtggtgaagatctgtgacttgg 146
XX |||||||||||||||||||
XX DB 2509 gtggtgaagatctgtgacttgg 2531
XX
XX
XX RESULT 28
XX ID AA079068 standard; cDNA: 3453 BP.
XX
XX AC AA079068;
XX
XX
XX 04-JUL-1995 (first entry)
XX
XX
XX Mouse flk-2 cDNA.
XX
XX
XX Fetal liver kinase-2; flk-2; protein tyrosine-kinase receptor;
XX hematopoiesis; stem cell; ds.
XX
XX
XX Mus sp.
XX
XX
XX Key Location/Qualifiers
XX FH CDS 58..3039
XX FT sig_peptide /tag= a
XX 58..138
XX

```

```

FT      mat_peptide      /*tag= b
FT      139..3036
FT      /*tag= c
PN      US5367057-A.
XX      PD      22-NOV-1994.
XX      PF      02-APR-1991; 91US-0679666.
XX      PR      02-APR-1991; 91US-0679666.
XX      PR      28-JUN-1991; 91US-0728913.
XX      PR      15-NOV-1991; 91US-0793065.
XX      PR      24-DEC-1991; 91US-0813593.
XX      PR      26-JUN-1992; 92US-0906397.
XX      PR      12-NOV-1992; 92US-0975049.
XX      PR      19-NOV-1992; 92US-0977451.
XX      PR      30-APR-1993; 93US-0055269.
XX      PA      (UYPR-) UNIV PRINCETON.
XX      PI      Lemischka IR:
XX      DR      WPI: 1995-005894/01.
XX      DR      P-PSDB; AAR67535.
XX      PT      Murine flk-2 receptor protein tyrosine kinase - used to stimulate
XX      PT      proliferation and/or stimulation of primitive mammalian
XX      PT      haematopoietic stem cells in vitro or in vivo.
XX      PS      Disclosure; Fig. 1A-1F; 69pp; English.
XX      CC      CDNAs encoding receptor protein tyrosine-kinases, mouse foetal liver
XX      CC      kinase-2 (flk-2), human flk-2 and mouse flk-1 are given in AAG79068-70,
XX      CC      respectively, and the deduced amino acid sequences in AAR67535-37,
XX      CC      respectively.
SO      Sequence 3453 BP; 946 A; 822 C; 876 G; 809 T; 0 other:

Query Match      4.9%; Score 23; DB 16; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      124 gtggtaagatctgtgacttgg 146
DB      2509 gtggtaagatctgtgacttgg 2531

RESULT 29
AAT38733
ID      AAT38733 standard; cDNA: 3453 BP.
XX      AC      AAT38733;
XX      DT      11-DEC-1996 (first entry)
XX      DE      Human foetal liver kinase 2 cDNA.
XX      KW      Human; foetal liver kinase 2; flk-2; protein tyrosine kinase;
XX      KW      monoclonal; antibody; extracellular domain; receptor assay;
XX      KW      haematopoietic stem cell; ligand; stimulation; proliferation;
XX      KW      differentiation; treatment; anaemia; bone marrow damage;
XX      KW      cancer chemotherapy; radiation; ds.
XX      OS      Homo sapiens.
XX      FH      Key      Location/Qualifiers
XX      FT      CDS      31..3009
XX      FT      sig_peptide /*tag= a
XX      FT      31..111 /*tag= b
XX      FT      mat_peptide 112..3006
XX      FT

```

```

FT      US5448065-A.      /*tag= c
XX      PD      20-AUG-1996.
XX      PF      02-APR-1991; 91US-0679666.
XX      PR      19-NOV-1992; 92US-0977451.
XX      PR      02-APR-1991; 91US-0679666.
XX      PR      28-JUN-1991; 91US-0728913.
XX      PR      15-NOV-1991; 91US-0793065.
XX      PR      24-DEC-1991; 91US-0813593.
XX      PR      26-JUN-1992; 92US-0906397.
XX      PR      12-NOV-1992; 92US-0975049.
XX      PR      30-APR-1993; 93US-0055269.
XX      PR      31-OCT-1994; 94US-0252517.
XX      PA      (UYPR-) UNIV PRINCETON.
XX      PI      Lemischka IR:
XX      DR      WPI: 1996-392678/39.
XX      DR      P-PSDB; AAR97418.
XX      PT      Anti-foetal liver kinase 2 (flk-2) antibodies - useful in assays,
XX      PT      for isolating haematopoietic stem cells expressing receptor and for
XX      PT      obtaining ligands
XX      PS      Disclosure; Columns 27-34; 50pp; English.
XX      CC      The present sequence encodes human foetal liver kinase 2 (flk-2), a
XX      CC      protein tyrosine kinase. Isolated antibodies, pref. monoclonal,
XX      CC      raised against the extracellular portion of flk-2 can be used to
XX      CC      assay for flk receptors on the surface of primitive haematopoietic
XX      CC      stem cells, and to isolate positive cells. The antibodies can also
XX      CC      be used as, or to obtain ligands, which stimulate the proliferation
XX      CC      and/or differentiation of stem cells. The ligands can be used, e.g.
XX      CC      for treating anaemia, or bone marrow damage resulting from cancer
XX      CC      chemotherapy, or radiation.
SO      Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:

Query Match      4.9%; Score 23; DB 17; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      124 gtggtaagatctgtgacttgg 146
DB      2509 gtggtaagatctgtgacttgg 2531

RESULT 30
AAT72118
ID      AAT72118 standard; cDNA: 3453 BP.
XX      AC      AAT72118;
XX      DT      19-AUG-1997 (first entry)
XX      DE      Murine flk-2 receptor coding sequence.
XX      KW      Human; foetal liver kinase 2; flk2; receptor protein tyrosine kinase;
XX      KW      PTK; liver; spleen; thymus; adult; brain; bone marrow/primitive portion;
XX      KW      haematopoietic hierarchy; extracellular domain; soluble form; ligand;
XX      KW      proliferation; differentiation; mammalian; haematopoietic stem cell;
XX      KW      macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse; ss.
XX      OS      Mus musculus.
XX      FH      Key      Location/Qualifiers
XX      FT      CDS      31..3009
XX      FT

```

```

FT      /*tag= a
FT      /product= Murine_flk-2
FT      sig_peptide 31..111
FT      /*tag= b
FT      mat_peptide 112..3006
FT      /*tag= c
XX
XX      US5621090-A.
XX
XX      15-APR-1997.
XX
XX      02-APR-1991; 91US-0679666.
XX
XX      26-JUN-1992; 92US-0906397.
XX      02-APR-1991; 91US-0679666.
XX      28-JUN-1991; 91US-0728913.
XX      15-NOV-1991; 91US-0793065.
XX      24-DEC-1991; 91US-0813593.
XX      (UYP- ) UNIV PRINCETON.
XX
XX      Lemischka IR:
XX
XX      WPI: 1997-235228/21.
XX      P-PSDB: AAM19874.
XX
XX      Protein containing the extracellular domain of human flk-2 - used
XX      for identification of primitive haematopoietic cell proliferation
XX      and differentiation stimulatory ligands, e.g. for treating anaemia
XX
XX      Disclosure: Fig 1A; 55pp; English.
XX
XX      This sequence encodes the murine fetal liver kinase 2 (flk2). flk-2 is
XX      a receptor protein tyrosine kinase (PTK) and is important in transducing
XX      putative self-renewal signals from the environment. flk-2 is expressed
XX      in fetal liver, spleen, fetal thymus, adult brain and adult bone marrow,
XX      and it is thought that flk-2 is expressed in the entire primitive portion
XX      of the hematopoietic hierarchy. The invention concerns a recombinant
XX      nucleic acid, preferably mRNA, which encodes a protein containing only
XX      the extracellular domain of human flk-2 and lacking the flk-2 intra-
XX      cellular catalytic domain. The resultant protein represents a soluble
XX      form of flk-2 which is used to isolate specific ligands for flk-2. These
XX      ligands can be used to stimulate proliferation and/or differentiation of
XX      mammalian hematopoietic stem cells, in vivo or in vitro, e.g. for
XX      treatment of macrocytic or aplastic anaemia or bone marrow damage caused
XX      by cancer treatment or radiation.
XX
XX      Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:
XX
XX      Query Match 4.9%; Score 23; DB 18; Length 3453;
XX      Best Local Similarity 100.0%; Pred. No. 0.13;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      124 gtggtgaagatcgtgacttgg 146
OY      ||||||||||||||||||||
DB      2509 gtggtgaagatcgtgacttgg 2531

```

RESULT 31

```

AAAT77514
ID AAX77514 standard; cDNA; 3453 BP.
XX
XX      AAX77514:
XX
XX      05-AUG-1999 (first entry)
XX
XX      Murine flk-2 cDNA.
XX
XX      Murine: flk-2; flk-1; cell isolation; fetal liver kinase; receptor;
XX      monoclonal; polyclonal; antibody; tyrosine kinase; ds.
XX
XX      Mus sp.
OS

```

```

XX      XX      Location/Qualifiers
XX      FT      CDS 31..3009
XX      FT      /*tag= a
XX      FT      /product= "flk-2"
XX
XX      US5912133-A.
XX
XX      15-JUN-1999.
XX
XX      10-FEB-1998; 98US-0021324.
XX
XX      19-NOV-1992; 92US-0977451.
XX      02-APR-1991; 91US-0679666.
XX      28-JUN-1991; 91US-0728913.
XX      15-NOV-1991; 91US-0793065.
XX      24-DEC-1991; 91US-0813593.
XX      26-JUN-1992; 92US-0906397.
XX      12-NOV-1992; 92US-0975049.
XX      30-APR-1993; 93US-0055269.
XX      31-OCT-1994; 94US-0252498.
XX      15-FEB-1996; 96US-0601891.
XX      (UYP- ) UNIV PRINCETON.
XX
XX      Lemischka IR:
XX
XX      WPI: 1999-357194/30.
XX      P-PSDB: AAT08616.
XX
XX      Isolating hematopoietic cells expressing fetal liver kinase 1
XX      receptors
XX
XX      Disclosure: Fig 1a; 59pp; English.
XX
XX      This invention describes a novel method of isolating cells expressing
XX      fetal liver kinase 1 (flk-1) receptors on their surface and comprises
XX      binding the cells to a polyclonal or monoclonal antibody specific to
XX      the flk-1 receptor and isolating the cells that have bound to the
XX      antibody. The method can be used to isolate hematopoietic stem cells in
XX      any mammal but preferably a rat, mouse, rabbit or human. The proteins of
XX      the invention belong to the receptor protein family. This sequence
XX      encodes the murine flk-2 protein which is used in the method of the
XX      invention.
XX
XX      Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:
XX
XX      Query Match 4.9%; Score 23; DB 20; Length 3453;
XX      Best Local Similarity 100.0%; Pred. No. 0.13;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      124 gtggtgaagatcgtgacttgg 146
OY      ||||||||||||||||||||
DB      2509 gtggtgaagatcgtgacttgg 2531

```

RESULT 32

```

AAT00801
ID AAT00801 standard; DNA; 3521 BP.
XX
XX      AAT00801:
XX
XX      29-FEB-1996 (first entry)
XX
XX      flk2/flt3 tyrosine kinase receptor gene.
XX
XX      Tyrosine kinase receptor; flk2; flt3; agonist; monoclonal antibody;
XX      haematopoiesis; hypoplasemia; anaemia; thrombocytopenia; stem cell; ss.
XX
XX      Mus sp.
OS
XX
XX      Key Location/Qualifiers

```


Query Match 4.5%; Score 21; DB 18; Length 2574;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 catcacacagagacctgctgc 95
|||||
DB 1566 catcacacagagacctgctgc 1586

RESULT 37

AAC62208
ID AAC62208 standard; DNA: 20 BP.

AC AAC62208;

DT 06-MAR-2001 (first entry)

DE PCR primer used to amplify cDNA encoding flt-4.

XX Antisense oligonucleotide; flt-4; receptor type tyrosine kinase;
KM lymphangioemesis; prostate cancer; prostate cell; PCR primer: ss.
XX

OS Homo sapiens.

PN WO200062063-A1.

PD 19-OCT-2000.

PF 13-APR-1999; 99WO-US08079.

PR 13-APR-1999; 99WO-US08079.

PA (NMBI-) NORTHWEST BIOTHERAPEUTICS INC.

PI Su SL:

DR WPI: 2000-687067/67.

PT Detecting metastatic potential, diagnosing metastatic prostate cancer

PT or determining the prognosis of a subject with prostate cancer

PT comprises detecting the expression of flt-4 in a prostate cell

PS Example: Page 50; 78pp; English.

XX PCR primers AAC62208-09 were used to amplify cDNA encoding flt-4. Flt-4

CC is a receptor type tyrosine kinase with 7 Ig-like domains similar to

CC other VEGF receptors. Flt-4 may play a role in lymphangioemesis.

CC Antisense oligonucleotides can be used for detecting the metastatic

CC potential, diagnosing metastatic prostate cancer or determining the

CC prognosis of a subject with prostate cancer. The method comprises

CC identifying the prostate cell in a body fluid sample and detecting the

CC expression of flt-4 in the cell. Expression of flt-4 in a prostate cell

CC indicates that the cell is a cancerous prostate cell that has metastatic

CC potential or is a secondary tumour metastasis of a primary prostate

CC tumour.

XX Sequence 20 BP: 4 A; 3 C; 9 G; 4 T; 0 other;

Query Match 4.2%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 agaggagatgagcttctgc 62
|||||
DB 1 agaggagatgagcttctgc 20

RESULT 38

AAV62479
ID AAV62479 standard; CDNA: 1611 BP.

XX

AC AAV62479;

DT 18-JAN-1999 (first entry)

DE Human MAP kinase, ERK-2 cDNA sequence.

XX ERK-1; ERK-2; mitogen-activated protein kinase; MAP kinase; human;

XX inhibition; malignant; neoplastic growth; epithelial cell; mammary;

XX endothelial cell; antisense oligonucleotide; primary cancer;

XX metastatic cancer; breast cancer; prostate cancer; angiosarcoma;

XX endocrine tissue cancer; ds.

XX Homo sapiens.

OS

PN WO9844101-A1.

PD 08-OCT-1998.

PF 19-MAR-1998; 98WO-US05471.

PR 12-AUG-1997; 97US-0909742.

PR 28-MAR-1997; 97US-0827520.

PR 01-APR-1997; 97US-0831994.

PA (UYNV) UNIV NEW YORK STATE RES FOUND.

PI Malbon CC, Sivaraman VS, Wang H:

PD WPI: 1998-557109/47.

PT Treatment of e.g. breast or prostate cancer or angiosarcoma - by

PT administering antisense oligonucleotides to genes encoding

PT mitogen-activating protein kinases ERK1 and ERK2

PS Disclosure: Page 12; 59pp; English.

XX This represents the cDNA sequence of the human ERK-2, a

CC mitogen-activated protein (MAP) kinase. The invention provides a method

CC of inhibiting malignant neoplastic growth of epithelial or endothelial

CC cell in a mammal which comprises administering to the mammal an effective

CC amount of an oligonucleotide complementary to part of the mRNA for the

CC MAP kinases, ERK-1 or ERK2 which is over-expressed in the mammal. Also

CC provided is a method for identifying and monitoring potentially malignant

CC neoplastic cells by measuring the levels of ERK1 and ERK2 mRNA in

CC epithelial or endothelial cells and comparing it to the levels from

CC normal cells of the same origin. Administering to the ERK1 and ERK2

CC antisense oligonucleotides (AAV62480 and AAV62481) to neoplastic

CC endothelial or epithelial cells inhibits over-expression of ERK1 and

CC ERK2. This can be used to treat epithelial and endothelial malignancies

CC including primary or metastatic cancers of e.g. the breast, prostate,

CC other endocrine tissue or angiosarcoma.

XX Sequence 1611 BP: 403 A; 421 C; 407 G; 380 T; 0 other;

Query Match 4.2%; Score 20; DB 19; Length 1611;

Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtgacttgacct 149
|||||
DB 817 aagatctgtgacttgacct 836

RESULT 39

AAV62479/C
ID AAV62479 standard; CDNA: 1611 BP.

AC AAV62479;

DT 18-JAN-1999 (first entry)

DE Human MAP kinase, ERK-2 cDNA sequence.

```
XX ERK-1; ERK-2; mitogen-activated protein kinase; MAP kinase; human;
XX inhibition; malignant; neoplastic growth; epithelial cell; mammary;
XX endometrial cell; antisense oligonucleotide; primary cancer;
XX metastatic cancer; breast cancer; prostate cancer; angiosarcoma;
XX endocrine tissue cancer; ds.
XX Homo sapiens.
XX MO9844101-A1.
XX 08-OCT-1998.
XX 19-MAR-1998; 98MO-US05471.
XX 12-AUG-1997; 97US-0909742.
XX 28-MAR-1997; 97US-0827520.
XX 01-APR-1997; 97US-0831994.
XX (UYNV ) UNIV NEW YORK STATE RES FOUND.
XX Malbon CC, Sivaraman VS, Wang H;
XX WPI; 1998-557109/47.
XX Treatment of e.g. breast or prostate cancer or angiosarcoma - by
XX administering antisense oligonucleotides to genes encoding
XX mitogen-activating protein kinases ERK1 and ERK2
XX Disclosure; Page 12; 59pp; English.
XX PS
XX This represents the cDNA sequence of the human ERK-2, a
XX mitogen-activated protein (MAP) kinase. The invention provides a method
XX of inhibiting malignant neoplastic growth of epithelial or endothelial
XX cell in a mammal which comprises administering to the mammal an effective
XX amount of an oligonucleotide complementary to part of the mRNA for the
XX MAP kinases, ERK-1 or ERK2 which is over-expressed in the mammal. Also
XX provided is a method for identifying and monitoring potentially malignant
XX neoplastic cells by measuring the levels of ERK1 and ERK2 mRNA in
XX epithelial or endothelial cells and comparing it to the levels from
XX normal cells of the same origin. Administration of the ERK1 and ERK2
XX antisense oligonucleotides (AAV62460 and AAV62481) to neoplastic
XX endothelial or epithelial cells inhibits over-expression of ERK1 and
XX ERK2. This can be used to treat epithelial and endothelial malignancies
XX including primary or metastatic cancers of e.g. the breast, prostate,
XX other endocrine tissue or angiosarcoma.
XX SO
XX Sequence 1611 BP; 403 A; 421 C; 407 G; 380 T; 0 other;
XX
XX Query Match 4.2%; Score 20; DB 19; Length 1611;
XX Best Local Similarity 100.0%; Pred. No. 4.1;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 130 aagatctgagcttggcct 149
XX |||||||||||||||||||
XX Db 109 AAGATCTGTGACTTGGCCT 90
XX
XX RESULT 40
XX AAX89336
XX ID AAX89336 standard; cDNA to mRNA; 2463 BP.
XX AC AAX89336;
XX 27-SEP-1999 (first entry)
XX DE Platelet-derived growth factor beta receptor gene sequence.
XX XX
XX Chimera gene; chromosome translocation; t(5;14)(q33;q32); CEV14 gene;
XX platelet-derived growth factor beta receptor; PDGFR-beta; ds.
XX OS
XX Homo sapiens.
```

```
XX JP11187885-A.
XX 13-JUL-1999.
XX 26-DEC-1997; 97JP-0361020.
XX 26-DEC-1997; 97JP-0361020.
XX (M1TP ) MITSUBISHI YUKA BCL KK.
XX WPI; 1999-451550/38.
XX P-PSDB; AAY28935.
XX New DNA - and sensitive method for its detection
XX Claim 6; Page 10-13; 13pp; Japanese.
XX PS
XX The invention describes a new DNA containing a chimera gene specific to
XX the chromosome translocation t(5;14)(q33;q32) formed by fusing the CEV14
XX gene (1-2287 basepairs of the present sequence) with a platelet-derived
XX growth factor beta receptor (PDGFR-beta) gene. A method for the detection
XX of a chimera gene produced by t(5;14)(q33;q32) in a sample by preparing
XX cDNA from the DNA or mRNA in the sample as the template and using an
XX oligonucleotide designed to bind the CEV14 gene region of the above
XX chimera and an oligonucleotide designed to bind the PDGFR gene region as
XX the primers and detecting the amplified product formed by the PCR is also
XX provided. The method can detect a gene specific to the presence of
XX t(5;14)(q33;q32) specifically at a high sensitivity. The present sequence
XX represents the PDGFR-beta gene sequence.
XX SO
XX Sequence 2463 BP; 681 A; 631 C; 629 G; 522 T; 0 other;
XX
XX Query Match 4.2%; Score 20; DB 20; Length 2463;
XX Best Local Similarity 100.0%; Pred. No. 4;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 130 aagatctgagcttggcct 149
XX |||||||||||||||||||
XX Db 1810 aagatctgagcttggcct 1829
XX
XX RESULT 41
XX AAN90355
XX ID AAN90355 standard; cDNA; 4544 BP.
XX AC AAN90355;
XX 01-NOV-1989 (first entry)
XX DE cDNA encoding platelet derived growth factor receptor.
XX XX
XX Platelet derived growth factor receptor; human;
XX ligand binding receptor analogues; isoforms; assays; antibodies;
XX atherosclerosis; wound healing; peptide dimer; cDNA.
XX OS
XX Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 354
XX FT /*tag= a
XX PN EP325224-A.
XX 26-JUL-1989.
XX 18-JAN-1989; 89EP-0100787.
XX 22-JAN-1988; 88US-0146877.
XX (2YWO ) ZYMOGENETICS INC.
```

PI Sledziewski AZ, Bell LA, Kindsvogel WR;
XX AAT34552 standard; cDNA; 4544 BP.
DR WPI: 1989-214434/30.
DR P-PSDB: AAP90127.
XX
PT Secreted ligand-binding receptor analogues eg PDGF receptor
PT - used in assays, in purifications and as, or with,
PT therapeutic agents.
XX
PS Claim 2; fig 1: 45pp; English.
XX
CC cDNA encoding platelet derived growth factor receptor (see corresp.
CC AAP90127). Used in the invention to make analogues that are secreted
CC (pref. Ile-29 - Met-441, and Ile-29 - Lys-531; see specification for
CC details). These analogues are easily purified, produced in large
CC quantities recombinantly, used to produce antibodies, to screen ligands,
CC as imaging agents, as (ant-)agonists, or therapeutically for
CC atherosclerosis and wound healing, and assays.
XX
XX
SQ Sequence 4544 BP; 947 A; 1398 C; 1263 G; 936 T; 0 other;

Query Match 4.2%; Score 20; DB 10; Length 4544;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtgacttgacct 149
|||||
Db 2874 aagatctgtgacttgacct 2893

RESULT 42
AAT34552
ID AAT34552 standard; cDNA; 4544 BP.
XX
AC AAT34552;
XX
DT 11-OCT-1996 (first entry)
XX
DE Platelet-derived growth factor receptor cDNA.
XX
KM Platelet-derived growth factor receptor; PDGF-R; peptide dimer;
KM protein secretion; agonist; antagonist; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 354..3674
PT /*tag= a
XX
XX EP721983-A1.
XX
XX 17-JUL-1996.
XX
XX 18-JAN-1989; 89EP-0100787.
XX
XX 22-JAN-1988; 88US-0146877.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Bell LA, Kindsvogel WR, Sledziewski AZ;
XX
XX WPI: 1996-322833/33.
XX
XX P-PSDB: AAR99690.
XX
XX Prodn. of biologically active peptide dimers, esp. platelet-derived
XX growth factor receptor analogues - useful for systematic designing
XX of novel (ant)agonists
XX
XX Disclosure: Fig 1: 45pp; English.
XX
XX A cDNA sequence (AAT34552) codes for human platelet-derived growth
XX factor receptor (PDGF-R) (AAR99690). It was obcd. from a human

CC diploid dermal fibroblast library using probes (see also
CC AAT34555-57) complementary to sequences of the mouse PDGF-R.
CC The cDNA can be used in novel constructs that allow the prodn.
CC of secreted biologically active PDGF-R analogues. This may
CC comprise linking a sequence coding for PDGF-R, or the ligand-
CC binding domain of the PDGF-R extracellular region, to a protein
CC secretion signal (e.g. SUC2) and promoter, and expression in
CC transformed host cells, esp. Saccharomyces cerevisiae. The
CC secreted PDGF-R analogues are used in ligand screening procedures,
CC to screen for (ant)agonists, and in diagnostic assays.
XX
XX
SQ Sequence 4544 BP; 948 A; 1397 C; 1263 G; 936 T; 0 other;

Query Match 4.2%; Score 20; DB 17; Length 4544;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtgacttgacct 149
|||||
Db 2874 aagatctgtgacttgacct 2893

RESULT 43
AAC59189
ID AAC59189 standard; cDNA; 5279 BP.
XX
AC AAC59189;
XX
DT 30-JAN-2001 (first entry)
XX
XX Human secreted protein cDNA sequence #33.
XX
DE
XX
KM Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KM antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;
KM vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KM cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
KM neurological disease; infection; human; secreted protein; ss.
XX
XX Homo sapiens.
XX
XX
XX PN WO200055201-A1.
XX
XX 21-SEP-2000.
XX
XX 09-MAR-2000; 2000WO-US06059.
XX
XX 12-MAR-1999; 99US-0124096.
XX
XX 03-DEC-1999; 99US-0168622.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX PI Rosen CA, Ruben SM, Komatsoulis G;
XX
XX WPI: 2000-628182/60.
XX
XX P-PSDB: AAB27714.
XX
XX Novel human secreted proteins useful for diagnosis, prevention and
XX treatment of disorders including neurological, cell proliferative,
XX cardiovascular, autoimmune/inflammatory disorders and microbial
XX infections -
XX
XX
XX Claim 1; Page 355-356; 427pp; English.
XX
XX
XX The invention relate to the isolation of genes AAC59157-C59205 encoding
XX 49 human secreted proteins AAB27682-827730. The genes can be used to
XX generate fusion proteins by linking to the gene for the human
XX immunoglobulin G Fc portion for increasing the stability of
XX the fusion protein as compared to the human protein only. The genes and
XX proteins are useful for preventing, ameliorating or treating medical
XX conditions, e.g. by protein or gene therapy. The genes are isolated
XX from a range of human tissues disclosed in the specification. The
XX nucleic acids, proteins, antibodies and (ant)agonists are useful in

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
SQ Sequence 5279 BP; 1404 A; 1145 C; 1121 G; 1596 T; 13 other:

Query Match 4.2%; Score 20; DB 21; Length 5279;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtacttgacct 149
Db 547 aagatctgtacttgacct 566

RESULT 44
AAO27447
ID AAO27447 standard; DNA: 5427 BP.
XX
AC AAO27447:
XX
DT 09-FEB-1993 (first entry)
XX
DE Type B human platelet-derived growth factor receptor.
XX
KM PGCF: PDGF-R; mesenchyme; tyrosine kinase; ligand binding region: ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 187..3507
FT /*tag= a
XX
PN WO9213867-A.
XX
PD 20-AUG-1992.
XX
PF 28-JAN-1992: 92MO-US00730.
XX
PR 31-JAN-1991: 91US-0650793.
XX
PA (COR-) COR THERAPEUTICS INC.
XX
PI Escobedo JA, Fretto LJ, Glese NA, Tomlinson JE, Williams LT;
PI Wolf D;
XX
DR MPI: 1992-289970/36.
DR P-PSDB: AAR26205.
XX
PT Platelet derived growth factor receptor (PDGF-R) polypeptide(s)
PT - useful as therapeutic and diagnostic agents e.g. for assaying
PT PGCF activity in sample
XX
PS Disclosure: Page 75; 109pp; English.
XX
CC The sequence given encodes one allele of type B human platelet-
CC derived growth factor (PDGF) receptor (PDGF-R). This receptor is
CC typically found on cells of mesenchymal origin. It acts while in
CC the form of two transmembrane glycoproteins, each of which is about
CC 180 kD. This receptor has three major regions. The first is a
CC transmembrane region, which spans the membrane once, separating the
CC regions of the receptor exterior to the cell from those interior to
CC the cell. The second region is an extracellular region which
CC contains the domains which bind the PDGF. The third region is an
CC intracellular region which possesses a tyrosine kinase activity.

CC This tyrosine kinase domain is notable in having an insert of approx.
CC 100 amino acids, as compared with most other receptor tyrosine kinase
CC domains which are contiguous or have shorter insert sequences.
CC Fragments of this sequence between 8 and 400 amino acids comprising
CC one or more PDGF ligand binding region from the extracellular domain
CC may be used to bind a PDGF ligand.
XX
SQ Sequence 5427 BP; 1177 A; 1604 C; 1494 G; 1152 T; 0 other:

Query Match 4.2%; Score 20; DB 13; Length 5427;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtacttgacct 149
Db 2707 aagatctgtacttgacct 2726

RESULT 45
AAS84940
ID AAS84940 standard; cDNA: 5602 BP.
XX
AC AAS84940:
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #20744.
XX
KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder: ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001: 2001WO-US08631.
XX
PR 31-MAR-2000: 2000US-0540217.
XX
PR 23-AUG-2000: 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
PI
XX
DR MPI: 2001-639362/73.
DR P-PSDB: ABG20753.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID NO 20744; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5602 BP; 1201 A; 1682 C; 1539 G; 1180 T; 0 other;

Query Match 4.2%; Score 20; DB 23; Length 5602;
Best Local Similarity 100.0%; Pred No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgtgacttggcct 149
|||||
Db 2877 aagatctgtgacttggcct 2896

Search completed: July 15, 2002, 23:10:10
Job time: 18428 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:25:30 ; Search time 9532.94 Seconds

(without alignments)
1033.931 Million cell updates/sec

Title: US-09-375-248-1_COPY_3044_3514

Perfect score: 471

Sequence: 1 ctgacatcgaagatctgt.....gacctgcatctcggagctg 471

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 segs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_r:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_in:*
18: em_mu:*
19: em_om:*
20: em_ov:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
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1	471	100.0	4195	6	AR016568	AR016568 Sequence
2	471	100.0	4195	6	AR106405	AR106405 Sequence
3	471	100.0	4416	6	AR112506	AR112506 Sequence
4	471	100.0	4416	6	HSF1T4	HSF1T4
5	471	100.0	4425	6	HSU43143	HSU43143
6	471	100.0	4425	6	AR016569	AR016569 Sequence
7	471	100.0	4795	6	AR106406	AR106406 Sequence
8	471	100.0	4795	6	AR106406	AR106406 Sequence
9	420	89.2	6827	6	144515	144515 Sequence
10	305	64.8	4450	9	HSF1T4X	HSF1T4X
11	113	24.0	127488	2	AC022095	AC022095
12	113	24.0	130129	2	AC108083	AC108083
13	113	24.0	168347	2	AC025336	AC025336
14	113	24.0	173341	2	AC106813	AC106813
15	103	21.9	130129	2	AC108083	AC108083
16	76	16.1	160	6	144509	144509 Sequence
17	31	6.6	5284	10	MUSPRKA	MUSPRKA
18	31	6.6	260266	2	AL646088	AL646088 Mus muscu
19	28	5.9	534	4	AB017155	AB017155 Oryctolag
20	27	5.7	2753	5	XELXFGFRA2	M62322 Xenopus lae
21	27	5.7	3634	5	XLU24491	U24491 Xenopus lae
22	27	5.7	3815	5	XELXJGFGR	M55163 Xenopus lae
23	27	5.7	4254	10	AF402785	AF402785 Rattus no
24	27	5.7	4360	10	AF402785	AF402785 Rattus no
25	27	5.7	161580	2	AC098957	AC098957 Rattus no
26	26	5.5	1256	10	MMMAPK42	X58712 Mouse MAPK
27	26	5.5	1467	6	AR016532	AR016532 Sequence
28	26	5.5	1467	6	AR036245	AR036245 Sequence
29	26	5.5	1467	6	AR171291	AR171291 Sequence
30	26	5.5	1467	6	AR172792	AR172792 Sequence
31	26	5.5	1467	6	134200	134200 Sequence
32	26	5.5	1467	10	RATERRK2	M64300 Rat extrace
33	26	5.5	1534	5	S65207	S65207 endothe1a1
34	26	5.5	1747	10	MUSERK2	D10939 Mouse mRNA
35	26	5.5	1815	6	A84443	A84443 Sequence
36	26	5.5	1818	6	A84425	A84425 Sequence
37	26	5.5	4617	5	CCOUERK2	X83287 C.cotturmix
38	26	5.5	4696	10	RATIGFIRF	L29232 Rattus norv
39	25	5.3	786	10	D87264S4	D87267 Mus musculu
40	23	4.9	159	6	AR062728	AR062728 Sequence
41	23	4.9	272	9	D50001S13	D50013 Human DNA f
42	23	4.9	429	10	MUS3RKT	L36163 Mus musculu
43	23	4.9	1525	5	AP178759	AP178759 Danio rer
44	23	4.9	1894	6	AR149571	AR149571 Sequence
45	23	4.9	2538	14	AC2TRKSEA	M25158 Avian retro

ALIGNMENTS

RESULT	1	4195 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	AR016568				
DEFINITION	Sequence 1 from patent US 5776755.				
ACCESSION	AR016568				
VERSION	AR016568.1	GI:3972845			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 4195)				
AUTHORS	Altaiio,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J. and Kaipainen,A.				
TITLE	FLR4, a receptor tyrosine kinase				
JOURNAL	Patent: US 5776755-A 1 07-JUL-1998;				
FEATURES	Location/Qualifiers				
source	1..4195				
BASE COUNT	889 a 1279 c 1305 g 722 t				
ORIGIN	/organism="unknown"				

Query Match	Score 471:	DB 6:	Length 4195:
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Best Local Similarity 100.0%; Pred. No. 2,1e-263;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ctgacacatgaagaatctgtctgtctacagcttcccaagtgccagagagatgagcttcctg 60
Db 3044 CTGACCATGACAGATCTTGTCTGTCTACAGCTTCAGCTGCCAGAGAGATGAGATTCCTG 3103
OY 61 gcttccgaaagatgacatccacagagaccttgctgcttcgaaacttcgtctcgaaagc 120
Db 3104 GCTTCCGAAAGTGCATTCACAGACCTGCTGCTCGAACAATTGCTGCTCGAAGC 3163
OY 121 gacgtgtaagaatctgtactgtgcttgcctgcgagacatctacaagaacctgaactc 180
Db 3164 GAGCTGTGAAGATCTGTGACTTTGGCTTGCCGGACATCTACAAAGACCTGACTTAC 3223
OY 181 gtccgaaagggcagtgccgagctgccttgaaatgagtgagccctgaagacatcttcgac 240
Db 3224 GTCCGAAAGGCACTGCCGCTGCCCTGAGTGTGAGTGGCCCTGAAACATCTTCGAC 3283
OY 241 aaggtgtaaccaacagcagagtgacgtgtgcttcttgagggtactctctcgagagatctc 300
Db 3284 AAGGTGTACACACAGCAGAGATGAGCTGTGCTTGGGTGCTTCTGTGAGATCTTC 3343
OY 301 tctctggggcctcccgtaacctgaggtgacatcaatgaagagtgcttcgacagcgctg 360
Db 3344 TCTCTGGGGCCTCCCGTACCCCTGAGCTGACATCAATGAGAGTCTCTGCGACGGCTG 3403
OY 361 agagaagcgaagaagatgagagggcccgagctgacaccccgcaataagccgacatcatg 420
Db 3404 AGAGACGGCACAGAGATGAGAGGGCCCGGACCTGGCACCTCCGCAATACCCCGCATCATG 3463
OY 421 ctgaactgtgctgcgagagaccccaagcgagacatcttcgagagcg 471
Db 3464 CTGAACGTGCTGCTCGAGACCCCAAGCGAGACCTGCATTTCTCGAGCTG 3514

RESULT 2
ARI06405 4195 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 1 from patent US 6107046.
DEFINITION ARI06405
ACCESSION ARI06405
VERSION ARI06405.1 GI:12820935
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4195)
AUTHORS Allitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.,
TITLE Antihodles to Flt4, a receptor tyrosine kinase and uses thereof
JOURNAL Patent: US 6107046-A 1 22-AUG-2000;
FEATURES
source 1..4195
location/Qualifiers
BASE COUNT 889 a 1279 c 1305 g 722 t
ORIGIN
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Query Match 100.0%; Score 471; DB 6; Length 4195;
Best Local Similarity 100.0%; Pred. No. 2,1e-263;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgacacatgaagaatctgtctgtctacagcttcccaagtgccagagagatgagcttcctg 60
Db 3044 CTGACCATGACAGATCTTGTCTGTCTACAGCTTCAGCTGCCAGAGAGATGAGATTCCTG 3103
OY 61 gcttccgaaagatgacatccacagagaccttgctgcttcgaaacttcgtctcgaaagc 120
Db 3104 GCTTCCGAAAGTGCATTCACAGACCTGCTGCTCGAACAATTGCTGCTCGAAGC 3163
OY 121 gacgtgtaagaatctgtactgtgcttgcctgcgagacatctacaagaacctgaactc 180
Db 3164 GAGCTGTGAAGATCTGTGACTTTGGCTTGCCGGACATCTACAAAGACCTGACTTAC 3223
OY 181 gtccgaaagggcagtgccgagctgccttgaaatgagtgagccctgaagacatcttcgac 240
Db 3224 GTCCGAAAGGCACTGCCGCTGCCCTGAGTGTGAGTGGCCCTGAAACATCTTCGAC 3283
OY 241 aaggtgtaaccaacagcagagtgacgtgtgcttcttgagggtactctctcgagagatctc 300
Db 3284 AAGGTGTACACACAGCAGAGATGAGCTGTGCTTGGGTGCTTCTGTGAGATCTTC 3343
OY 301 tctctggggcctcccgtaacctgaggtgacatcaatgaagagtgcttcgacagcgctg 360
Db 3344 TCTCTGGGGCCTCCCGTACCCCTGAGCTGACATCAATGAGAGTCTTGTGCGACGGCTG 3403
OY 361 agagaagcgaagaagatgagagggcccgagctgacaccccgcaataagccgacatcatg 420
Db 3404 AGAGACGGCACAGAGATGAGAGGGCCCGGACCTGGCACCTCCGCAATACCCCGCATCATG 3463
OY 421 ctgaactgtgctgcgagagaccccaagcgagacatcttcgagagcg 471
Db 3464 CTGAACGTGCTGCTCGAGACCCCAAGCGAGACCTGCATTTCTCGAGCTG 3514
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```
OY 181 gtccgaaagggcagtgccgagctgccttgaaatgagtgagccctgaagacatcttcgac 240
Db 3224 GTCCGAAAGGCACTGCCGCTGCCCTGAGTGTGAGTGGCCCTGAAACATCTTCGAC 3283
OY 241 aaggtgtaaccaacagagtgacgtgtgcttcttgagggtactctctcgagagatctc 300
Db 3284 AAGGTGTACACACAGCAGAGATGAGCTGTGCTTGGGTGCTTCTGTGAGATCTTC 3343
OY 301 tctctggggcctcccgtaacctgaggtgacatcaatgaagagtgcttcgacagcgctg 360
Db 3344 TCTCTGGGGCCTCCCGTACCCCTGAGCTGACATCAATGAGAGTCTTGTGCGACGGCTG 3403
OY 361 agagaagcgaagaagatgagagggcccgagctgacaccccgcaataagccgacatcatg 420
Db 3404 AGAGACGGCACAGAGATGAGAGGGCCCGGACCTGGCACCTCCGCAATACCCCGCATCATG 3463
OY 421 ctgaactgtgctgcgagagaccccaagcgagacatcttcgagagcg 471
Db 3464 CTGAACGTGCTGCTCGAGACCCCAAGCGAGACCTGCATTTCTCGAGCTG 3514
```

```
RESULT 3
ARI12506 4416 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 1 from patent US 6130071.
DEFINITION ARI12506
ACCESSION ARI12506
VERSION ARI12506.1 GI:14092406
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4416)
AUTHORS Allitalo,K. and Joukov,V.
TITLE Vascular endothelial growth factor C (VEGF-C). DELTA.Cys.sub.156
JOURNAL Protein and gene,
PATENT: US 6130071-A 1 10-OCT-2000;
FEATURES
source 1..4416
location/Qualifiers
BASE COUNT 941 a 1345 c 1355 g 774 t 1 others
ORIGIN
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Query Match 100.0%; Score 471; DB 6; Length 4416;
Best Local Similarity 100.0%; Pred. No. 2,1e-263;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgacacatgaagaatctgtctgtctacagcttcccaagtgccagagagatgagcttcctg 60
Db 3044 CTGACCATGACAGATCTTGTCTGTCTACAGCTTCAGCTGCCAGAGAGATGAGATTCCTG 3103
OY 61 gcttccgaaagatgacatccacagagaccttgctgcttcgaaacttcgtctcgaaagc 120
Db 3104 GCTTCCGAAAGTGCATTCACAGACCTGCTGCTCGAACAATTGCTGCTCGAAGC 3163
OY 121 gacgtgtaagaatctgtactgtgcttgcctgcgagacatctacaagaacctgaactc 180
Db 3164 GAGCTGTGAAGATCTGTGACTTTGGCTTGCCGGACATCTACAAAGACCTGACTTAC 3223
OY 181 gtccgaaagggcagtgccgagctgccttgaaatgagtgagccctgaagacatcttcgac 240
Db 3224 GTCCGAAAGGCACTGCCGCTGCCCTGAGTGTGAGTGGCCCTGAAACATCTTCGAC 3283
OY 241 aaggtgtaaccaacagcagagtgacgtgtgcttcttgagggtactctctcgagagatctc 300
Db 3284 AAGGTGTACACACAGCAGAGATGAGCTGTGCTTGGGTGCTTCTGTGAGATCTTC 3343
OY 301 tctctggggcctcccgtaacctgaggtgacatcaatgaagagtgcttcgacagcgctg 360
Db 3344 TCTCTGGGGCCTCCCGTACCCCTGAGCTGACATCAATGAGAGTCTTGTGCGACGGCTG 3403
OY 361 agagaagcgaagaagatgagagggcccgagctgacaccccgcaataagccgacatcatg 420
Db 3404 AGAGACGGCACAGAGATGAGAGGGCCCGGACCTGGCACCTCCGCAATACCCCGCATCATG 3463
OY 421 ctgaactgtgctgcgagagaccccaagcgagacatcttcgagagcg 471
Db 3464 CTGAACGTGCTGCTCGAGACCCCAAGCGAGACCTGCATTTCTCGAGCTG 3514
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:28:08 ; Search time 9532.94 Seconds
(without alignments)
2.195 Million cell updates/sec

Title: US-09-375-248-1_COPY_3150_3150

Perfect score: 1 t 1

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmb1:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

C	1	100.0	2	6	AX081326	AX081326 Sequence
C	2	100.0	2	6	AX081327	AX081327 Sequence
C	3	100.0	2	6	AX081328	AX081328 Sequence
C	4	100.0	2	6	AX092440	AX092440 Sequence
C	5	100.0	2	6	AX092441	AX092441 Sequence
C	6	100.0	2	6	AX092442	AX092442 Sequence
C	7	100.0	2	6	AX092443	AX092443 Sequence
C	8	100.0	2	6	AX092444	AX092444 Sequence
C	9	100.0	2	6	AX092445	AX092445 Sequence
C	10	100.0	2	6	AX092446	AX092446 Sequence
C	11	100.0	2	6	AX092447	AX092447 Sequence
C	12	100.0	2	6	AX092448	AX092448 Sequence
C	13	100.0	2	6	AX092451	AX092451 Sequence
C	14	100.0	2	6	AX092452	AX092452 Sequence
C	15	100.0	2	6	AX092453	AX092453 Sequence
C	16	100.0	2	6	AX092454	AX092454 Sequence
C	17	100.0	2	6	AX092455	AX092455 Sequence
C	18	100.0	2	6	AX092528	AX092528 Sequence
C	19	100.0	2	6	AX092530	AX092530 Sequence
C	20	100.0	2	6	AX092538	AX092538 Sequence
C	21	100.0	2	6	AX092539	AX092539 Sequence
C	22	100.0	2	6	AX175286	AX175286 Sequence
C	23	100.0	2	6	AX175287	AX175287 Sequence
C	24	100.0	2	6	AX235098	AX235098 Sequence
C	25	100.0	2	6	AX235098	AX235098 Sequence
C	26	100.0	2	6	BD001933	BD001933 Sequence
C	27	100.0	2	8	CNS01C99	AL115237 Botrytis
C	28	100.0	3	2	AC079635	AC079635 Mus muscu
C	29	100.0	3	2	AC079635	AC079635 Mus muscu
C	30	100.0	3	5	CHKNCA65	M23994 Chicken car
C	31	100.0	3	6	AX092456	AX092456 Sequence
C	32	100.0	3	6	AX092457	AX092457 Sequence
C	33	100.0	3	6	AX092458	AX092458 Sequence
C	34	100.0	3	6	AX092459	AX092459 Sequence
C	35	100.0	3	6	AX092459	AX092459 Sequence
C	36	100.0	3	6	AX092460	AX092460 Sequence
C	37	100.0	3	6	AX092461	AX092461 Sequence
C	38	100.0	3	6	AX092462	AX092462 Sequence
C	39	100.0	3	6	AX092463	AX092463 Sequence
C	40	100.0	3	6	AX092463	AX092463 Sequence
C	41	100.0	3	6	AX092464	AX092464 Sequence
C	42	100.0	3	6	AX092465	AX092465 Sequence
C	43	100.0	3	6	AX092466	AX092466 Sequence
C	44	100.0	3	6	AX092467	AX092467 Sequence
C	45	100.0	3	6	AX092467	AX092467 Sequence

ALIGNMENTS

RESULT 1
AX081326/c
LOCUS AX081326 2 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 5 from Patent WO0108707.
ACCESSION AX081326
VERSION AX081326.1 GI:13170168
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequence.
REFERENCE
AUTHORS Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.
TITLE Conjugates and methods for the production thereof, and their use
JOURNAL for transporting molecules via biological membranes
Patent: WO 0108707-A 5 08-FEB-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
SOURCE
1.2
location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT 1 a 0 c 0 g 0 t 1 others

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 T 2

RESULT 2
AX081327/c
LOCUS Sequence 6 from Patent WO0108707.
DEFINITION
ACCESSION AX081327
VERSION AX081327.1 GI:13170169
KEYWORDS
SOURCE .
ORGANISM synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 2)
AUTHORS Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.
TITLE Conjugates and methods for the production thereof, and their use
JOURNAL for transporting molecules via biological membranes
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source 1..2
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT 1 a 0 c 0 g 0 t 1 others
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 T 2

RESULT 3
AX081328/c
LOCUS Sequence 7 from Patent WO0108707.
DEFINITION
ACCESSION AX081328
VERSION AX081328.1 GI:13170170
KEYWORDS
SOURCE .
ORGANISM synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 2)
AUTHORS Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.
TITLE Conjugates and methods for the production thereof, and their use
JOURNAL for transporting molecules via biological membranes
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source 1..2
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT 1 a 0 c 0 g 0 t 1 others
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 T 2

RESULT 4
AX092440/c
LOCUS Sequence 1 from Patent WO0116366.
DEFINITION
ACCESSION AX092440
VERSION AX092440.1 GI:13444535
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 1 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)
FEATURES
source 1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 2 a 0 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 T 2

RESULT 5
AX092441/c
LOCUS Sequence 2 from Patent WO0116366.
DEFINITION
ACCESSION AX092441
VERSION AX092441.1 GI:13444536
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 2 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)
FEATURES
source 1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 T 2

RESULT 5
AX092441/c
LOCUS Sequence 2 from Patent WO0116366.
DEFINITION
ACCESSION AX092441
VERSION AX092441.1 GI:13444536
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 2 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)
FEATURES
source 1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 T 2

RESULT 5
AX092441/c
LOCUS Sequence 2 from Patent WO0116366.
DEFINITION
ACCESSION AX092441
VERSION AX092441.1 GI:13444536
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 2 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)
FEATURES
source 1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 T 2

RESULT 5
AX092441/c
LOCUS Sequence 2 from Patent WO0116366.
DEFINITION
ACCESSION AX092441
VERSION AX092441.1 GI:13444536
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 2 08-MAR-2001;
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)
FEATURES
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 0 t
ORIGIN

Db 1 T 1

RESULT 6 AX092442 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092442/c
DEFINITION Sequence 3 from Patent WO0116366.
ACCESSION AX092442
VERSION AX092442.1 GI:13444537
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 3 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide:"

BASE COUNT 1 a 0 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
1
Db 1 T 1

RESULT 7 AX092443 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092443
DEFINITION Sequence 4 from Patent WO0116366.
ACCESSION AX092443
VERSION AX092443.1 GI:13444538
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 4 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide:"

BASE COUNT 1 a 0 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
1
Db 2 T 2

RESULT 8 AX092443 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092443/c
DEFINITION Sequence 4 from Patent WO0116366.
ACCESSION AX092443
VERSION AX092443.1 GI:13444538
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 4 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide:"

BASE COUNT 1 a 0 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
1
Db 1 T 1

RESULT 9 AX092444 2 bp DNA linear PAT 23-MAR-2001
LOCUS AX092444/c
DEFINITION Sequence 5 from Patent WO0116366.
ACCESSION AX092444
VERSION AX092444.1 GI:13444539
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 5 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide:"

BASE COUNT 1 a 1 c 0 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
1
Db 2 T 2

RESULT 10 AX092447 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092447

DEFINITION Sequence 8 from Patent WO0116366.
ACCESSION AX092447
VERSION AX092447.1 GI:13444542
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 8 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 1 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 T 2

RESULT 11
AX092448/C
LOCUS AX092448 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 9 from Patent WO0116366.
ACCESSION AX092448
VERSION AX092448.1 GI:13444543
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 9 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 T 2

RESULT 12
AX092451
LOCUS AX092451 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 12 from Patent WO0116366.
ACCESSION AX092451
VERSION AX092451.1 GI:13444546

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 12 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 T 2

RESULT 13
AX092452
LOCUS AX092452 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 13 from Patent WO0116366.
ACCESSION AX092452
VERSION AX092452.1 GI:13444547
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 13 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 T 2

RESULT 14
AX092452/C
LOCUS AX092452 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 13 from Patent WO0116366.
ACCESSION AX092452
VERSION AX092452.1 GI:13444547
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

unclassified.
1 (bases 1 to 2)
REFERENCE Kless, H.
AUTHORS
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 13 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source 1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 ↑ 2

RESULT 15
AX092453 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092453
DEFINITION Sequence 14 from Patent WO0116366.
ACCESSION AX092453
VERSION AX092453.1 GI:13444548
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE Kless, H.
AUTHORS 1 (bases 1 to 2)
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 14 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 1 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 ↑ 1

RESULT 16
AX092454 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092454
DEFINITION Sequence 15 from Patent WO0116366.
ACCESSION AX092454
VERSION AX092454.1 GI:13444549
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE Kless, H.
AUTHORS 1 (bases 1 to 2)

TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 15 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 ↑ 1

RESULT 17
AX092455 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092455
DEFINITION Sequence 16 from Patent WO0116366.
ACCESSION AX092455
VERSION AX092455.1 GI:13444550
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE Kless, H.
AUTHORS 1 (bases 1 to 2)
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 16 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source 1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 0 g 2 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 ↑ 1

RESULT 18
AX092528 2 bp DNA linear PAT 21-MAR-2001
LOCUS AX092528/c
DEFINITION Sequence 89 from Patent WO0116366.
ACCESSION AX092528
VERSION AX092528.1 GI:13444523
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE Kless, H.
AUTHORS 1 (bases 1 to 2)
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 89 08-MAR-2001;

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source 1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 T 2

RESULT 19
AX092530/c

LOCUS AX092530 2 bp DNA linear PAT 21-MAR-2001

DEFINITION Sequence 91 from Patent WO0116366.

ACCESSION AX092530

VERSION AX092530.1 GI:13444625

KEYWORDS

SOURCE .
unidentified.
unclassified.

ORGANISM
unclassified.
unclassified.
1 (bases 1 to 2)

REFERENCE
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 91 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 T 1

RESULT 20
AX092538

LOCUS AX092538 2 bp DNA linear PAT 21-MAR-2001

DEFINITION Sequence 99 from Patent WO0116366.

ACCESSION AX092538

VERSION AX092538.1 GI:13444633

KEYWORDS

SOURCE .
unidentified.
unclassified.

ORGANISM
unclassified.
unclassified.
1 (bases 1 to 2)

REFERENCE
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 99 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
Location/Qualifiers

source 1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 T 2

RESULT 21
AX092539/c

LOCUS AX092539 2 bp DNA linear PAT 21-MAR-2001

DEFINITION Sequence 100 from Patent WO0116366.

ACCESSION AX092539

VERSION AX092539.1 GI:13444634

KEYWORDS

SOURCE .
unidentified.
unclassified.

ORGANISM
unclassified.
unclassified.
1 (bases 1 to 2)

REFERENCE
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 100 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 2 a 0 c 0 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 T 2

RESULT 22
AX175286

LOCUS AX175286 2 bp DNA linear PAT 03-JUL-2001

DEFINITION Sequence 50 from Patent WO0144465.

ACCESSION AX175286

VERSION AX175286.1 GI:14598654

KEYWORDS

SOURCE .
synthetic construct.
artificial construct.
artificial sequence.

ORGANISM
synthetic construct.
artificial construct.
1 (bases 1 to 2)

REFERENCE
AUTHORS Phillips,N.C. and Fillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 50 21-JUN-2001;
Bloniche Life Sciences Inc. (CA)

FEATURES
source 1..2
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 2 T 2

RESULT 23
AX175287
LOCUS AX175287 2 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 51 from Patent WO0144465.
ACCESSION AX175287
VERSION AX175287.1 GI:14598655
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 2)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 51 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source 1..2
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 T 1

RESULT 24
AX235098
LOCUS AX235098 2 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 55 from Patent WO0163540.
ACCESSION AX235098
VERSION AX235098.1 GI:15593746
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 2)
AUTHORS Bureau,T.
TITLE Method for identifying transposons from a nucleic acid database
JOURNAL Patent: WO 0163540-A 55 30-AUG-2001;
MCGILL UNIVERSITY (CA)
FEATURES
source 1..2
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="sequence from g1 3243214"
BASE COUNT 1 a 0 c 0 g 1 t
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Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1

Db 2 T 2

RESULT 25
AX235098/c
LOCUS AX235098 2 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 55 from Patent WO0163540.
ACCESSION AX235098
VERSION AX235098.1 GI:15593746
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 2)
AUTHORS Bureau,T.
TITLE Method for identifying transposons from a nucleic acid database
JOURNAL Patent: WO 0163540-A 55 30-AUG-2001;
MCGILL UNIVERSITY (CA)
FEATURES
source 1..2
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="sequence from g1 3243214"
BASE COUNT 1 a 0 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 T 1

RESULT 26
BD001933
LOCUS BD001933 2 bp DNA linear PAT 31-JAN-2002
DEFINITION Sensitized method for detecting DNA.
ACCESSION BD001933
VERSION BD001933.1 GI:18628673
KEYWORDS JP 2000146894-A/2.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 2)
AUTHORS Takenaka,S. and Takagi,M.
TITLE Sensitized method for detecting DNA
JOURNAL Patent: JP 2000146894-A 2 26-MAY-2000;
FUJI PHOTO FILM CO LTD
COMMENT
OS Artificial Sequence
PN JP 2000146894-A/2
PD 26-MAY-2000
PF 04-NOV-1998 JP 1998328872
PI
PR SHIGEO TAKENAKA,MAKOTO TAKAGI
PC G01N27/327,C12N15/09,C12Q1/68,G01N33/483,G01N33/50,G01N27/30,
PC C12N15/00
CC
FH
FT
FT key Location/Qualifiers
FT source 1..2
/organism="Artificial Sequence".
Location/Qualifiers
1..2
/organism="synthetic construct"
/db_xref="taxon:32630"

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;

Oy 1 t 1
Db 1

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 t 1
1
Db 1 t 1

RESULT 27
CNS01C99
LOCUS 2 bp mRNA linear PLN 02-SEP-1999
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ACCESSION AL115237.1 GI:5829856
VERSION cDNA library: nitrogen deprivation.
KEYWORDS Botryotinia fuckelliana.
SOURCE Botryotinia fuckelliana
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniales; Botryotinia.

REFERENCE 1 (bases 1 to 2)
AUTHORS Bilton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 2)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBS11 vector.

FEATURES
source Location/Qualifiers
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/organism="Botryotinia fuckelliana"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W04F091"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 8; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 1 t 1
1
Db 2 t 2

RESULT 28
AC079635
LOCUS 3 bp DNA linear HTG 14-AUG-2001
DEFINITION Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.
AC079635
AC079635.3 GI:14647267
KEYWORDS HTG; HTGS_PHASE0.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3)
AUTHORS McCombie, W.R., Baker, J.P., Bahret, A., Yang, C., Ballja, V., Dedhia, N.N., de la Bastide, M., Kuit, K., King, L., Kirchhoff, K.A., Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Palmer, L., Vill, M.D. and Zutavern, T.
TITLE Mouse Genomic Sequence

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3)
AUTHORS McCombie, W.R.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
On Jul 10, 2001 this sequence version replaced gi:14595773.

COMMENT * NOTE: This record contains 1 individual
* sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
* 1
* 3: contig of 3 bp in length.
This entry has been temporarily removed. An update for RP23-152L20 will be submitted as soon as it becomes available.
Location/Qualifiers
1..3
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-152L20"

BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 1 t 1
1
Db 3 t 3

RESULT 29
AC079635/c
LOCUS 3 bp DNA linear HTG 14-AUG-2001
DEFINITION Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.
AC079635
AC079635.3 GI:14647267
KEYWORDS HTG; HTGS_PHASE0.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3)
AUTHORS McCombie, W.R., Baker, J.P., Bahret, A., Yang, C., Ballja, V., Dedhia, N.N., de la Bastide, M., Kuit, K., King, L., Kirchhoff, K.A., Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Palmer, L., Vill, M.D. and Zutavern, T.
TITLE Mouse Genomic Sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3)
AUTHORS McCombie, W.R.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
On Jul 10, 2001 this sequence version replaced gi:14595773.
* NOTE: This record contains 1 individual
* sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 3: contig of 3 bp in length.
This entry has been temporarily removed. An update for RP23-152L20
will be submitted as soon as it becomes available.

FEATURES

source

1..3
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-152L20"

BASE COUNT

1 a 0 c 1 g 1 t

Query Match

100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

Db 2 t 2

RESULT 30
CHKNCAMC5/c 3 bp DNA linear VRT 17-JUL-2000
LOCUS CHICKEN cardiac neural cell adhesion (NCAM) gene, exon 12D.
DEFINITION M23994 J04140
ACCESSION M23994.1 GI:212442
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 3)
Prediger,E.A., Hoffman,S., Edelman,G.M. and Cunningham,B.A.
Four exons encode a 93-base-pair insert in three neural cell
adhesion molecule mRNAs specific for chicken heart and skeletal
muscle

REFERENCE
AUTHORS
TITLE
JOURNAL,
MEDLINE
PUBMED
COMMENT
FEATURES
source

Proc. Natl. Acad. Sci. U.S.A. 85 (24), 9616-9620 (1988)

89071747
3200847
Exon 12D represents a very small exon.
Location/Qualifiers

FEATURES

1..3
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="PEC101B"
/tissue_type="cardiac muscle"
/dev_stage="day 10 embryo"

exon

1..3
/gene="NACM"
/number=12

BASE COUNT 2 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

Db 2 t 2

RESULT 31
AX092456/c 3 bp DNA linear PAT 21-MAR-2001
LOCUS AX092456

DEFINITION Sequence 17 from Patent WO0116366.
ACCESSION AX092456
VERSION AX092456.1 GI:13444551
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 3)
Kless,H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 17 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

DEFINITION
AUTHORS
TITLE
JOURNAL

FEATURES

1..3
Location/Qualifiers

source
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 3 a 0 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

Db 3 t 3

RESULT 32
AX092457/c 3 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 18 from Patent WO0116366.
DEFINITION AX092457
ACCESSION AX092457
VERSION AX092457.1 GI:13444552
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

unidentified.
unclassified.
1 (bases 1 to 3)
Kless,H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 18 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

DEFINITION
AUTHORS
TITLE
JOURNAL

unclassified.
unclassified.
1 (bases 1 to 3)
Kless,H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 18 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

DEFINITION
AUTHORS
TITLE
JOURNAL

unclassified.
unclassified.
1 (bases 1 to 3)
Kless,H.
Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 18 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

Db 2 t 2

RESULT 33
AX092458/c 3 bp DNA linear PAT 21-MAR-2001
LOCUS AX092458
DEFINITION Sequence 19 from Patent WO0116366.
ACCESSION AX092458
VERSION AX092458.1 GI:13444553

KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE
AUTHORS Kless,H.
TITLE 1 (bases 1 to 3)
JOURNAL Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 19 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..3
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN 2 a 0 c 1 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 T 2

RESULT 34
AX092459
LOCUS AX092459 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 20 from Patent WO0116366.
ACCESSION AX092459
VERSION AX092459.1 GI:13444554
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 20 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..3
Location/Qualifiers
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN 2 a 0 c 0 g 1 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 3 T 3

RESULT 35
AX092459/C
LOCUS AX092459 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 20 from Patent WO0116366.
ACCESSION AX092459
VERSION AX092459.1 GI:13444554
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 20 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..3
Location/Qualifiers
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN 2 a 0 c 0 g 1 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 2 T 2

RESULT 36
AX092460
LOCUS AX092460 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 21 from Patent WO0116366.
ACCESSION AX092460
VERSION AX092460.1 GI:13444555
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
Patent: WO 0116366-A 21 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source 1..3
Location/Qualifiers
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT
ORIGIN 2 a 1 c 0 g 0 t

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
|
Db 3 T 3

RESULT 37
AX092461/C
LOCUS AX092461 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 22 from Patent WO0116366.
ACCESSION AX092461
VERSION AX092461.1 GI:13444556
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.

TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 22 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 T 1

RESULT 38
AX092462/c 3 bp DNA linear PAT 21-MAR-2001
LOCUS AX092462
DEFINITION Sequence 23 from Patent WO0116366.
ACCESSION AX092462
VERSION AX092462.1 GI:13444557
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 23 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 T 1

RESULT 39
AX092463 3 bp DNA linear PAT 21-MAR-2001
LOCUS AX092463
DEFINITION Sequence 24 from Patent WO0116366.
ACCESSION AX092463
VERSION AX092463.1 GI:13444558
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 24 08-MAR-2001;

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 T 1

RESULT 40
AX092463/c 3 bp DNA linear PAT 21-MAR-2001
LOCUS AX092463
DEFINITION Sequence 24 from Patent WO0116366.
ACCESSION AX092463
VERSION AX092463.1 GI:13444558
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 24 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 T 1

RESULT 41
AX092464 3 bp DNA linear PAT 21-MAR-2001
LOCUS AX092464
DEFINITION Sequence 25 from Patent WO0116366.
ACCESSION AX092464
VERSION AX092464.1 GI:13444559
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 25 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source Location/Qualifiers

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source 1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide:"
BASE COUNT 2 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
1
Db 3 T 3

RESULT 42
AX092465/c AX092465 3 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 26 from Patent WO0116366.
DEFINITION AX092465
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS
SOURCE
ORGANISM
unidentified.
AUTHORS Kless,H.
REFERENCE 1 (bases 1 to 3)
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 26 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source 1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide:"
BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
1
Db 1 T 1

RESULT 43
AX092466/c AX092466 3 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 27 from Patent WO0116366.
DEFINITION AX092466
ACCESSION AX092466
VERSION AX092466.1 GI:13444561
KEYWORDS
SOURCE
ORGANISM
unidentified.
AUTHORS Kless,H.
REFERENCE 1 (bases 1 to 3)
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 27 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source 1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide:"
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BASE COUNT 1 a 0 c 2 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
1
Db 1 T 1

RESULT 44
AX092467 AX092467 3 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 28 from Patent WO0116366.
DEFINITION AX092467
ACCESSION AX092467
VERSION AX092467.1 GI:13444562
KEYWORDS
SOURCE
ORGANISM
unidentified.
AUTHORS Kless,H.
REFERENCE 1 (bases 1 to 3)
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 28 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source 1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide:"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
1
Db 3 T 3

RESULT 45
AX092467/c AX092467 3 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 28 from Patent WO0116366.
DEFINITION AX092467
ACCESSION AX092467
VERSION AX092467.1 GI:13444562
KEYWORDS
SOURCE
ORGANISM
unidentified.
AUTHORS Kless,H.
REFERENCE 1 (bases 1 to 3)
TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 28 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)

FEATURES
source 1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide:"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN
```

Query Match 100.0%; Score 1; DB 6; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 L 1
 1 1
 1 1 1

Search completed: July 15, 2002, 23:28:08
 Job time: 24541 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:38 ; Search time 223.79 Seconds
(without alignments)
1.098 Million cell updates/sec

Title: US-09-375-248-1_COPY_3150_3150
Perfect score: 1
Sequence: 1 t 1

Scoring table: OLIGO-NUC
Capopt 60.0 , Capext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/2/lna/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/2/lna/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/2/lna/5A.COMB.seq:*
- 4: /cgn2_6/ptodata/2/lna/5B.COMB.seq:*
- 5: /cgn2_6/ptodata/2/lna/PTCDS.COMB.seq:*
- 6: /cgn2_6/ptodata/2/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
c 1	1	100.0	2	1	US-08-457-274A-16
c 2	1	100.0	2	3	US-09-016-520-35
c 3	1	100.0	2	4	US-09-130-973-35
c 4	1	100.0	2	4	US-09-477-902-35
c 5	1	100.0	2	5	PCT-US95-05758-16
c 6	1	100.0	3	1	US-07-791-213D-46
c 7	1	100.0	3	1	US-07-791-213D-62
c 8	1	100.0	3	1	US-08-268-679B-7
c 9	1	100.0	3	1	US-08-295-743-22
c 10	1	100.0	3	1	US-08-602-036A-2
c 11	1	100.0	3	1	US-08-293-150A-46
c 12	1	100.0	3	1	US-08-293-150A-62
c 13	1	100.0	3	2	US-08-502-374A-2
c 14	1	100.0	3	2	US-08-642-407A-2
c 15	1	100.0	3	4	US-08-793-634B-12
c 16	1	100.0	3	4	US-08-793-634B-12
c 17	1	100.0	3	4	US-08-793-634B-13
c 18	1	100.0	3	4	US-08-793-634B-13
c 19	1	100.0	3	4	US-08-973-568-55
c 20	1	100.0	4	1	US-07-755-462-2
c 21	1	100.0	4	1	US-07-755-462-2
c 22	1	100.0	4	1	US-07-630-288A-7
c 23	1	100.0	4	1	US-07-630-288A-11
c 24	1	100.0	4	1	US-07-630-288A-11
c 25	1	100.0	4	1	US-07-630-288A-34
c 26	1	100.0	4	1	US-07-630-288A-34
c 27	1	100.0	4	1	US-08-188-943-1

c 28	1	100.0	4	1	US-08-188-943-1	Sequence 1, Appl1
c 29	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
c 30	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
c 31	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1
c 32	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1
c 33	1	100.0	4	1	US-08-393-219-11	Sequence 9, Appl1
c 34	1	100.0	4	1	US-08-510-032A-9	Sequence 7, Appl1
c 35	1	100.0	4	1	US-08-510-032A-9	Sequence 7, Appl1
c 36	1	100.0	4	1	US-08-468-049-11	Sequence 11, Appl1
c 37	1	100.0	4	1	US-08-468-049-11	Sequence 11, Appl1
c 38	1	100.0	4	1	US-08-468-049-11	Sequence 11, Appl1
c 39	1	100.0	4	1	US-08-468-049-11	Sequence 11, Appl1
c 40	1	100.0	4	1	US-08-468-049-11	Sequence 11, Appl1
c 41	1	100.0	4	1	US-08-468-049-11	Sequence 11, Appl1
c 42	1	100.0	4	1	US-08-468-049-11	Sequence 11, Appl1
c 43	1	100.0	4	1	US-08-351-365-3	Sequence 3, Appl1
c 44	1	100.0	4	1	US-08-351-365-3	Sequence 3, Appl1
c 45	1	100.0	4	1	US-08-351-365-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-457-274A-16/c
; Sequence 16, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; TITLE OF INVENTION: Cytochrome P4501pr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P. O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Musca domestica
; STRAIN: Learn-Pyr
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
; US-08-457-274A-16

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 t 2

RESULT 2

US-09-016-520-35
Sequence 35, Application US/09016520A
Patent No. 6127533
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/016,520A
CURRENT FILING DATE: 1998-01-30
EARLIER APPLICATION NUMBER: 60/037,143
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 2
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: Sequence
NAME/KEY: misc-feature
LOCATION: (1)..(2)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-35

Query Match 100.0%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 3

US-09-130-973-35
Sequence 35, Application US/09130973
Patent No. 6172209
GENERAL INFORMATION:
APPLICANT: Manoharan, Muthiah
APPLICANT: Cook, Phillip Dan
APPLICANT: Prakash, Thazna P
APPLICANT: Kawasaki, Andrew M
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
FILE REFERENCE: ISIS2955
CURRENT APPLICATION NUMBER: US/09/130,973
CURRENT FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 2
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)..(2)
OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1

OTHER INFORMATION: Sequence
US-09-130-973-35

Query Match 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 4

US-09-477-902-35
Sequence 35, Application US/09477902
Patent No. 6194598
GENERAL INFORMATION:
APPLICANT: Cook, Phillip D
APPLICANT: Manoharan, Muthiah
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
FILE REFERENCE: ISIS2824
CURRENT APPLICATION NUMBER: US/09/477,902
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 09/016,520
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/037,143
PRIOR FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 2
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
NAME/KEY: misc-feature
LOCATION: (1)..(2)
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-477-902-35

Query Match 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 5

PCT-US95-05758-16/c
Sequence 16, Application PC/TUS9505758
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Cytochrome P450lpr Gene and Its
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P. O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Musca domestica
STRAIN: learn-pyr
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 1
PCT-US95-05758-16

Query Match 100.0%; Score 1; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 t 1
Db 2 T 2

RESULT 6
US-07-791-213D-46
Sequence 46, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 t 1
Db 1 T 1

RESULT 7
US-07-791-213D-62
Sequence 62, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 1 t 1

RESULT 8

US-08-268-679B-7/C
; Sequence 7, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD; MOLIA, V.
; APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; TITLE OF INVENTION: SYNTHESIS PICOINAVIRUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,679B
; FILING DATE: 30-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07\846,914
; FILING DATE: 06-MAR-1992
; CLASSIFICATION: 435
; APPLICATION NUMBER: 07719,761
; FILING DATE: 24-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MARIA C.H. LIN
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 0887-4095 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: OLIGONUCLEOTIDE
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE: N.A.
; POSITION IN GENOME: N.A.
; US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 t 1

RESULT 9
US-08-295-743-22

; Sequence 22, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,743
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Luccl
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: hexylamine modified uridine
; OTHER INFORMATION: moiety
; US-08-295-743-22

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 t 1

RESULT 10

US-08-602-036A-2
; Sequence 2, Application US/08602036A
; Patent No. 5789248
; GENERAL INFORMATION:
; APPLICANT: Oeystein, Fodstad
; APPLICANT: Hoyt, Eivind
; APPLICANT: Engebraten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street

```

: CITY: Boston
: STATE: MA
: COUNTRY: United States of America
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/602,036A
: FILING DATE: 16-FEB-1996
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Kerner, Ann-Louise
: REGISTRATION NUMBER: 33,523
: REFERENCE/DOCKET NUMBER: HY2-039CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 526-6000
: TELEFAX: (617) 526-5000
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: RNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
:
: US-08-602-036A-2
:
Query Match          100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
:
Db 2 U 2

RESULT 11
US-08-293-150A-46
: Sequence 46, Application US/08293150A
: Patent No. 5792629
: GENERAL INFORMATION:
: APPLICANT: MORISHITA, Hideaki
: APPLICANT: KANAMORI, Toshinori
: APPLICANT: NOBUHARA, Masahito
: TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
: TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
: TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
: TITLE OF INVENTION: TREATING USING THE SAME
: NUMBER OF SEQUENCES: 110
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/293,150A
: FILING DATE: 19-AUG-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/791,213
: FILING DATE: 13-NOV-1990
```

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 2-306745
: FILING DATE: 13-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Meuth, Donna M.
: REGISTRATION NUMBER: 36,607
: REFERENCE/DOCKET NUMBER: 029650-049
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 46:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
:
: US-08-293-150A-46
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Query Match          100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 t 1
:
Db 1 T 1
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```

RESULT 12
US-08-293-150A-62
: Sequence 62, Application US/08293150A
: Patent No. 5792629
: GENERAL INFORMATION:
: APPLICANT: MORISHITA, Hideaki
: APPLICANT: KANAMORI, Toshinori
: APPLICANT: NOBUHARA, Masahito
: TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
: TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
: TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
: TITLE OF INVENTION: TREATING USING THE SAME
: NUMBER OF SEQUENCES: 110
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/293,150A
: FILING DATE: 19-AUG-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/791,213
: FILING DATE: 13-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 2-306745
: FILING DATE: 13-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Meuth, Donna M.
: REGISTRATION NUMBER: 36,607
: REFERENCE/DOCKET NUMBER: 029650-049
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
```

LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-62

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;
Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 1 t 1

RESULT 13
US-08-502-374A-2
Sequence 2, Application US/08502374A
Patent No. 5872007
GENERAL INFORMATION:
APPLICANT: Fodstad, Oegystein
APPLICANT: Hovig, Eivind
APPLICANT: Engbraaten, Olav
APPLICANT: Maeldansmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502.374A
FILING DATE: 14-Jul-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-502-374A-2

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 3;
Pred. No. 0;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 u 2

RESULT 14
US-08-642-407A-2
Sequence 2, Application US/08642407A
Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oegystein, Fodstad
APPLICANT: Hovig, Eivind
APPLICANT: Engbraaten, Olav
APPLICANT: Maeldansmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642.407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-2

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 3;
Pred. No. 0;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
1
Db 2 u 2

RESULT 15
US-08-793-634B-12
Sequence 12, Application US/08793634B
Patent No. 6211431
GENERAL INFORMATION:
APPLICANT: Boevink, Petra C.
APPLICANT: Surin, Brian P.
APPLICANT: Keese, Paul K.
APPLICANT: Chu, Paul W.-G.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Khan, Rafiqul I.
APPLICANT: Larkin, Philip J.
APPLICANT: Taylor, William C.
APPLICANT: Marshall, Jerry S.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES

NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,634B
FILING DATE: June 9, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10530
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-793-634B-12

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 1 T 1

RESULT 16
US-08-793-634B-12/c
Sequence 12, Application US/08793634B
Patent No. 6211431
GENERAL INFORMATION:
APPLICANT: Boevink, Petra C.
APPLICANT: Surin, Brian P.
APPLICANT: Keese, Paul K.
APPLICANT: Chu, Paul W.G.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Khan, Rafiqul I.
APPLICANT: Larkin, Philip J.
APPLICANT: Taylor, William C.
APPLICANT: Marchall, Jerry S.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,634B
FILING DATE: June 9, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10530
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FILING DATE: June 9, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10530
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-793-634B-12

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 3 T 3

RESULT 17
US-08-793-634B-13
Sequence 13, Application US/08793634B
Patent No. 6211431
GENERAL INFORMATION:
APPLICANT: Boevink, Petra C.
APPLICANT: Surin, Brian P.
APPLICANT: Keese, Paul K.
APPLICANT: Chu, Paul W.G.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Khan, Rafiqul I.
APPLICANT: Larkin, Philip J.
APPLICANT: Taylor, William C.
APPLICANT: Marchall, Jerry S.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,634B
FILING DATE: June 9, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10530
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA
US-08-793-634B-13

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 1 T 1

RESULT 18
US-08-793-634B-13/C
Sequence 13, Application US/08793634B
Patent No. 6211431
GENERAL INFORMATION:
APPLICANT: Boevink, Petra C.
APPLICANT: Surlin, Brian P.
APPLICANT: Keese, Paul K.
APPLICANT: Chu, Paul W. G.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Khan, Rafiqul I.
APPLICANT: Larkin, Philip J.
APPLICANT: Taylor, William C.
APPLICANT: Matchall, Jerry S.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,634B
FILING DATE: June 9, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10530
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-793-634B-13

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 3 T 3

RESULT 19
US-08-973-568-55/C

Sequence 55, Application US/08973568B
Patent No. 6277634
GENERAL INFORMATION:
APPLICANT: McCall, Maxine J.
APPLICANT: Hendry, Philip
APPLICANT: Lockett, Trevor
TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF
FILE REFERENCE: 47203bpcplus
CURRENT APPLICATION NUMBER: US/08/973,568B
CURRENT FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 55
LENGTH: 3
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
FEATURE: Synthetic Ribozyme or portion thereof
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
US-08-973-568-55

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 3 T 3

RESULT 20
US-07-755-462-2
Sequence 2, Application US/07755462
Patent No. 5273881
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Zarlino, David A.
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,462
FILING DATE: 19910904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4255-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
|
Db 3 T 3

RESULT 21
US-07-755-462-2/C
Sequence 2, Application US/07755462
Patent No. 5273881
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calhoun, Cornelia J.
APPLICANT: Zarling, David A.
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
TITLE OF INVENTION: Formation
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,462
FILING DATE: 19910904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4255-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
|
Db 2 T 2

RESULT 22
US-07-630-288A-7/C
Sequence 7, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Giesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Giesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2430
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-7

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
|
Db 4 T 4

RESULT 23
US-07-630-288A-11
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glessner
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glessner, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 3 t 3

RESULT 24
US-07-630-288A-11/C
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glessner
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glessner, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 2 t 2

RESULT 25
US-07-630-288A-34
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glessner
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glessner, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 1 u 1

RESULT 26
US-07-630-288A-34/c
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
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INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 3 t 3

RESULT 27
US-08-188-943-1
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
Db 2 t 2

RESULT 28
US-08-188-943-1/c
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification